

NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH PLANTS

Field of the Invention

The present invention is in the field of plant genetics. More specifically the invention relates to nucleic acid molecules and nucleic acid molecules that contain markers, in particular, single nucleotide polymorphism (SNP) and repetitive element markers. In addition, the present invention provides nucleic acid molecules having regulatory elements or encoding proteins or fragments thereof and nucleic acid molecules present in non-coding regions.. The invention also relates to proteins and fragments of proteins so encoded and antibodies capable of binding the proteins. The invention also relates to methods of using the nucleic acid molecules, for example, for gene identification and analysis, markers, repetitive elements and fragments of repetitive elements, regulatory elements, proteins and fragments of proteins.

Background of the Invention

I. SEQUENCE TAGGED CONNECTOR NUCLEIC ACID MOLECULES AND THE BACTERIAL ARTIFICIAL CHROMOSOMES (BACS) CONTAINING THESE SEQUENCES.

Sequence tagged connectors, or STCs, are sequences of insert data generated from both ends (at the vector-insert point) of a BAC clone in a genomic library. These sequences, and BACs containing these STC sequences, can be used, for example, for marker development, genetic mapping or linkage analysis, marker assisted breeding, and physical genome mapping (Venter, *et al.*, *Nature*, 381:364-366 (1996), the entirety of which is herein incorporated by reference; Choi and Wing, <http://www.genome.clemson.edu/protocols2-nj.html> July, 1998). STCs can represent a copy of up to a full length of a mRNA transcript, a promoter element or

part of a promoter, can contain simple sequence repeats (also called microsatellites) repetitive elements or fragments of repetitive elements, other DNA markers, or any combination thereof.

Markers have been used in genetic mapping which can be a step in isolating a gene. Genetic mapping or linkage analysis is based on the level at which markers and genes are co-inherited (Rothwell, *Understanding Genetics*, 4th Ed., Oxford University Press, New York, p. 703 (1988). Statistical tests like chi-square analysis can be used to test the randomness of segregation or linkage (Kochert, *The Rockefeller Foundation International Program on Rice Biotechnology*, University of Georgia, Athens, GA, pp 1-14 (1989), the entirety of which is herein incorporated by reference. In linkage mapping, the proportion of recombinant individuals out of the total mapping population provides the information for determining the genetic distance between the loci (Young, *Encyclopedia of Agricultural Science*, Vol. 3, pp 275-282 (1994), the entirety of which is herein incorporated by reference).

Classical mapping studies utilize easily observable, visible traits instead of molecular markers. These visible traits are also known as naked eye polymorphisms. These traits can be morphological like plant height, fruit size, shape and color or physiological like disease response, photoperiod sensitivity or crop maturity. Visible traits are useful and are still in use because they represent actual phenotypes and are easy to score without any specialized lab equipment. By contrast, the other types of genetic markers are arbitrary loci for use in linkage mapping and often not associated to specific plant phenotypes (Young, *Encyclopedia of Agricultural Science*, Vol. 3, pp. 275-282 (1994). Many morphological markers cause such large effects on phenotype that they are undesirable in breeding programs. Many other visible traits have the disadvantage of being developmentally regulated (i.e., expressed only at certain stages; or in specific tissues and organs). Often times, visible traits mask the effects of linked minor genes making it nearly

impossible to identify desirable linkages for selection (Tanksey, *et al.*, *Biotech.* 7:257-264 (1989), the entirety of which is herein incorporated by reference).

Although a number of important agronomic characters are controlled by loci having major effects on phenotype, many economically important traits, such as yield and some forms of disease resistance, are quantitative in nature. This type of phenotypic variation in a trait is characterized by continuous, normal distribution of phenotypic values in a particular population (Beckmann and Soller, *Oxford Surveys of Plant Molecular Biology*, Miffen. (ed.), Vol. 3, Oxford University Press, UK., pp. 196-250 (1986), the entirety of which is herein incorporated by reference). Such traits are governed by a large number of loci, Quantitative Trait Loci (QTL), each of which can make a small positive or negative effect to the final phenotype value of the trait (Beckmann and Soller, *Oxford Surveys of Plant Molecular Biology*, Miffen. (ed.), Vol. 3, Oxford University Press, U.K., pp. 196-250 (1986). Loci contributing to such genetic variation are often termed minor genes as opposed to major genes with large effects that follow a Mendelian pattern of inheritance. Polygenic traits are also predicted to follow a Mendelian type of inheritance, however the contribution of each locus is expressed as an increase or decrease in the final trait value.

Markers have been used in physical mapping studies with BAC libraries made from plant genomes. Such mapping studies have been carried out in rice (Kim *et al.*, *Genomics* 34:213-218 (1996), herein incorporated by reference; Hang, *Plant Mol. Biol.* 35:129-133 (1997), herein incorporated by reference; Zhang and Wing, *Plant Mol. Bio.* 35:115-127 (1997) herein incorporated by reference; Chen *et al.*, *Proc. Acad. Sci. (U.S.A.)* 94:3431-3435 (1997) herein incorporated by reference; Wang *et al.*, *Plant J.* 7:525-533 (1995) herein incorporated by reference) sorghum (Zwick *et al.*, *Genetics* 148:1983-1992 (1998) herein incorporated by

reference; Zhang, *et al.*, *Molecular Breeding* 2:11-24 (1996) the entirety of which is herein incorporated by reference) maize, (Chen, *et al.*, *Proc. Acad. Sci. (U.S.A.)* 94:3431-3435 (1997), and *Arabidopsis* (Kim, *et al.*, *Genomics* 34:213-218 (1996) the entirety of which is herein incorporated by reference).

Repetitive elements have been used in physical mapping in cereals (Ananiev, *et al.*, *Proc. Acad. Sci. (U.S.A.)* 95:13073-8 (1998), the entirety of which is herein incorporated by reference; McLean *et al.*, *Mol Gen Genet* 253:687-694 (1997), the entirety of which is herein incorporated by reference).

II. SEQUENCE COMPARISONS

STCs and sequenced BACs can be compared, for example, to sequences that encode promoters or proteins. These homologies can be determined by similarity searches (Adams, *et al.*, *Science* 252:1651-1656 (1991), herein incorporated by reference).

A characteristic feature of a DNA sequence is that it can be compared with other DNA sequences. Sequence comparisons can be undertaken by determining the similarity of the test or query sequence with sequences in publicly available or propriety databases ("similarity analysis") or by searching for certain motifs ("intrinsic sequence analysis")(e.g., *cis* elements)(Coulson, *Trends in Biotechnology*, 12:76-80 (1994), the entirety of which is herein incorporated by reference; Birren, *et al.*, *Genome Analysis*, 1:543-559 (1997), the entirety of which is herein incorporated by reference).

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ)(<http://www.ddbj.nig.ac.jp/>); Genebank (<http://www.ncbi.nlm.nih.gov/web/Genbank/Index.html>); and the European Molecular Biology

Laboratory Nucleic Acid Sequence Database (EMBL)

(http://www.ebi.ac.uk/ebi_docs/embl_db.html). A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology*, 12:76-80 (1994); Birren, *et al.*, *Genome Analysis*, 1:543-559 (1997)).

BLASTN takes a nucleotide sequence (the query sequence) and its reverse complement and searches them against a nucleotide sequence database. BLASTN was designed for speed, not maximum sensitivity, and may not find distantly related coding sequences. BLASTX takes a nucleotide sequence, translates it in three forward reading frames and three reverse complement reading frames, and then compares the six translations against a protein sequence database. BLASTX is useful for sensitive analysis of preliminary (single-pass) sequence data and is tolerant of sequencing errors (Gish and States, *Nature Genetics*, 3:266-272 (1993), the entirety of which is herein incorporated by reference). BLASTN and BLASTX may be used in concert for analyzing STC data (Coulson, *Trends in Biotechnology*, 12:76-80 (1994); Birren, *et al.*, *Genome Analysis*, 1:543-559 (1997)).

Given a coding nucleotide sequence and the protein it encodes, it is often preferable to use the protein as the query sequence to search a database because of the greatly increased sensitivity to detect more subtle relationships. This is due to the larger alphabet of proteins (20 amino acids) compared with the alphabet of nucleic acid sequences (4 bases), where it is far easier to obtain a match by chance. In addition, with nucleotide alignments, only a match (positive score) or a mismatch (negative score) is obtained, but with proteins, the presence of

conservative amino acid substitutions can be taken into account. Here, a mismatch may yield a positive score if the non-identical residue has physical/chemical properties similar to the one it replaced. Various scoring matrices are used to supply the substitution scores of all possible amino acid pairs. A general purpose scoring system is the BLOSUM62 matrix (Henikoff and Henikoff, *Proteins*, 17:49-61 (1993), the entirety of which is herein incorporated by reference), which is currently the default choice for BLAST programs. BLOSUM62 is tailored for alignments of moderately diverged sequences and thus may not yield the best results under all conditions. Altschul, *J. Mol. Biol.* 36:290-300 (1993), the entirety of which is herein incorporated by reference, uses a combination of three matrices to cover all contingencies. This may improve sensitivity, but at the expense of slower searches. In practice, a single BLOSUM62 matrix is often used but others (PAM40 and PAM250) may be attempted when additional analysis is necessary. Low PAM matrices are directed at detecting very strong but localized sequence similarities, whereas high PAM matrices are directed at detecting long but weak alignments between very distantly related sequences.

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package available that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol.* 25:351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance between each pair is calculated; from this distance matrix, a guide tree is calculated, and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied to encourage the insertion of gaps in probable loop regions instead of in the

middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both the pairwise alignments and the multiple alignments. CLUSTAL W for UNIX and VMS systems is available at: [ftp.ebi.ac.uk](ftp://ftp.ebi.ac.uk). Another program is MACAW (Schuler *et al.*, *Proteins, Struct. Func. Genet.*, 9:180-190 (1991), the entirety of which is herein incorporated by reference, for which both Macintosh and Microsoft Windows versions are available. MACAW uses a graphical interface, provides a choice of several alignment algorithms, and is available by anonymous ftp at: [ncbi.nlm.nih.gov](ftp://ncbi.nlm.nih.gov) (directory/pub/macaw).

Sequence motifs are derived from multiple alignments and can be used to examine individual sequences or an entire database for subtle patterns. With motifs, it is sometimes possible to detect distant relationships that may not be demonstrable based on comparisons of primary sequences alone. Currently, the largest collection of sequence motifs in the world is PROSITE (Bairoch and Bucher, *Nucleic Acid Research*, 22:3583-3589 (1994), the entirety of which is herein incorporated by reference). PROSITE may be accessed via either the ExPASy server on the World Wide Web or anonymous ftp site. Many commercial sequence analysis packages also provide search programs that use PROSITE data.

A resource for searching protein motifs is the BLOCKS E-mail server developed by S. Henikoff, *Trends Biochem Sci.*, 18:267-268 (1993), the entirety of which is herein incorporated by reference; Henikoff and Henikoff, *Nucleic Acid Research*, 19:6565-6572 (1991), the entirety of which is herein incorporated by reference; Henikoff and Henikoff, *Proteins*, 17:49-61 (1993). BLOCKS searches a protein or nucleotide sequence against a database of protein motifs or "blocks." Blocks are defined as short, ungapped multiple alignments that represent highly conserved protein patterns. The blocks themselves are derived from entries in PROSITE as well

as other sources. Either a protein or nucleotide query can be submitted to the BLOCKS server; if a nucleotide sequence is submitted, the sequence is translated in all six reading frames and motifs are sought in these conceptual translations. Once the search is completed, the server will return a ranked list of significant matches, along with an alignment of the query sequence to the matched BLOCKS entries.

Conserved protein domains can be represented by two-dimensional matrices, which measure either the frequency or probability of the occurrences of each amino acid residue and deletions or insertions in each position of the domain. This type of model, when used to search against protein databases, is sensitive and usually yields more accurate results than simple motif searches. Two popular implementations of this approach are profile searches (such as GCG program ProfileSearch) and Hidden Markov Models (HMMs) (Krough, *et al.*, *J. Mol. Biol.* 235:1501-1531 (1994); Eddy, *Current Opinion in Structural Biology* 6:361-365 (1996), both of which are herein incorporated by reference in their entirety). In both cases, a large number of common protein domains have been converted into profiles, as present in the PROSITE library, or HMM models, as in the Pfam protein domain library (Sonnhammer, *et al.*, *Proteins* 28:405-420 (1997), the entirety of which is herein incorporated by reference). Pfam contains more than 500 HMM models for enzymes, transcription factors, signal transduction molecules, and structural proteins. Protein databases can be queried with these profiles or HMM models, which will identify proteins containing the domain of interest. For example, HMMSW or HMMFS, two programs in a public domain package called HMMER (Sonnhammer, *et al.*, *Proteins* 28:405-420 (1997)) can be used.

PROSITE and BLOCKS represent collected families of protein motifs. Thus, searching these databases entails submitting a single sequence to determine whether or not that sequence is

similar to the members of an established family. Programs working in the opposite direction compare a collection of sequences with individual entries in the protein databases. An example of such a program is the Motif Search Tool, or MoST (Tatusov, *et al.*, *Proc. Natl. Acad. Sci.* 91:12091-12095 (1994), the entirety of which is herein incorporated by reference). On the basis of an aligned set of input sequences, a weight matrix is calculated by using one of four methods (selected by the user); a weight matrix is simply a representation, position by position in an alignment, of how likely a particular amino acid will appear. The calculated weight matrix is then used to search the databases. To increase sensitivity, newly found sequences are added to the original data set, the weight matrix is recalculated, and the search is performed again. This procedure continues until no new sequences are found.

Summary of the Invention

The present invention provides a substantially purified nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof.

The present invention also provides a substantially purified nucleic acid molecule, the nucleic acid molecule capable of specifically hybridizing to a second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof.

The present invention also provides a substantially purified nucleic acid molecule encoding a protein or fragment thereof, wherein the protein or fragment thereof is selected from the group consisting a *Glycine max* protein or fragment thereof from Table 1.

The present invention also provides a substantially purified nucleic acid molecule encoding a *Glycine max* protein or fragment thereof, wherein the *Glycine max* protein or

fragment thereof is encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof or fragments of either.

The present invention also provides a substantially purified protein or fragment thereof encoded by a nucleic acid sequence selected from the group that encodes a *Glycine max* protein or fragment thereof from Table 1.

The present invention also provides a substantially purified protein or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule selected from the group that encodes a *Glycine max* protein or fragments thereof from Table 1.

The present invention also provides a substantially purified protein or fragment thereof encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof or fragments of either.

The present invention also provides a transformed cell having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in the cell to cause the production of a mRNA molecule; which is linked to (B) a structural nucleic acid molecule, wherein the structural nucleic acid molecule encodes a protein or fragment thereof selected from the group consisting of a *Glycine max* protein or fragment thereof in Table 1; which is linked to (C) a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a plant cell, a mammalian cell, a bacterial cell, an insect cell and a fungal cell transformed with a nucleic acid molecule of the present invention.

The present invention also provides a computer readable medium having recorded thereon one or more of the nucleotide sequences depicted in SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof.

The present invention also provides a computer readable medium having recorded thereon one or more of the nucleotide sequences encoding a protein or fragment thereof, wherein the protein or fragment thereof is selected from the group consisting of a *Glycine max* protein or fragment thereof in Table 1.

The present invention provides a computer readable medium having recorded thereon one or more of the nucleotide sequences depicted in SEQ ID NO:1 through SEQ ID NO: 20082.

The present invention provides a method of introgressing a trait into a plant comprising using a nucleic acid marker for marker assisted selection of the plant, the nucleic acid marker complementary to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof, and introgressing the trait into a plant.

The present invention provides a method for screening for a trait comprising interrogating genomic DNA for the presence or absence of a marker molecule that is genetically linked to a nucleic acid sequence complementary to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof; and detecting the presence or absence of the marker.

The present invention provides a method for determining the likelihood of the level, presence or absence of a trait in a plant comprising the steps of: (A) obtaining genomic DNA from the plant; (B) detecting a marker nucleic acid molecule; the marker nucleic acid molecule wherein the marker nucleic acid molecule specifically hybridizes with a nucleic acid sequence that is genetically linked to a nucleic acid sequence complementary to a nucleic acid sequence

selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof; (C) and determining the level, presence or absence of the marker nucleic acid molecule, wherein the level, presence or absence of the marker nucleic acid molecule is indicative of the likely presence in the plant of the trait.

The present invention provides a method for determining a genomic polymorphism in a plant that is predictive of a trait comprising the steps: (A) incubating a marker nucleic acid molecule, under conditions permitting nucleic acid hybridization, and a complementary nucleic acid molecule obtained from the plant, the marker nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant; and (C) detecting the presence of the polymorphism.

The present invention provides a method of determining an association between a polymorphism and a plant trait comprising: (A) hybridizing a nucleic acid molecule specific for the polymorphism to genetic material of a plant, wherein the nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof; and (B) calculating the degree of association between the polymorphism and the plant trait.

Detailed Description of the Invention

Agents of the invention:

(a) Nucleic Acid Molecules

Agents of the present invention include nucleic acid molecules and more specifically BACs and STC nucleic acid molecules or nucleic acid fragment molecules thereof.

A subset of the nucleic acid molecules of the present invention includes nucleic acid molecules that are marker molecules. Another subset of the nucleic molecules of the present invention include nucleic acid molecules that are promoters and/or regulatory elements. Another subset of the nucleic acid molecules of the present invention include nucleic acid molecules that encode proteins or fragments of proteins. In a preferred embodiment the nucleic acid molecules of the present invention are derived from *Glycine max* (soybean) and more preferably *Glycine max*, genotype A3244 (Asgrow, Des Moines, Iowa).

Fragment STC nucleic acid molecules and fragments of BACs may encode significant portion(s) of, or indeed most of, the STC or BAC nucleic acid molecule. In addition, a fragment nucleic acid molecule can encode a *Glycine max* protein or fragment thereof. Alternatively, the fragments may comprise smaller oligonucleotides (having from about 15 to about 250 nucleotide residues, and more preferably, about 15 to about 30 nucleotide residues).

The term "substantially purified", as used herein, refers to a molecule separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of

solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state.

The agents of the present invention will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic, and thus involve the capacity of the agent to mediate a chemical reaction or response.

The agents of the present invention may also be recombinant. As used herein, the term recombinant means any agent (e.g., DNA, peptide etc.), that is, or results, however indirect, from human manipulation of a nucleic acid molecule.

It is understood that the agents of the present invention may be labeled with reagents that facilitate detection of the agent (e.g., fluorescent labels (Prober, *et al.*, *Science* 238:336-340 (1987); Albarella *et al.*, EP 144914, chemical labels (Sheldon *et al.*, U.S. Patent 4,582,789; Albarella *et al.*, U.S. Patent 4,563,417, modified bases (Miyoshi *et al.*, EP 119448, all of which are hereby incorporated by reference in their entirety).

It is further understood, that the present invention provides bacterial, viral, microbial, insect, fungal and plant cells comprising the agents of the present invention.

The genetic variability resulting from transposable elements ranges from changes in the size and arrangement of whole genomes to changes in single nucleotides. They may produce major effects on phenotypic traits or small silent changes detectable only at the DNA sequence level. Transposable elements may also produce variation when they excise, leaving small footprints of their previous presence (Kidwell and Lisch, *Proc. Natl. Acad. Sci. (U.S.A.)* 94:7704-7711 (1997)).

In addition, other markers such as AFLP markers, RFLP markers, RAPD markers, phenotypic markers or isozyme markers can be utilized (Walton, Seed World 22-29 (July, 1993), the entirety of which is herein incorporated by reference; Burow and Blake, *Molecular Dissection of Complex Traits*, 13-29, Eds. Paterson, CRC Press, New York (1988), the entirety of which is herein incorporated by reference). DNA markers can be developed from nucleic acid molecules using restriction endonucleases, the PCR and/or DNA sequence information. RFLP markers result from single base changes or insertions/deletions. These codominant markers are highly abundant in plant genomes, have a medium level of polymorphism and are developed by a combination of restriction endonuclease digestion and Southern blotting hybridization. CAPS are similarly developed from restriction nuclease digestion but only of specific PCR products. These markers are also codominant, have a medium level of polymorphism and are highly abundant in the genome. The CAPS result from single base changes and insertions/deletions. Another marker type, RAPDs, are developed from DNA amplification with random primers and result from single base changes and insertions/deletions in plant genomes. They are dominant markers with a medium level of polymorphisms and are highly abundant. AFLP markers require using the PCR on a subset of restriction fragments from extended adapter primers. These markers are both dominant and codominant, are highly abundant in genomes and exhibit a medium level of polymorphism. SSRs require DNA sequence information. These codominant markers result from repeat length changes, are highly polymorphic, and do not exhibit as high a degree of abundance in the genome as CAPS, AFLPs and RAPDs. SNPs also require DNA sequence information. These codominant markers result from single base substitutions. They are highly abundant and exhibit a medium of polymorphism (Rafalski, *et al.*, In: *Nonmammalian Genomic Analysis*, ed. Birren and Lai, Academic Press, San Diego, CA, pp. 75-134 (1996), the

entirety of which is herein incorporated by reference). Methods to isolate such markers are known in the art.

Long Terminal repeat retrotransposons and *MITEs* have been found to be associated with the genes of many plants where some of the transposable elements contribute regulatory sequences. *MITEs* such as the *Tourist* element in maize and the *Stowaway* element in Sorghum are found frequently in the 5' and 3' noncoding regions of genes and are frequently associated with the regulatory regions of genes of diverse flowering plants (Kidwell and Lisch, *Proc. Natl. Acad. Sci. (U.S.A.)* 94:7704-7711 (1997)). It is understood that one or more of the Long Terminal repeat retrotransposons and/or *MITEs* may be a marker, and even more preferably a marker for a gene.

(ii) **Nucleic Acid Molecules Comprising Regulatory Elements**

Another class of agents of the present invention are nucleic acid molecules having promoter regions or partial promoter regions, including those located within SEQ ID NO: 1 through SEQ ID NO:20082. Such promoter regions are typically found upstream of the trinucleotide ATG sequence at the start site of a protein coding region.

As used herein, a promoter region is a region of a nucleic acid molecule that is capable, when located in *cis* to a nucleic acid sequence that encodes for a protein or fragment thereof to function in a way that directs expression of one or more mRNA molecules that encodes for the protein or fragment thereof.

Promoters of the present invention can include between about 300bp upstream and about 10kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region. Promoters of the present invention can preferably include between about 300bp upstream and about 5kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region.

Promoters of the present invention can more preferably include between about 300bp upstream and about 2kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region. Promoters of the present invention can include between about 300bp upstream and about 1kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region. While in many circumstances a 300bp promoter may be sufficient for expression, additional sequences may act to further regulate expression, for example, in response to biochemical, developmental or environmental signals.

It is also preferred that the promoters of the present invention contain a CAAT and a TATA *cis* element. Moreover, the promoters of the present invention can contain one or more *cis* elements in addition to a CAAT and a TATA box.

By "regulatory element" it is intended a series of nucleotides that determines if, when, and at what level a particular gene is expressed. The regulatory DNA sequences specifically interact with regulatory or other proteins. Many regulatory elements act in *cis* ("*cis* elements") and are believed to affect DNA topology, producing local conformations that selectively allow or restrict access of RNA polymerase to the DNA template or that facilitate selective opening of the double helix at the site of transcriptional initiation. *Cis* elements occur within, but are not limited to promoters, and promoter modulating sequences (inducible elements). *Cis* elements can be identified using known *cis* elements as a target sequence or target motif in the BLAST programs of the present invention.

Promoters of the present invention include homologues of *cis* elements known to effect gene regulation that show homology with the nucleic acid molecules of the present invention. These *cis* elements include, but are not limited to, oxygen responsive *cis* elements (Cowen, *et al.*, *J Biol. Chem.* 268(36):26904-26910 (1993) the entirety of which is herein incorporated by

reference), light regulatory elements (Bruce and Quail, *Plant Cell* 2 (11):1081-1089 (1990) the entirety of which is herein incorporated by reference; Bruce, *et al.*, *EMBO J.* 10:3015-3024 (1991), the entirety of which is herein incorporated by reference; Rocholl, *et al.*, *Plant Sci.* 97:189-198 (1994), the entirety of which is herein incorporated by reference; Block, *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 87:5387-5391 (1990), the entirety of which is herein incorporated by reference; Giuliano, *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 85:7089-7093 (1988), the entirety of which is herein incorporated by reference; Staiger, *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 86:6930-6934 (1989), the entirety of which is herein incorporated by reference; Izawa, *et al.*, *Plant Cell* 6:1277-1287 (1994), the entirety of which is herein incorporated by reference; Menkens, *et al.*, *Trends in Biochemistry* 20:506-510 (1995), the entirety of which is herein incorporated by reference; Foster, *et al.*, *FASEB J.* 8:192-200 (1994), the entirety of which is herein incorporated by reference; Plesse, *et al.*, *Mol Gen Gene* 254:258-266 (1997), the entirety of which is herein incorporated by reference; Green, *et al.*, *EMBO J.* 6:2543-2549 (1987), the entirety of which is herein incorporated by reference; Kuhlemeier *et al.*, *Ann. Rev Plant Physiol.* 38:221-257 (1987), the entirety of which is herein incorporated by reference; Villain *et al.*, *J. Biol. Chem.* 271:32593-32598 (1996), the entirety of which is herein incorporated by reference; Lam *et al.*, *Plant Cell* 2:857-866 (1990), the entirety of which is herein incorporated by reference; Gilmartin, *et al.*, *Plant Cell* 2:369-378 (1990), the entirety of which is herein incorporated by reference; Datta, *et al.*, *Plant Cell* 1:1069-1077 (1989) the entirety of which is herein incorporated by reference; Gilmartin, *et al.*, *Plant Cell* 2:369-378 (1990), the entirety of which is herein incorporated by reference; Castresana, *et al.*, *EMBO J.* 7:1929-1936 (1988), the entirety of which is herein incorporated by reference; Ueda, *et al.*, *Plant Cell* 1:217-227 (1989), the entirety of which is herein incorporated by reference; Terzaghi, *et al.*, *Annu. Rev. Plant Physiol. Plant Mol.*

Biol. 46:445-474 (1995), the entirety of which is herein incorporated by reference; Green *et al.*, *EMBO J.* 6:2543-2549 (1987), the entirety of which is herein incorporated by reference; Villain, *et al.*, *J. Biol. Chem.* 271:32593-32598 (1996), the entirety of which is herein incorporated by reference; Tjaden, *et al.*, *Plant Cell* 6:107-118 (1994), the entirety of which is herein incorporated by reference; Tjaden, *et al.*, *Plant Physiol.* 108:1109-1117 (1995), the entirety of which is herein incorporated by reference; Ngai, *et al.*, *Plant J.* 12:1021-1234 (1997), the entirety of which is herein incorporated by reference; Bruce, *et al.*, *EMBO J.* 10:3015-3024 (1991), the entirety of which is herein incorporated by reference; Ngai, *et al.*, *Plant J.* 12:1021-1034 (1997), the entirety of which is herein incorporated by reference), elements responsive to gibberellin, (Muller, *et al.*, *J. Plant Physiol.* 145:606-613 (1995), the entirety of which is herein incorporated by reference; Croissant, *et al.*, *Plant Science* 116:27-35 (1996), the entirety of which is herein incorporated by reference; Lohmer, *et al.*, *EMBO J.* 10:617-624 (1991), the entirety of which is herein incorporated by reference; Rogers, *et al.*, *Plant Cell* 4:1443-1451 (1992), the entirety of which is herein incorporated by reference; Lanahan *et al.*, *Plant Cell* 4:203-211 (1992) the entirety of which is herein incorporated by reference; Skriver *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 88:7266-7270 (1991) the entirety of which is herein incorporated by reference; Gilmartin, *et al.*, *Plant Cell* 2:369-378 (1990), the entirety of which is herein incorporated by reference; Huang, *et al.*, *Plant Mol. Biol.* 14:655-668 (1990), the entirety of which is herein incorporated by reference, Gubler, *et al.*, *Plant Cell* 7:1879-1891 (1995), the entirety of which is herein incorporated by reference), elements responsive to abscisic acid, (Busk, *et al.*, *Plant Cell* 9:2261-2270 (1997), the entirety of which is herein incorporated by reference; Gultinan, *et al.*, *Science* 250:267-270 (1990), the entirety of which is herein incorporated by reference; Shen, *et al.*, *Plant Cell* 7:295-307 (1995) the entirety of which is herein incorporated by reference; Shen

et al., *Plant Cell* 8:1107-1119 (1996), the entirety of which is herein incorporated by reference; Seo *et al.*, *Plant Mol. Biol.* 27:1119-1131 (1995), the entirety of which is herein incorporated by reference; Marcotte *et al.*, *Plant Cell* 1:969-976 (1989) the entirety of which is herein incorporated by reference; Shen *et al.*, *Plant Cell* 7:295-307 (1995), the entirety of which is herein incorporated by reference; Iwasaki *et al.*, *Mol Gen Genet* 247:391-398 (1995), the entirety of which is herein incorporated by reference; Hattori *et al.*, *Genes Dev.* 6:609-618 (1992), the entirety of which is herein incorporated by reference; Thomas *et al.*, *Plant Cell* 5:1401-1410 (1993), the entirety of which is herein incorporated by reference), elements similar to abscisic acid responsive elements, (Ellerstrom *et al.*, *Plant Mol. Biol.* 32:1019-1027 (1996), the entirety of which is herein incorporated by reference), auxin responsive elements (Liu *et al.*, *Plant Cell* 6:645-657 (1994) the entirety of which is herein incorporated by reference; Liu *et al.*, *Plant Physiol.* 115:397-407 (1997), the entirety of which is herein incorporated by reference; Kosugi *et al.*, *Plant J.* 7:877-886 (1995), the entirety of which is herein incorporated by reference; Kosugi *et al.*, *Plant Cell* 9:1607-1619 (1997), the entirety of which is herein incorporated by reference; Ballas *et al.*, *J. Mol. Biol.* 233:580-596 (1993), the entirety of which is herein incorporated by reference), a *cis* element responsive to methyl jasmonate treatment (Beaudoin and Rothstein, *Plant Mol. Biol.* 33:835-846 (1997), the entirety of which is herein incorporated by reference), a *cis* element responsive to abscisic acid and stress response (Straub *et al.*, *Plant Mol. Biol.* 26:617-630 (1994), the entirety of which is herein incorporated by reference), ethylene responsive *cis* elements (Itzhaki *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 91:8925-8929 (1994), the entirety of which is herein incorporated by reference; Montgomery *et al.*, *Proc. Acad. Sci. (U.S.A.)* 90:5939-5943 (1993), the entirety of which is herein incorporated by reference; Sessa *et al.*, *Plant Mol. Biol.* 28:145-153 (1995), the entirety of which is herein

incorporated by reference; Shinshi *et al.*, *Plant Mol. Biol.* 27:923-932 (1995), the entirety of which is herein incorporated by reference), salicylic acid *cis* responsive elements, (Strange *et al.*, *Plant J.* 11:1315-1324 (1997), the entirety of which is herein incorporated by reference; Qin *et al.*, *Plant Cell* 6:863-874 (1994), the entirety of which is herein incorporated by reference), a *cis* element that responds to water stress and abscisic acid (Lam *et al.*, *J. Biol. Chem.* 266:17131-17135 (1991), the entirety of which is herein incorporated by reference; Thomas *et al.*, *Plant Cell* 5:1401-1410 (1993), the entirety of which is herein incorporated by reference; Pla *et al.*, *Plant Mol Biol* 21:259-266 (1993), the entirety of which is herein incorporated by reference), a *cis* element essential for M phase-specific expression (Ito *et al.*, *Plant Cell* 10:331-341 (1998), the entirety of which is herein incorporated by reference), sucrose responsive elements (Huang *et al.*, *Plant Mol. Biol.* 14:655-668 (1990), the entirety of which is herein incorporated by reference; Hwang *et al.*, *Plant Mol Biol* 36:331-341 (1998), the entirety of which is herein incorporated by reference; Grierson *et al.*, *Plant J.* 5:815-826 (1994), the entirety of which is herein incorporated by reference), heat shock response elements (Pelham *et al.*, *Trends Genet.* 1:31-35 (1985), the entirety of which is herein incorporated by reference), elements responsive to auxin and/or salicylic acid and also reported for light regulation (Lam *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 86:7890-7897 (1989), the entirety of which is herein incorporated by reference; Benfey *et al.*, *Science* 250:959-966 (1990), the entirety of which is herein incorporated by reference), elements responsive to ethylene and salicylic acid (Ohme-Takagi *et al.*, *Plant Mol. Biol.* 15:941-946 (1990), the entirety of which is herein incorporated by reference), elements responsive to wounding and abiotic stress (Loake *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 89:9230-9234 (1992), the entirety of which is herein incorporated by reference; Mhiri *et al.*, *Plant Mol. Biol.* 33:257-266 (1997), the entirety of which is herein incorporated by reference), antioxidant response

elements (Rushmore *et al.*, *J. Biol. Chem.* 266:11632-11639, the entirety of which is herein incorporated by reference; Dalton *et al.*, *Nucleic Acids Res.* 22:5016-5023 (1994), the entirety of which is herein incorporated by reference), Sph elements (Suzuki *et al.*, *Plant Cell* 9:799-807 (1997), the entirety of which is herein incorporated reference), Elicitor responsive elements, (Fukuda *et al.*, *Plant Mol. Biol.* 34:81-87 (1997), the entirety of which is herein incorporated by reference; Rushton *et al.*, *EMBO J.* 15:5690-5700 (1996), the entirety of which is herein incorporated by reference), metal responsive elements (Stuart *et al.*, *Nature* 317:828-831 (1985), the entirety of which is herein incorporated by reference; Westin *et al.*, *EMBO J.* 7:3763-3770 (1988), the entirety of which is herein incorporated by reference; Thiele *et al.*, *Nucleic Acids Res.* 20:1183-1191 (1992), the entirety of which is herein incorporated by reference; Faisst *et al.*, *Nucleic Acids Res.* 20:3-26 (1992), the entirety of which is herein incorporated by reference), low temperature responsive elements, (Baker *et al.*, *Plant Mol. Biol.* 24:701-713 (1994), the entirety of which is herein incorporated by reference; Jiang *et al.*, *Plant Mol. Biol.* 30:679-684 (1996), the entirety of which is herein incorporated by reference; Nordin *et al.*, *Plant Mol. Biol.* 21:641-653 (1993), the entirety of which is herein incorporated by reference; Zhou *et al.*, *J. Biol. Chem.* 267:23515-23519 (1992), the entirety of which is herein incorporated by reference), drought responsive elements, (Yamaguchi *et al.*, *Plant Cell* 6:251-264 (1994), the entirety of which is herein incorporated by reference; Wang *et al.*, *Plant Mol. Biol.* 28:605-617 (1995), the entirety of which is herein incorporated by reference; Bray EA, *Trends in Plant Science* 2:48-54 (1997), the entirety of which is herein incorporated by reference) enhancer elements for glutenin, (Colot *et al.*, *EMBO J.* 6:3559-3564 (1987), the entirety of which is herein incorporated by reference; Thomas *et al.*, *Plant Cell* 2:1171-1180 (1990), the entirety of which is incorporated by reference; Kreis *et al.*, *Philos. Trans. R. Soc. Lond.*, B314:355-365 (1986), the entirety of which is herein

incorporated by reference), light-independent regulatory elements, (Lagrange *et al.*, *Plant Cell* 9:1469-1479 (1997), the entirety of which is herein incorporated by reference; Villain *et al.*, *J. Biol. Chem.* 271:32593-32598 (1996), the entirety of which is herein incorporated by reference), OCS enhancer elements, (Bouchez *et al.*, *EMBO J.* 8:4197-4204 (1989), the entirety of which is herein incorporated by reference; Foley *et al.*, *Plant J.* 3:669-679 (1993), the entirety of which is herein incorporated by reference), ACGT elements, (Foster *et al.*, *FASEB J.* 8:192-200 (1994), the entirety of which is herein incorporated by reference; Izawa *et al.*, *Plant Cell* 6:1277-1287 (1994), the entirety of which is herein incorporated by reference; Izawa *et al.*, *J. Mol. Biol.* 230:1131-1144 (1993) the entirety of which is herein incorporated by reference), negative *cis* elements in plastid related genes, (Zhou *et al.*, *J. Biol. Chem.* 267:23515-23519 (1992), the entirety of which is herein incorporated by reference; Lagrange *et al.*, *Mol. Cell Biol.* 13:2614-2622 (1993), the entirety of which is herein incorporated by reference; Lagrange *et al.*, *Plant Cell* 9:1469-1479 (1997), the entirety of which is herein incorporated by reference; Zhou *et al.*, *J. Biol. Chem.* 267:23515-23519 (1992), the entirety of which is herein incorporated by reference), prolamins box elements, (Forde *et al.*, *Nucleic Acids Res.* 13:7327-7339 (1985), the entirety of which is herein incorporated by reference; Colot *et al.*, *EMBO J.* 6:3559-3564 (1987), the entirety of which is herein incorporated by reference; Thomas *et al.*, *Plant Cell* 2:1171-1180 (1990), the entirety of which is herein incorporated by reference; Thompson *et al.*, *Plant Mol. Biol.* 15:755-764 (1990), the entirety of which is herein incorporated by reference; Vicente *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 94:7685-7690 (1997), the entirety of which is herein incorporated by reference), elements in enhancers from the IgM heavy chain gene (Gillies *et al.*, *Cell* 33:717-728 (1983), the entirety of which is herein incorporated by reference; Whittier *et al.*, *Nucleic Acids Res.* 15:2515-2535 (1987), the entirety of which is herein incorporated by reference).

(iii) Nucleic Acid Molecules Comprising Genes or Fragments Thereof

Nucleic acid molecules of the present invention can comprise one or more genes or fragments thereof. Such genes or fragments thereof include homologues of known genes or protein coding regions in other organisms or genes or fragments thereof that elicit only limited or no matches with known genes or protein coding regions. Table 1 sets forth a list of nucleic acid molecules that encode *Glycine max* proteins or fragments thereof which are homologues of known proteins.

Genomic sequences can be screened for the presence of proteins or genes utilizing one or a number of different search algorithms have that been developed, one example of which are the suite of programs referred to as BLAST programs. Other examples of suitable programs that can be utilized are known in the art, several of which are described above in the Background and under the section titled "Uses of the Agents of the Invention." In addition, unidentified reading frames may be screened for protein coding regions by prediction software such as GenScan, which is located at <http://gnomic.stanford.edu/GENSCANW.html>.

In a preferred embodiment of the present invention, the *Glycine max* protein or fragment thereof of the present invention is a homologue of another plant protein. In another preferred embodiment of the present invention, the *Glycine max* protein or fragment thereof of the present invention is a homologue of a fungal protein. In another preferred embodiment of the present invention, the *Glycine max* protein or fragment thereof of the present invention is a homologue of a mammalian protein. In another preferred embodiment of the present invention, the *Glycine max* protein or fragment thereof of the present invention is a homologue of a bacterial protein.

In a preferred embodiment of the present invention, the *Glycine max* protein or fragments thereof or nucleic acid molecule or fragment thereof has a BLAST score of more than 200,

preferably a BLAST score of more than 300, even more preferably a BLAST score of more than 400.

In another preferred embodiment of the present invention, the nucleic acid molecule encoding the *Glycine max* protein or fragment thereof and/or nucleic acid molecule or fragment thereof exhibits a % identity with its homologue of between about 25% and about 40%, more preferably of between about 40 and about 70%, even more preferably of between about 70% and about 90%, and even more preferably between about 90% and 99%. In another preferred embodiment, of the present invention, the *Glycine max* the nucleic acid molecule encoding the *Glycine max* protein or fragment thereof exhibits a % identity with its homologue of 100%.

In a preferred embodiment of the present invention, the *Glycine max* protein or fragment thereof or nucleic acid molecule or fragment thereof exhibits a % coverage of between about 0 % and about 33%, more preferably of between about 34% and about 66%, and even more preferably of between about 67% and about 100%.

Genomic sequences can be screened for the presence of proteins utilizing one or a number of different search algorithms have that been developed, one example of which are the suite of programs referred to as BLAST programs. Other examples of suitable programs that can be utilized are known in the art, several of which are described above in the Background. Nucleic acid molecules of the present invention also include non-*Glycine max* homologues. Preferred non-*Glycine max* homologues are selected from the group consisting of alfalfa, *Arabidopsis* barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, maize, pea, peanut, pepper, potato, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, and *Phaseolus*.

In a preferred embodiment, nucleic acid molecules having SEQ ID NO: 1 through SEQ ID NO: 20082 or complements and fragments of either can be utilized to obtain such homologues.

The degeneracy of the genetic code, which allows different nucleic acid sequences to code for the same protein or peptide, is known in the literature. (U.S. Patent No. 4,757,006, the entirety of which is herein incorporated by reference).

In an aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a soybean protein or fragment thereof in SEQ ID NO: 1 through SEQ ID NO: 20082 due to the degeneracy in the genetic code in that they encode the same protein but differ in nucleic acid sequence.

In another further aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a soybean protein or fragment thereof in SEQ ID NO: 1 through SEQ ID NO: 20082 due to the fact that the different nucleic acid sequences encode a protein having one or more conservative amino acid residues.

It is understood that codons capable of coding for such conservative amino acid substitutions are known in the art.

It is well known in the art that one or more amino acids in a native sequence can be substituted with another amino acid(s), the charge and polarity of which are similar to that of the native amino acid, *i.e.*, a conservative amino acid substitution, resulting in a silent change. Conserved substitutes for an amino acid within the native polypeptide sequence can be selected from other members of the class to which the naturally occurring amino acid belongs. Amino acids can be divided into the following four groups: (1) acidic amino acids, (2) basic amino

acids, (3) neutral polar amino acids, and (4) neutral nonpolar amino acids. Representative amino acids within these various groups include, but are not limited to, (1) acidic (negatively charged) amino acids such as aspartic acid and glutamic acid; (2) basic (positively charged) amino acids such as arginine, histidine, and lysine; (3) neutral polar amino acids such as glycine, serine, threonine, cysteine, cystine, tyrosine, asparagine, and glutamine; and (4) neutral nonpolar (hydrophobic) amino acids such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine.

Conservative amino acid changes within the native polypeptides sequence can be made by substituting one amino acid within one of these groups with another amino acid within the same group. Biologically functional equivalents of the proteins or fragments thereof of the present invention can have 10 or fewer conservative amino acid changes, more preferably seven or fewer conservative amino acid changes, and most preferably five or fewer conservative amino acid changes. The encoding nucleotide sequence will thus have corresponding base substitutions, permitting it to encode biologically functional equivalent forms of the proteins or fragments of the present invention.

It is understood that certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Because it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence and, of course, its underlying DNA coding sequence and, nevertheless, obtain a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the peptide sequences of the proteins or fragments of the present invention, or corresponding DNA

sequences that encode said peptides, without appreciable loss of their biological utility or activity. It is understood that codons capable of coding for such amino acid changes are known in the art.

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte and Doolittle, *J. Mol. Biol.* 157, 105-132 (1982), herein incorporated by reference in its entirety). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like.

Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, 1982); these are isoleucine (+4.5), valine (+4.2), leucine (+3.8), phenylalanine (+2.8), cysteine/cystine (+2.5), methionine (+1.9), alanine (+1.8), glycine (-0.4), threonine (-0.7), serine (-0.8), tryptophan (-0.9), tyrosine (-1.3), proline (-1.6), histidine (-3.2), glutamate (-3.5), glutamine (-3.5), aspartate (-3.5), asparagine (-3.5), lysine (-3.9), and arginine (-4.5).

In making such changes, the substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those which are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, incorporated herein by reference in its entirety, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein

As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0), lysine (+3.0), aspartate (+3.0 \pm 1), glutamate (+3.0 \pm 1), serine (+0.3), asparagine (+0.2), glutamine (+0.2), glycine (0), threonine (-0.4), proline (-0.5 \pm 1), alanine (-0.5), histidine (-0.5), cysteine (-1.0), methionine (-1.3), valine (-1.5), leucine (-1.8), isoleucine (-1.8), tyrosine (-2.3), phenylalanine (-2.5), and tryptophan (-3.4). In making such changes, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those which are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a protein or fragment thereof set forth in SEQ ID NO: 1 through SEQ ID NO: 20082 or fragment thereof due to the fact that one or more codons encoding an amino acid has been substituted for a codon that encodes a nonessential substitution of the amino acid originally encoded.

(iv) Nucleic Acid Molecules Comprising Introns and/or Intron/Exon Junctions

Nucleic acid molecules of the present invention can comprise an intron and/or one or more intron/exon junction. Sequences of the present invention can be screened for introns and intron/exon junctions utilizing one or a number of different search algorithms that have that been developed, one example of which are the suite of programs referred to as BLAST programs. Other examples of suitable programs that can be utilized are known in the art, several of which are described above in the Background and in the section entitled "Uses of the Agents of the Present Invention".

(b) **Protein and Peptide Molecules**

A class of agents comprises one or more of the protein or peptide molecules encoded by SEQ ID NO: 1 through SEQ ID NO:20082, fragments thereof or complements thereof or one or more of the proteins encoded by a nucleic acid molecule or fragment thereof or peptide molecules encoded by other nucleic acid agents of the present invention. Protein and peptide molecules can be identified using known protein or peptide molecules as a target sequence or target motif in the BLAST programs of the present invention. In a preferred embodiment, the protein or peptide molecules of the present invention are derived from *Glycine max* (soybean) and more preferably *Glycine max*, genotype A3244.

As used herein, the term "protein molecule" or "peptide molecule" includes any molecule that comprises five or more amino acids. It is well known in the art that proteins or peptides may undergo modification, including post-translational modifications, such as, but not limited to, disulfide bond formation, glycosylation, phosphorylation, or oligomerization. Thus, as used herein, the term "protein molecule" or "peptide molecule" includes any protein molecule that is modified by any biological or non-biological process. The terms "amino acid" and "amino acids" refer to all naturally occurring L-amino acids. This definition is meant to include norleucine, ornithine, homocysteine, and homoserine.

One or more of the protein or fragments of peptide molecules may be produced via chemical synthesis, or more preferably, by expression in a suitable bacterial or eukaryotic host. Suitable methods for expression are described by Sambrook, *et al.*, *Molecular Cloning, A Laboratory Manual, 2nd Edition*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989), or similar texts.

A "protein fragment" is a peptide or polypeptide molecule whose amino acid sequence comprises a subset of the amino acid sequence of that protein. A protein or fragment thereof that comprises one or more additional peptide regions not derived from that protein is a "fusion" protein. Such molecules may be derivatized to contain carbohydrate or other moieties (such as keyhole limpet hemocyanin, etc.). Fusion protein or peptide molecules of the present invention are preferably produced via recombinant means.

Another class of agents comprises protein or peptide molecules encoded by SEQ ID NO: 1 through SEQ ID NO:20082 or complements thereof or, fragments or fusions thereof in which conservative, non-essential, or not relevant, amino acid residues have been added, replaced, or deleted. An example of such a homologue is the homologue protein of all non-*Glycine max* plant species, including but not limited to alfalfa, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, maize, an ornamental plant, pea, peanut, pepper, potato, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eukalyptus, apple, lettuce, peas, lentils, grape, banana, tea, turf grasses, etc. Particularly preferred non-*Glycine max* plants to utilize for the isolation of homologues would include alfalfa, barley, cotton, corn, oat, oilseed rape, rice, corn, canola, ornamentals, sugarcane, sugarbeet, tomato, potato, wheat, and turf grasses. Such a homologue can be obtained by any of a variety of methods. Most preferably, as indicated above, one or more of the disclosed sequences (SEQ ID NO: 1 through SEQ ID NO:20082 or complements thereof) will be used to define a pair of primers that may be used to isolate the homologue-encoding nucleic acid molecules from any desired species. Such molecules can be expressed to yield homologues by recombinant means.

(c) **Antibodies**

One aspect of the present invention concerns antibodies, single-chain antigen binding molecules, or other proteins that specifically bind to one or more of the protein or peptide molecules of the present invention and their homologues, fusions or fragments. Such antibodies may be used to quantitatively or qualitatively detect the protein or peptide molecules of the present invention. As used herein, an antibody or peptide is said to "specifically bind" to a protein or peptide molecule of the present invention if such binding is not competitively inhibited by the presence of non-related molecules. In a preferred embodiment the antibodies of the present invention bind to proteins derived from *Glycine max* (soybean) and more preferably bind to proteins or fragments thereof of *Glycine max*, genotype A3244.

Nucleic acid molecules that encode all or part of the protein of the present invention can be expressed, via recombinant means, to yield protein or peptides that can in turn be used to elicit antibodies that are capable of binding the expressed protein or peptide. Such antibodies may be used in immunoassays for that protein. Such protein-encoding molecules, or their fragments may be a "fusion" molecule (i.e., a part of a larger nucleic acid molecule) such that, upon expression, a fusion protein is produced. It is understood that any of the nucleic acid molecules of the present invention may be expressed, via recombinant means, to yield proteins or peptides encoded by these nucleic acid molecules.

The antibodies that specifically bind proteins and protein fragments of the present invention may be polyclonal or monoclonal, and may comprise intact immunoglobulins, or antigen binding portions of immunoglobulins (such as (F(ab'), F(ab')₂ fragments), or single-chain immunoglobulins producible, for example, via recombinant means). It is understood that practitioners are familiar with the standard resource materials which describe specific conditions

and procedures for the construction, manipulation and isolation of antibodies (see, for example, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1988), the entirety of which is herein incorporated by reference).

Murine monoclonal antibodies are particularly preferred. BALB/c mice are preferred for this purpose, however, equivalent strains may also be used. The animals are preferably immunized with approximately 25 µg of purified protein (or fragment thereof) that has been emulsified in a suitable adjuvant (such as TiterMax adjuvant (Vaxcel, Norcross, GA)). Immunization is preferably conducted at two intramuscular sites, one intraperitoneal site, and one subcutaneous site at the base of the tail. An additional i.v. injection of approximately 25 µg of antigen is preferably given in normal saline three weeks later. After approximately 11 days following the second injection, the mice may be bled and the blood screened for the presence of anti-protein or peptide antibodies. Preferably, a direct binding Enzyme-Linked Immunoassay (ELISA) is employed for this purpose.

More preferably, the mouse having the highest antibody titer is given a third i.v. injection of approximately 25 µg of the same protein or fragment. The splenic leukocytes from this animal may be recovered 3 days later, and are then permitted to fuse, most preferably, using polyethylene glycol, with cells of a suitable myeloma cell line (such as, for example, the P3X63Ag8.653 myeloma cell line). Hybridoma cells are selected by culturing the cells under "HAT" (hypoxanthine-aminopterin-thymine) selection for about one week. The resulting clones may then be screened for their capacity to produce monoclonal antibodies ("mAbs"), preferably by direct ELISA.

In one embodiment, anti-protein or peptide monoclonal antibodies are isolated using a fusion of a protein, protein fragment, or peptide of the present invention, or conjugate of a

protein, protein fragment, or peptide of the present invention, as immunogens. Thus, for example, a group of mice can be immunized using a fusion protein emulsified in Freund's complete adjuvant (e.g., approximately 50 μ g of antigen per immunization). At three week intervals, an identical amount of antigen is emulsified in Freund's incomplete adjuvant and used to immunize the animals. Ten days following the third immunization, serum samples are taken and evaluated for the presence of antibody. If antibody titers are too low, a fourth booster can be employed. Polysera capable of binding the protein or peptide can also be obtained using this method.

In a preferred procedure for obtaining monoclonal antibodies, the spleens of the above-described immunized mice are removed, disrupted, and immune splenocytes are isolated over a ficoll gradient. The isolated splenocytes are fused, using polyethylene glycol with BALB/c-derived HGPRT (hypoxanthine guanine phosphoribosyl transferase) deficient P3x63xAg8.653 plasmacytoma cells. The fused cells are plated into 96-well microtiter plates and screened for hybridoma fusion cells by their capacity to grow in culture medium supplemented with hypoxanthine, aminopterin and thymidine for approximately 2-3 weeks.

Hybridoma cells that arise from such incubation are preferably screened for their capacity to produce an immunoglobulin that binds to a protein of interest. An indirect ELISA may be used for this purpose. In brief, the supernatants of hybridomas are incubated in microtiter wells that contain immobilized protein. After washing, the titer of bound immunoglobulin can be determined using, for example, a goat anti-mouse antibody conjugated to horseradish peroxidase. After additional washing, the amount of immobilized enzyme is determined (for example through the use of a chromogenic substrate). Such screening is performed as quickly as possible after the identification of the hybridoma in order to ensure that a desired clone is not overgrown

by non-secreting neighbors. Desirably, the fusion plates are screened several times since the rates of hybridoma growth vary. In a preferred sub-embodiment, a different antigenic form of immunogen may be used to screen the hybridoma. Thus, for example, the splenocytes may be immunized with one immunogen, but the resulting hybridomas can be screened using a different immunogen. It is understood that any of the protein or peptide molecules of the present invention may be used to raise antibodies.

As discussed below, such antibody molecules or their fragments may be used for diagnostic purposes. Where the antibodies are intended for diagnostic purposes, it may be desirable to derivatize them, for example with a ligand group (such as biotin) or a detectable marker group (such as a fluorescent group, a radioisotope or an enzyme).

The ability to produce antibodies that bind the protein or peptide molecules of the present invention permits the identification of mimetic compounds of those molecules. A "mimetic compound" is a compound that is not that compound, or a fragment of that compound, but which nonetheless exhibits an ability to specifically bind to antibodies directed against that compound.

It is understood that any of the agents of the present invention can be substantially purified and/or be biologically active and/or recombinant.

Uses of the Agents of the Invention

Nucleic acid molecules and fragments thereof of the present invention may be employed for genetic mapping studies using linkage analysis (genetic markers). A genetic linkage map shows the relative locations of specific DNA markers along a chromosome. Maps are used for the identification of genes associated with genetic diseases or phenotypic traits, comparative genomics, and as a guide for physical mapping. Through genetic mapping, a fine scale linkage map can be developed using DNA markers, and, then, a genomic DNA library of large-sized

fragments can be screened with molecular markers linked to the desired trait. In a preferred embodiment of the present invention, the genomic library screened with the nucleic acid molecules of the present invention is a genomic library of *Glycine max*.

Mapping marker locations is based on the observation that two markers located near each other on the same chromosome will tend to be passed together from parent to offspring. During gamete production, DNA strands occasionally break and rejoin in different places on the same chromosome or on the homologous chromosome. The closer the markers are to each other, the more tightly linked and the less likely a recombination event will fall between and separate them. Recombination frequency thus provides an estimate of the distance between two markers.

In segregating populations, target genes have been reported to have been placed within an interval of 5-10 cM with a high degree of certainty (Tanksley *et al.*, *Trends in Genetics* 11(2):63-68 (1995), the entirety of which is herein incorporated by reference). The markers defining this interval are used to screen a larger segregating population to identify individuals derived from one or more gametes containing a crossover in the given interval. Such individuals are useful in orienting other markers closer to the target gene. Once identified, these individuals can be analyzed in relation to all molecular markers within the region to identify those closest to the target.

Markers of the present invention can be employed to construct linkage maps and to locate genes with qualitative and quantitative effects. The genetic linkage of additional marker molecules can be established by a genetic mapping model such as, without limitation, the flanking marker model reported by Lander and Botstein, *Genetics*, 121:185-199 (1989), and the interval mapping, based on maximum likelihood methods described by Lander and Botstein, *Genetics*, 121:185-199 (1989), the entirety of which is herein incorporated by reference and

implemented in the software package MAPMAKER/QTL (Lincoln and Lander, *Mapping Genes Controlling Quantitative Traits Using MAPMAKER/QTL*, Whitehead Institute for Biomedical Research, Massachusetts, (1990)). Additional software includes Qgene, Version 2.23 (1996), Department of Plant Breeding and Biometry, 266 Emerson Hall, Cornell University, Ithaca, NY, the manual of which is herein incorporated by reference in its entirety). Use of the Qgene software is a particularly preferred approach.

A maximum likelihood estimate (MLE) for the presence of a marker is calculated, together with an MLE assuming no QTL effect, to avoid false positives. A \log_{10} of an odds ratio (LOD) is then calculated as: $\text{LOD} = \log_{10}(\text{MLE for the presence of a QTL} / \text{MLE given no linked QTL})$.

The LOD score essentially indicates how much more likely the data are to have arisen assuming the presence of a QTL than in its absence. The LOD threshold value for avoiding a false positive with a given confidence, say 95%, depends on the number of markers and the length of the genome. Graphs indicating LOD thresholds are set forth in Lander and Botstein, *Genetics*, 121:185-199 (1989), the entirety of which is herein incorporated by reference and further described by Arús and Moreno-González, *Plant Breeding*, Hayward, Rosemark, Romagosa (eds.) Chapman & Hall, London, pp. 314-331 (1993).

Additional models can be used. Many modifications and alternative approaches to interval mapping have been reported, including the use of non-parametric methods (Kruglyak and Lander, *Genetics*, 139:1421-1428 (1995), the entirety of which is herein incorporated by reference). Multiple regression methods or models can be also be used, in which the trait is regressed on a large number of markers (Jansen, *Biometrics in Plant Breed*, van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding,

The Netherlands, pp. 116-124 (1994); Weber and Wricke, *Advances in Plant Breeding*, Blackwell, Berlin, 16 (1994). Procedures combining interval mapping with regression analysis, whereby the phenotype is regressed onto a single putative QTL at a given marker interval, and at the same time onto a number of markers that serve as 'cofactors,' have been reported by Jansen and Stam, *Genetics*, 136:1447-1455 (1994) and Zeng, *Genetics*, 136:1457-1468 (1994). Generally, the use of cofactors reduces the bias and sampling error of the estimated QTL positions (Utz and Melchinger, *Biometrics in Plant Breeding*, van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp.195-204 (1994), thereby improving the precision and efficiency of QTL mapping (Zeng, *Genetics*, 136:1457-1468 (1994). These models can be extended to multi-environment experiments to analysis genotype-environment interactions (Jansen *et al.*, *Theo. Appl. Genet.* 91:33-37 (1995).

Selection of an appropriate mapping population is important to map construction. The choice of appropriate mapping population depends on the type of marker systems employed (Tanksley *et al.*, J.P. Gustafson and R. Appels (eds.), Plenum Press, New York, pp. 157-173 (1988), the entirety of which is herein incorporated by reference). Consideration must be given to the source of parents (adapted vs. exotic) used in the mapping population. Chromosome pairing and recombination rates can be severely disturbed (suppressed) in wide crosses (adapted x exotic) and generally yield greatly reduced linkage distances. Wide crosses will usually provide segregating populations with a relatively large array of polymorphisms when compared to progeny in a narrow cross (adapted x adapted).

An F₂ population is the first generation of selfing after the hybrid seed is produced. Usually a single F₁ plant is selfed to generate a population segregating for all the genes in

Mendelian (1:2:1) fashion. Maximum genetic information is obtained from a completely classified F_2 population using a codominant marker system (Mather, Measurement of Linkage in Heredity: Methuen and Co., (1938), the entirety of which is herein incorporated by reference). In the case of dominant markers, progeny tests (e.g., F_3 , BCF_2) are required to identify the heterozygotes, thus making it equivalent to a completely classified F_2 population. However, this procedure is often prohibitive because of the cost and time involved in progeny testing. Progeny testing of F_2 individuals is often used in map construction where phenotypes do not consistently reflect genotype (e.g., disease resistance) or where trait expression is controlled by a QTL. Segregation data from progeny test populations (e.g., F_3 or BCF_2) can be used in map construction. Marker-assisted selection can then be applied to cross progeny based on marker-trait map associations (F_2 , F_3), where linkage groups have not been completely disassociated by recombination events (i.e., maximum disequilibrium).

Recombinant inbred lines (RIL) (genetically related lines; usually $>F_5$, developed from continuously selfing F_2 lines towards homozygosity) can be used as a mapping population. Information obtained from dominant markers can be maximized by using RIL because all loci are homozygous or nearly so. Under conditions of tight linkage (i.e., about $<10\%$ recombination), dominant and co-dominant markers evaluated in RIL populations provide more information per individual than either marker type in backcross populations (Reiter, *Proc. Natl. Acad. Sci. (U.S.A.)* 89:1477-1481 (1992). However, as the distance between markers becomes larger (i.e., loci become more independent), the information in RIL populations decreases dramatically when compared to codominant markers.

Backcross populations (e.g., generated from a cross between a successful variety (recurrent parent) and another variety (donor parent) carrying a trait not present in the former)

can be utilized as a mapping population. A series of backcrosses to the recurrent parent can be made to recover most of its desirable traits. Thus a population is created consisting of individuals nearly like the recurrent parent but each individual carries varying amounts or mosaic of genomic regions from the donor parent. Backcross populations can be useful for mapping dominant markers if all loci in the recurrent parent are homozygous and the donor and recurrent parent have contrasting polymorphic marker alleles (Reiter *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 89:1477-1481 (1992). Information obtained from backcross populations using either codominant or dominant makers is less than that obtained from F_2 populations because one, rather than two, recombinant gametes are sampled per plant. Backcross populations, however, are more informative (at low marker saturation) when compared to RILs as the distance between linked loci increases in RIL populations (i.e., about 0.15% recombination). Increased recombination can be beneficial for resolution of tight linkages, but may be undesirable in the construction of maps with low marker saturation.

Near-isogenic lines (NIL)(created by many backcrosses to produce an array of individuals that are nearly identical in genetic composition except for the trait or genomic region under interrogation) can be used as a mapping population. In mapping with NILs, only a portion of the polymorphic loci are expected to map to a selected region.

Bulk segregant analysis (BSA) is a method developed for the rapid identification of linkage between markers and traits of interest (Michelmore, *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 88:9828-9832 (1991). In BSA, two bulked DNA samples are drawn from a segregating population originating from a single cross. These bulks contain individuals that are identical for a particular trait (resistant or susceptible to particular disease) or genomic region but arbitrary at

unlinked regions (i.e., heterozygous). Regions unlinked to the target region will not differ between the bulked samples of many individuals in BSA.

Applications for markers in plant breeding include: Quantitative Trait Loci (QTL) mapping (Edwards *et al*, *Genetics* 116:113-115 (1987), the entirety of which is herein incorporated by reference); Nienhuis *et al*, *Crop Sci.* 27:797-803 (1987); Osborn *et al*, *Theor. Appl. Genet.* 73:350-356 (1987); Romero-Severson *et al*, *Use of RFLPs In Analysis of Quantitative Trait Loci In Maize*, In Helentjaris and Burr (eds.) pp. 97-102 (1989), the entirety of which is herein incorporated by reference; Young *et al*, *Genetics* 120:570-585 (1988), the entirety of which is herein incorporated by reference; Martin *et al*, *Science* 243:1725-1728 (1989), the entirety of which is herein incorporated by reference; Sarfatti *et al.*, *Theor. Appl. Genet.* 78:22-26 (1989), the entirety of which is herein incorporated by reference; Tanksley, *et al.*, *Biotech.* 7:257-264 (1989); Barone *et al*, *Mol. Gen. Genet.* 224:177-182 (1990), the entirety of which is herein incorporated by reference; Jung *et al*, *Theor. Appl. Genet.* 79:663-672 (1990), the entirety of which is herein incorporated by reference; Keim *et al*, *Genetics* 126:735-742 (1990), the entirety of which is herein incorporated by reference, *Theor. Appl. Genet.* 79:465-369 (1990), the entirety of which is herein incorporated by reference; Paterson *et al.*, *Genetics* 124:735-742 (1990), the entirety of which is herein incorporated by reference; Martin *et al*, *Proc. Natl. Acad. Sci. (U.S.A.)* 88:2336-2340 (1991), the entirety of which is herein incorporated by reference; Messeguer *et al*, *Theor. Appl. Genet.* 82:529-536 (1991), the entirety of which is herein incorporated by reference; Michelmore *et al*, *Proc Natl. Acad. Sci. (U.S.A.)* 88:9828-9832 (1991), the entirety of which is herein incorporated by reference; Ottaviano *et al*, *Theor. Appl. Genet.* 81:713-719 (1991), the entirety of which is herein incorporated by reference; Yu *et al*, *Theor. Appl. Genet.* 81:471-476 (1991), the entirety of which is herein incorporated by

reference; Diers *et al*, *Crop Sci.* 32:77-383 (1992), the entirety of which is herein incorporated by reference; *Theor. Appl. Genet.* 83:608-612 (1992), the entirety of which is herein incorporated by reference; *J. Plant Nut.* 15:2127-2136 (1992), the entirety of which is herein incorporated by reference; Doebley *et al*, *Proc. Natl. Acad. Sci. (U.S.A.)* 87:9888-9892 (1990), the entirety of which is herein incorporated by reference), screening genetic resource strains for useful quantitative trait alleles and introgression of these alleles into commercial varieties (Beckmann and Soller, *Theor. Appl. Genet.* 67:35-43 (1983), the entirety of which is herein incorporated by reference; Tanksley *et al*, (1989) the entirety of which is incorporated by reference), or the mapping of mutations (Rafalski, *et al.*, In: *Nonmammalian Genomic Analysis*, ed. Birren and Lai, Academic Press, San Diego, CA, pp. 75-134 (1996). Additionally, markers can be used to characterize transformants or germplasm, as a genetic diagnostic test for plant breeding or to identify individuals or varieties (Soller and Beckmann, *Theor. Appl. Genet.* 67:25-33 (1983), the entirety of which is herein incorporated by reference; Tanksley *et al*, 1989). Markers also can be used to obtain information about: (1) the number, effect, and chromosomal location of each gene affecting a trait; (2) effects of multiple copies of individual genes (gene dosage); (3) interaction between/among genes controlling a trait (epistasis); (4) whether individual genes affect more than one trait (pleiotropy); and (5) stability of gene function across environments (G x E interactions).

It is understood that one or more of the nucleic acid molecules of the present invention may in one embodiment be used as markers in genetic mapping. In a preferred embodiment, nucleic acid molecules of the present invention may in one embodiment be used as markers with *Glycine max*.

The nucleic acid molecules of the present invention may be used for physical mapping. Physical mapping, in conjunction with linkage analysis, can enable the isolation of genes. Physical mapping has been reported to identify the markers closest in terms of genetic recombination to a gene target for cloning. Once a DNA marker is linked to a gene of interest, the chromosome walking technique can be used to find the genes via overlapping clones. For chromosome walking, random molecular markers or established molecular linkage maps are used to conduct a search to localize the gene adjacent to one or more markers. A chromosome walk (Bukanov and Berg, *Mo. Microbiol.* 11:509-523 (1994), the entirety of which is herein incorporated by reference; Birkenbihl and Vielmetter *Nucleic Acids Res.* 17:5057-5069 (1989), the entirety of which is herein incorporated by reference; Wenzel and Herrmann, *Nucleic Acids Res.* 16:8323-8336, (1988), the entirety of which is herein incorporated by reference) is then initiated from the closest linked marker. Starting from the selected clones, labeled probes specific for the ends of the insert DNA are synthesized and used as probes in hybridizations against a representative library. Clones hybridizing with one of the probes are picked and serve as templates for the synthesis of new probes; by subsequent analysis, contigs are produced.

The degree of overlap of the hybridizing clones used to produce a contig can be determined by comparative restriction analysis. Comparative restriction analysis can be carried out in different ways all of which exploit the same principle; two clones of a library are very likely to overlap if they contain a limited number of restriction sites for one or more restriction endonucleases located at the same distance from each other. The most frequently used procedures are, fingerprinting (Coulson *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 83:7821-7821, (1986), the entirety of which is herein incorporated by reference); Knott *et al.*, *Nucleic Acids Res.* 16:2601-2612 (1988), the entirety of which is herein incorporated by reference; Eiglmeier *et al.*,

Mol. Microbiol. 7(2):197-206 (1993), the entirety of which is herein incorporated by reference, 1993), restriction fragment mapping (Smith and Birnstiel, *Nucleic Acids Res.* 3:2387-2398 (1976), the entirety of which is herein incorporated by reference, or the "landmarking" technique (Charlebois *et al.*, *J. Mol. Biol.* 222:509-524 (1991), the entirety of which is herein incorporated by reference

To generate a physical map of a genome with BACs using the fingerprinting technique, a BAC library containing a number of clones equivalent to 4X-20X haploid genome can be used. (Zhang and Wing., *Plant Mol. Bio.* 35:115-127 (1997)). For example, BAC DNA can be purified with the conventional alkaline lysis procedure as used for plasmid DNA purification, digested with the restriction enzyme used for construction of the BAC libraries and end-labeled with ^{32}P -dATP, digested with *Sau3AI* and fractionated on a denaturing polyacrylamide gel. The gel is dried to chromatography paper and exposed to X-ray film. Fingerprints are scanned and then converted into database records, according to the positions of each band relative to the bands of the closest molecular-weight marker on a gel. The incoming database of fingerprints are first compared against each other to assemble contigs if overlapped, and then compared against all existing databases to place the incoming BACs and BAC contigs in established contigs if overlapped. The physical length of a contig in kb is estimated according to the number of restriction sites of the enzyme used for the first digestion prior to fragment end labeling

Restriction analysis of a certain clone can be carried out, for example, according to a method originally described by Smith and Berstiel, *Nucleic Acids Res.* 3:2387-2398 (1976). First, the number and size of cloned restriction fragments to be mapped are determined by complete digestion and agarose gel electrophoresis. Then, the clone is linearized at a unique restriction site outside of the cloned DNA. Aliquots of the linearized molecules are digested to

different extents with the enzyme selected for mapping. These partially cut samples are separated on agarose gels, blotted, and hybridized to a labeled fragment of vector DNA. This probe is derived entirely from one side or the other of the unique site used to linearize the clone.

The results show a ladder of DNA fragments that have the same unique end. By repeating these analyses in pairs with all the neighboring intermediate DNA fragments, the correct order of restriction fragments as well as the orientation of the cloned insert can be deduced. The order of restriction fragments produced by restriction enzymes other than the cloning enzyme can be determined similarly. Fragment data from different enzymes are then combined by a computer program and compared with the alignments of other clones of the library (Kohara *et al.*, *Cell* 50:495-508 (1987), the entirety of which is herein incorporated by reference).

The landmarking technique can be carried out without any labeling and relies on agarose gel analysis. Clones are first digested preferably with a 6 bp specific endonuclease A, if possible with the original clone enzyme. Clones are then digested with a second endonuclease B. Endonuclease B is chosen based on its ability to cut rarely in the genome, for example, on average only once in 30 kbp. Of the fragments generated by digestion of one clone with enzyme A, statistically only a small number (between zero and three fragments) will also be cut by enzyme B. The very specific pattern of those fragments which are produced by double digestion are easily recognized. Any of these fragments which have a restriction site for the rarely cutting endonuclease is called a "landmark". Generally one common landmark is sufficient for defining two overlapping clones.

Alternatively to chromosome walking and the associated comparative restriction analyses methods, chromosome landing also has been reported to be used to locate a gene of interest

(Tanksley *et al.*, *Trends in Genetics* 11(2):63-68 (1995), the entirety of which is herein incorporated by reference. For chromosome landing, a DNA marker is isolated at a physical distance from the targeted gene. High resolution linkage analysis is used to identify such a marker that cosegregates with the gene. The marker is isolated at a distance that is less than the average insert size of the genomic library used for clone isolation. The DNA marker is then used to screen the library and isolate (or "land" on) the clone containing the gene without chromosome walking. Genome coverage of a library can also be determined by cross-hybridization of individual large insert clones by screening a BAC library with single copy RFLP markers distributed randomly across the genome by hybridization. To assure accuracy of the physical map, the markers should be single-copy or of single-locus origin, if multiple-copy.

Chromosome landing of large-insert clones using chromosome-specific DNA markers such as STSs microsatellites, RFLPs, or other markers can correlate physical and genetic maps (Zwick *et al.*, *Genetics* 148:1983-1992 (1998), the entirety of which is herein incorporated by reference in its entirety). These strategies include chromosome landing of BACs containing markers or BAC contigs by BAC-FISH (Fluorescent *In Situ* Hybridization), a technique that involves tagging the DNA marker with an observable label. BAC clones giving positive hybridization signals are individually analyzed by FISH to metaphase chromosome spreads. The location of the labeled probe can be detected after it binds to its complementary DNA strand in an intact chromosome. The FISH of a BAC selected from a BAC contig will directly place the BAC contig to a specific chromosome region and establish a linkage relationships of the BAC contig to another BAC contig .

Likewise, BACs and STCs of the present invention can be used for contig mapping (Venter, *et al.*, *Nature*, 381:364-366 (1996), the entirety of which is herein incorporated by

reference). A "seed" BAC insert can be sequenced and then STCs and the corresponding BAC of each STC can be placed on the sequenced insert using the BLASTN program. Marker or gene containing STCs can be determined by the BLASTN program and their corresponding BACs can be hybridized to specific chromosomes using BAC-FISH (Zwick *et al.*, *Genetics* 148:1983-1992 (1998)).

STCs can be used to identify a minimum tiling path of BACs by computational procedures. Any nucleation sequence (the sequence of an entire BAC, for example) can be electronically compared to a database of STCs to identify the next clones to be sequenced to maximally extend a contig. Chosen STCs need to occupy correct positions in the tiling path. Several factors can contribute to errors in the positioning and selection of these clones. An STC that contains all or part of a repetitive element can appear to align at any part of the growing mosaic which contains that element. One method of selecting the appropriate BAC is to mask out all sections of DNA sequence which are known to be repetitive elements. The sequence symbols of these section are replaced with Ns. These sections of DNA are not used to align the STC. STCs which are completely comprised of Ns are discarded. In this way, the unmasked sections of DNA may be aligned against the growing mosaic without misplacing them due to redundant sequence. A program publicly available, PowerBLAST includes a number of options for masking repetitive elements and low complexity subsequences (Zhang and Madden, *Genome Res.* 7:649-56 (1997), the entirety of which is herein incorporated by reference. cDNA and genomic libraries also can be used as probe sources, thus directly combining the ordering of the genomic DNA with the localization of transcribed sequences. By a simultaneous hybridization to the genomic and back to the transcriptional libraries, results are produced on sequence homologies between transcribed sequences.

It is understood that the nucleic acid molecules of the present invention may in one embodiment be used in physical mapping. In a preferred embodiment, nucleic acid molecules of the present invention may in one embodiment be used in the physical mapping of *Glycine max*.

Nucleic acid molecules of the present invention can be used in comparative mapping (physical and genetic). Comparative mapping within families provides a method to the degree of sequence conservation, gene order, ploidy of species, ancestral relationships and the rates at which individual genomes are evolving. Comparative mapping has been carried out by cross-hybridizing molecular markers across species within a given family. As in genetic mapping, molecular markers are needed but instead of direct hybridization to mapping filters, the markers are used to select large insert clones from a total genomic DNA library of a related species. The selected clones, each a representative of a single marker, can then be used to physically map the region in the target species. The advantage of this method for comparative mapping is that no mapping population or linkage map of the target species is needed and the clones may also be used in other closely related species. By comparing the results obtained by genetic mapping in model plants, with those from other species, similarities of genomic structure among plants species can be established. Cross-hybridization of RFLP markers have been reported and conserved gene order has been established in many studies. Such macroscopic synteny is utilized for the estimation of correspondence of loci among these crops. These loci include not only Mendelian genes but also Quantitative Trait Loci (QTL) (Mohan *et al.*, *Molecular Breeding* 3:87-103 (1997), the entirety of which is herein incorporated by reference.

It is understood that markers of the present invention may in another embodiment be used in comparative mapping. In a preferred embodiment the markers of present invention may be

used in the comparative mapping of *Glycine clandestina*, *Glycine gracilis*, *Glycine soja*, *Glycine tomentella*, and *Glycine tabaina*

The nucleic acid molecules of the present invention can be used to identify polymorphisms. In one embodiment, one or more of the STC nucleic acid molecules or a BAC nucleic acid molecule (or a sub-fragment of either) may be employed as a marker nucleic acid molecule to identify such polymorphism(s). Alternatively, such polymorphisms can be detected through the use of a marker nucleic acid molecule or a marker protein that is genetically linked to (i.e., a polynucleotide that co-segregates with) such polymorphism(s).

In an alternative embodiment, such polymorphisms can be detected through the use of a marker nucleic acid molecule that is physically linked to such polymorphism(s). For this purpose, marker nucleic acid molecules comprising a nucleotide sequence of a polynucleotide located within 1 mb of the polymorphism(s), and more preferably within 100 kb of the polymorphism(s), and most preferably within 10 kb of the polymorphism(s) can be employed.

The genomes of animals and plants naturally undergo spontaneous mutation in the course of their continuing evolution (Gusella, *Ann. Rev. Biochem.* 55:831-854 (1986)). A "polymorphism" is a variation or difference in the sequence of the gene or its flanking regions that arises in some of the members of a species. The variant sequence and the "original" sequence co-exist in the species' population. In some instances, such co-existence is in stable or quasi-stable equilibrium.

A polymorphism is thus said to be "allelic," in that, due to the existence of the polymorphism, some members of a species may have the original sequence (i.e., the original "allele") whereas other members may have the variant sequence (i.e., the variant "allele"). In the simplest case, only one variant sequence may exist, and the polymorphism is thus said to be di-

allelic. In other cases, the species' population may contain multiple alleles, and the polymorphism is termed tri-allelic, etc. A single gene may have multiple different unrelated polymorphisms. For example, it may have a di-allelic polymorphism at one site, and a multi-allelic polymorphism at another site.

The variation that defines the polymorphism may range from a single nucleotide variation to the insertion or deletion of extended regions within a gene. In some cases, the DNA sequence variations are in regions of the genome that are characterized by short tandem repeats (STRs) that include tandem di- or tri-nucleotide repeated motifs of nucleotides. Polymorphisms characterized by such tandem repeats are referred to as "variable number tandem repeat" ("VNTR") polymorphisms. VNTRs have been used in identity analysis (Weber, U.S. Patent 5,075,217; Armour, *et al.*, *FEBS Lett.* 307:113-115 (1992); Jones, *et al.*, *Eur. J. Haematol.* 39:144-147 (1987); Horn, *et al.*, PCT Application WO91/14003; Jeffreys, European Patent Application 370,719; Jeffreys, U.S. Patent 5,175,082; Jeffreys *et al.*, *Amer. J. Hum. Genet.* 39:11-24 (1986); Jeffreys *et al.*, *Nature* 316:76-79 (1985); Gray, *et al.*, *Proc. R. Acad. Soc. Lond.* 243:241-253 (1991); Moore, *et al.*, *Genomics* 10:654-660 (1991); Jeffreys, *et al.*, *Anim. Genet.* 18:1-15 (1987); Hillel, *et al.*, *Anim. Genet.* 20:145-155 (1989); Hillel, *et al.*, *Genet.* 124:783-789 (1990), all of which are herein incorporated by reference in their entirety).

The detection of polymorphic sites in a sample of DNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis or other means.

The most preferred method of achieving such amplification employs the polymerase chain reaction ("PCR") (Mullis, *et al.*, *Cold Spring Harbor Symp. Quant. Biol.* 51:263-273 (1986); Erlich, *et al.*, European Patent Appln. 50,424; European Patent Appln. 84,796, European Patent Application 258,017, European Patent Appln. 237,362; Mullis, European Patent Appln. 201,184; Mullis, *et al.*, U.S. Patent No. 4,683,202; Erlich, U.S. Patent No. 4,582,788; and Saiki, *et al.*, U.S. Patent No. 4,683,194, all of which are herein incorporated by reference), using primer pairs that are capable of hybridizing to the proximal sequences that define a polymorphism in its double-stranded form.

In lieu of PCR, alternative methods, such as the "Ligase Chain Reaction" ("LCR") may be used (Barany, *Proc. Natl. Acad. Sci.(U.S.A.)* 88:189-193 (1991), the entirety of which is herein incorporated by reference. LCR uses two pairs of oligonucleotide probes to exponentially amplify a specific target. The sequences of each pair of oligonucleotides is selected to permit the pair to hybridize to abutting sequences of the same strand of the target. Such hybridization forms a substrate for a template-dependent ligase. As with PCR, the resulting products thus serve as a template in subsequent cycles and an exponential amplification of the desired sequence is obtained.

LCR can be performed with oligonucleotides having the proximal and distal sequences of the same strand of a polymorphic site. In one embodiment, either oligonucleotide will be designed to include the actual polymorphic site of the polymorphism. In such an embodiment, the reaction conditions are selected such that the oligonucleotides can be ligated together only if the target molecule either contains or lacks the specific nucleotide that is complementary to the polymorphic site present on the oligonucleotide. Alternatively, the oligonucleotides may be

selected such that they do not include the polymorphic site (see, Segev, PCT Application WO 90/01069, the entirety of which is herein incorporated by reference).

The "Oligonucleotide Ligation Assay" ("OLA") may alternatively be employed (Landegren, *et al.*, *Science* 241:1077-1080 (1988), the entirety of which is herein incorporated by reference). The OLA protocol uses two oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of a target. OLA, like LCR, is particularly suited for the detection of point mutations. Unlike LCR, however, OLA results in "linear" rather than exponential amplification of the target sequence.

Nickerson, *et al.* have described a nucleic acid detection assay that combines attributes of PCR and OLA (Nickerson, *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 87:8923-8927 (1990), the entirety of which is herein incorporated by reference). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA. In addition to requiring multiple, and separate, processing steps, one problem associated with such combinations is that they inherit all of the problems associated with PCR and OLA.

Schemes based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide, are also known (Wu, *et al.*, *Genomics* 4:560 (1989), the entirety of which is herein incorporated by reference), and may be readily adapted to the purposes of the present invention.

Other known nucleic acid amplification procedures, such as allele-specific oligomers, branched DNA technology, transcription-based amplification systems, or isothermal amplification methods may also be used to amplify and analyze such polymorphisms (Malek, *et al.*, U.S. Patent 5,130,238; Davey, *et al.*, European Patent Application 329,822; Schuster *et al.*,

U.S. Patent 5,169,766; Miller, *et al.*, PCT Application WO 89/06700; Kwoh, *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 86:1173-1177 (1989); Gingeras, *et al.*, PCT Application WO 88/10315; Walker, *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 89:392-396 (1992), all of which are herein incorporated by reference in their entirety).

The identification of a polymorphism can be determined in a variety of ways. By correlating the presence or absence of it in an plant with the presence or absence of a phenotype, it is possible to predict the phenotype of that plant. If a polymorphism creates or destroys a restriction endonuclease cleavage site, or if it results in the loss or insertion of DNA (e.g., a VNTR polymorphism), it will alter the size or profile of the DNA fragments that are generated by digestion with that restriction endonuclease. As such, individuals that possess a variant sequence can be distinguished from those having the original sequence by restriction fragment analysis. Polymorphisms that can be identified in this manner are termed "restriction fragment length polymorphisms" ("RFLPs"). RFLPs have been widely used in human and plant genetic analyses (Glassberg, UK Patent Application 2135774; Skolnick, *et al.*, *Cytogen. Cell Genet.* 32:58-67 (1982); Botstein, *et al.*, *Ann. J. Hum. Genet.* 32:314-331 (1980); Fischer, *et al.* (PCT Application WO90/13668); Uhlen, PCT Application WO90/11369).

Polymorphisms can also be identified by Single Strand Conformation Polymorphism (SSCP) analysis. The SSCP technique is a method capable of identifying most sequence variations in a single strand of DNA, typically between 150 and 250 nucleotides in length (Elles, *Methods in Molecular Medicine: Molecular Diagnosis of Genetic Diseases*, Humana Press (1996), the entirety of which is herein incorporated by reference); Orita *et al.*, *Genomics* 5:874-879 (1989), the entirety of which is herein incorporated by reference). Under denaturing conditions a single strand of DNA will adopt a conformation that is uniquely dependent on its

sequence conformation. This conformation usually will be different, even if only a single base is changed. Most conformations have been reported to alter the physical configuration or size sufficiently to be detectable by electrophoresis. A number of protocols have been described for SSCP including, but not limited to Lee *et al.*, *Anal. Biochem.* 205:289-293 (1992), the entirety of which is herein incorporated by reference; Suzuki *et al.*, *Anal. Biochem.* 192:82-84 (1991), the entirety of which is herein incorporated by reference; Lo *et al.*, *Nucleic Acids Research* 20:1005-1009 (1992), the entirety of which is herein incorporated by reference; Sarkar *et al.*, *Genomics* 13:441-443 (1992), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acids of the present invention, may be utilized as markers or probes to detect polymorphisms by SSCP analysis.

Polymorphisms may also be found using a DNA fingerprinting technique called amplified fragment length polymorphism (AFLP), which is based on the selective PCR amplification of restriction fragments from a total digest of genomic DNA to profile that DNA. Vos, *et al.*, *Nucleic Acids Res.* 23:4407-4414 (1995), the entirety of which is herein incorporated by reference. This method allows for the specific co-amplification of high numbers of restriction fragments, which can be visualized by PCR without knowledge of the nucleic acid sequence.

AFLP employs basically three steps. Initially, a sample of genomic DNA is cut with restriction enzymes and oligonucleotide adapters are ligated to the restriction fragments of the DNA. The restriction fragments are then amplified using PCR by using the adapter and restriction sequence as target sites for primer annealing. The selective amplification is achieved by the use of primers that extend into the restriction fragments, amplifying only those fragments in which the primer extensions match the nucleotide flanking the restriction sites. These amplified fragments are then visualized on a denaturing polyacrylamide gel.

AFLP analysis has been performed on *Salix* (Beismann, *et al.*, *Mol. Ecol.* 6:989-993 (1997), the entirety of which is herein incorporated by reference); *Acinetobacter* (Janssen, *et al.*, *Int. J. Syst. Bacteriol.* 47:1179-1187 (1997), the entirety of which is herein incorporated by reference), *Aeromonas popoffi* (Huys, *et al.*, *Int. J. Syst. Bacteriol.* 47:1165-1171 (1997), the entirety of which is herein incorporated by reference), rice (McCouch, *et al.*, *Plant Mol. Biol.* 35:89-99 (1997), the entirety of which is herein incorporated by reference); Nandi, *et al.*, *Mol. Gen. Genet.* 255:1-8 (1997); Cho, *et al.*, *Genome* 39:373-378 (1996), herein incorporated by reference), barley (*Hordeum vulgare*) (Simons, *et al.*, *Genomics* 44:61-70 (1997), the entirety of which is herein incorporated by reference; Waugh, *et al.*, *Mol. Gen. Genet.* 255:311-321 (1997), the entirety of which is herein incorporated by reference; Qi, *et al.*, *Mol. Gen. Genet.* 254:330-336 (1997), the entirety of which is herein incorporated by reference; Becker, *et al.*, *Mol. Gen. Genet.* 249:65-73 (1995), the entirety of which is herein incorporated by reference), potato (Van der Voort, *et al.*, *Mol. Gen. Genet.* 255:438-447 (1997), the entirety of which is herein incorporated by reference; Meksem, *et al.*, *Mol. Gen. Genet.* 249:74-81 (1995), the entirety of which is herein incorporated by reference), *Phytophthora infestans* (Van der Lee, *et al.*, *Fungal Genet. Biol.* 21:278-291 (1997), the entirety of which is herein incorporated by reference), *Bacillus anthracis* (Keim, *et al.*, *J. Bacteriol.* 179:818-824 (1997)), *Astragalus cremnophylax* (Travis, *et al.*, *Mol. Ecol.* 5:735-745 (1996), the entirety of which is herein incorporated by reference), *Arabidopsis* (Cnops, *et al.*, *Mol. Gen. Genet.* 253:32-41 (1996), the entirety of which is herein incorporated by reference), *Escherichia coli* (Lin, *et al.*, *Nucleic Acids Res.* 24:3649-3650 (1996), the entirety of which is herein incorporated by reference), *Aeromonas* (Huys, *et al.*, *Int. J. Syst. Bacteriol.* 46:572-580 (1996), the entirety of which is herein incorporated by reference), nematode (Folkertsma, *et al.*, *Mol. Plant Microbe Interact.* 9:47-54 (1996), the

entirety of which is herein incorporated by reference), tomato (Thomas, *et al.*, *Plant J.* 8:785-794 (1995), the entirety of which is herein incorporated by reference), and human (Latorra, *et al.*, *PCR Methods Appl.* 3:351-358 (1994) the entirety of which is herein incorporated by reference). AFLP analysis has also been used for fingerprinting mRNA (Money, *et al.*, *Nucleic Acids Res.* 24:2616-2617 (1996), the entirety of which is herein incorporated by reference; Bachem, *et al.*, *Plant J.* 9:745-753 (1996), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acid molecules of the present invention, may be utilized as markers or probes to detect polymorphisms by AFLP analysis for fingerprinting mRNA.

Polymorphisms may also be found using random amplified polymorphic DNA (RAPD) (Williams *et al.*, *Nucl. Acids Res.* 18:6531-6535 (1990), the entirety of which is herein incorporated by reference) and cleavable amplified polymorphic sequences (CAPS) (Lyamichev *et al.*, *Science* 260:778-783 (1993), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acid molecules of the present invention, may be utilized as markers or probes to detect polymorphisms by RAPD or CAPS analysis.

Nucleic acid molecules of the present invention can be used to monitor expression. A microarray-based method for high-throughput monitoring of plant gene expression may be utilized to measure gene-specific hybridization targets. This 'chip'-based approach involves using microarrays of nucleic acid molecules as gene-specific hybridization targets to quantitatively measure expression of the corresponding plant genes (Schena *et al.*, *Science* 270:467-470 (1995), the entirety of which is herein incorporated by reference; Shalon, Ph.D. Thesis. Stanford University (1996), the entirety of which is herein incorporated by reference).

Every nucleotide in a large sequence can be queried at the same time. Hybridization can be used to efficiently analyze nucleotide sequences.

Several microarray methods have been described. One method compares the sequences to be analyzed by hybridization to a set of oligonucleotides or cDNA molecules representing all possible subsequences (Bains and Smith, *J. Theor. Biol.* 135:303 (1989), the entirety of which is herein incorporated by reference). A second method hybridizes the sample to an array of oligonucleotide or cDNA probes. An array consisting of oligonucleotides or cDNA molecules complementary to subsequences of a target sequence can be used to determine the identity of a target sequence, measure its amount, and detect differences between the target and a reference sequence. Nucleic acid molecule microarrays may also be screened with protein molecules or fragments thereof to determine nucleic acid molecules that specifically bind protein molecules or fragments thereof.

Additionally, microarrays of BACs may be prepared to sufficiently cover 3X of an entire genome. Such microarrays can be used in a variety of genomics experiments including gene mapping, DNA fingerprinting and promoter identification. Microarrays of genomic DNA can also be used for parallel analysis of genomes at single gene resolution (Lemieux *et al.*, *Molecular Breeding* 277-289 (1988), the entirety of which is herein incorporated by reference). It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a genomic microarray based method. In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a genomic microarray based method. For example, Genomic Mismatch Scanning (GMS), a hybridization-based method of

linkage analysis that allows rapid identification of regions of identity-by-descent between two related individuals, can be carried out with microarrays. GMS is reported to have been used to identify genetically common chromosomal segments based on the ability of these DNA sequences to form extensive regions of mismatch-free heteroduplexes. A series of enzymatic steps, coupled with filter binding, is used to selectively remove heteroduplexes that contain mismatches (i.e., chromosomal regions that do not share identity-by descent.). Fragments of chromosomal DNA representing inherited regions are hybridized to a microarray of ordered genomic clones and positive hybridization signals pinpoint regions of identity-by-descent at high resolution (Lemieux *et al.*, *Molecular Breeding* 277-289 (1988))

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to locate regions of identity-by-descent between related individuals. In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to locate regions of identity-by-descent between related individuals. The GMS microarray approach can also be used as a tool to map mutigenic traits. For example, in yeast, the entire genomic sequence is known and it has been reported that the genes responsible for growth at elevated temperature, a trait required for the pathogenicity of certain yeast strains, may be determined using GMS (Lemieux *et al.*, *Molecular Breeding* 277-289 (1988)). By analyzing the inheritance of large numbers of tetrads derived from crosses of pathogenic and wild type strains, all the genes responsible for a yeast strain's ability to grow at 42°C, for example, could be identified.

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to map multigenic traits. In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to map multigenic traits.

Plant repeat elements may be used with GMS microarraying to identify species specific chromosomes in another species background. For example, the maize genome contains moderately repetitive DNA sequences (ZLRS) representing about 2500 copies per haploid genome; these sequences are present in the genus *Zea* and absent in other graminaceous species. Ananiev *et al.*, (*Proc. Natl. Acad. Sci. (U.S.A.)* 94:3526-3529 (1997)), all of which are herein incorporated by reference in their entirety) have reported unusual plants with individual maize chromosomes added to a complete oat genome generated by embryo rescue from oat (*Avena sativa*) x *Zea mays* crosses. By using highly repetitive maize-specific sequences as probes, Ananiev *et al.* (1997) were able to selectively isolate cosmid clones containing maize genomic DNA.

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method using repeat elements to selectively isolate clones containing species specific DNA. In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to selectively isolate clones containing species specific DNA. A particular preferred microarray

embodiment of the present invention is a microarray comprising nucleic acid molecules encoding genes that are homologues of known genes or nucleic acid molecules that comprise genes or fragments thereof that elicit only limited or no matches to known genes. A further preferred microarray embodiment of the present invention is a microarray comprising nucleic acid molecules encoding genes or fragments thereof that are homologues of known genes and nucleic acid molecules that comprise genes or fragments thereof that elicit only limited or no matches to known genes. A further preferred microarray embodiment of the present invention is a microarray comprising nucleic acid molecules encoding genes or fragments thereof that elicit only limited or no matches to known genes.

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a microarray based method. In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or protein molecules or fragments thereof of the present invention set forth in Table 1 may be utilized in a microarray based method.

Nucleic acid molecules of the present invention may be used in site directed mutagenesis. Site-directed mutagenesis may be utilized to modify nucleic acid sequences, particularly as it is a technique that allows one or more of the amino acids encoded by a nucleic acid molecule to be altered (e.g. a threonine to be replaced by a methionine). Three basic methods for site-directed mutagenesis are often employed. These are cassette mutagenesis (Wells *et al.*, *Gene* 34:315-23 (1985), the entirety of which is herein incorporated by reference), primer extension (Gilliam *et al.*, *Gene* 12:129-137 (1980), the entirety of which is herein incorporated by reference); Zoller and Smith, *Methods Enzymol.* 100:468-500 (1983), the entirety of which is herein incorporated

by reference; and Dalbadie-McFarland *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.)* 79:6409-6413 (1982), the entirety of which is herein incorporated by reference) and methods based upon PCR (Scharf *et al.*, *Science* 233:1076-1078 (1986), the entirety of which is herein incorporated by reference; Higuchi *et al.*, *Nucleic Acids Res.* 16:7351-7367 (1988), the entirety of which is herein incorporated by reference). Site-directed mutagenesis approaches are also described in European Patent 0 385 962, the entirety of which is herein incorporated by reference, European Patent 0 359 472, the entirety of which is herein incorporated by reference, and PCT Patent Application WO 93/07278, the entirety of which is herein incorporated by reference.

Site-directed mutagenesis strategies have been applied to plants for both *in vitro* as well as *in vivo* site-directed mutagenesis (Lanz *et al.*, *J. Biol. Chem.* 266:9971-6 (1991), the entirety of which is herein incorporated by reference; Kovgan and Zhdanov, *Biotechnologiya* 5:148-154, No. 207160n, Chemical Abstracts 110:225 (1989), the entirety of which is herein incorporated by reference; Ge *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 86:4037-4041 (1989), the entirety of which is herein incorporated by reference, Zhu *et al.*, *J. Biol. Chem.* 271:18494-18498 (1996), Chu *et al.*, *Biochemistry* 33:6150-6157 (1994), the entirety of which is herein incorporated by reference, Small *et al.*, *EMBO J.* 11:1291-1296 (1992), the entirety of which is herein incorporated by reference, Cho *et al.*, *Mol. Biotechnol.* 8:13-16 (1997), Kita *et al.*, *J. Biol. Chem.* 271:26529-26535 (1996), the entirety of which is herein incorporated by reference, Jin *et al.*, *Mol. Microbiol.* 7:555-562 (1993), the entirety of which is herein incorporated by reference, Hatfield and Vierstra, *J. Biol. Chem.* 267:14799-14803 (1992), the entirety of which is herein incorporated by reference, Zhao *et al.*, *Biochemistry* 31:5093-5099 (1992), the entirety of which is herein incorporated by reference).

Any of the nucleic acid molecules of the present invention may either be modified by site-directed mutagenesis or used as, for example, nucleic acid molecules that are used to target other nucleic acid molecules for modification. It is understood that mutants with more than one altered nucleotide can be constructed using techniques that practitioners skilled in the art are familiar with such as isolating restriction fragments and ligating such fragments into an expression vector (see, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989)). In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or fragments thereof of the present invention may be modified by site-directed mutagenesis.

Nucleic acid molecules of the present invention may be used in transformation. Exogenous genetic material may be transferred into a plant cell and the plant cell regenerated into a whole, fertile or sterile plant. Exogenous genetic material is any genetic material, whether naturally occurring or otherwise, from any source that is capable of being inserted into any organism. In a preferred embodiment of the present invention the exogenous genetic material can include *Glycine max* genetic material. In a preferred embodiment of the present invention, the exogenous genetic material comprises a nucleic acid molecule of the present invention. Such genetic material may be transferred into either monocotyledons and dicotyledons including but not limited to the plants, *Zea mays* and *Arabidopsis thaliana* and soybean (See specifically, Chistou, *Particle Bombardment for Genetic Engineering of Plants*, pp. 63-69 (*Zea mays*), pp50-60 (soybean), Biotechnology Intelligence Unit, Academic Press, San Diego, California (1996), the entirety of which is herein incorporated by reference and generally Chistou, *Particle Bombardment for Genetic Engineering of Plants*, Biotechnology Intelligence Unit, Academic Press, San Diego, California (1996), the entirety of which is herein incorporated by reference).

Transfer of a nucleic acid that encodes for a protein can result in overexpression of that protein in a transformed cell or transgenic plant. One or more of the proteins or fragments thereof encoded by nucleic acid molecules of the present invention may be overexpressed in a transformed cell or transformed plant. Such overexpression may be the result of transient or stable transfer of the exogenous material.

Exogenous genetic material may be transferred into a plant cell by the use of a DNA vector or construct designed for such a purpose. Vectors have been engineered for transformation of large DNA inserts into plant genomes. Vectors have been designed to replicate in both *E. coli* and *A. tumefaciens* and have all of the features required for transferring large inserts of DNA into plant chromosomes (Choi and Wing, <http://genome.clemson.edu/protocols2-nj.html> July, 1998). ApBACwch system has been developed to achieve site-directed integration of DNA into the genome. A 150 kb cotton BAC DNA is reported to have been transferred into a specific *lox* site in tobacco by biolistic bombardment and *Cre-lox* site specific recombination.

A construct or vector may include a plant promoter to express the protein or protein fragment of choice. A number of promoters which are active in plant cells have been described in the literature. These include the nopaline synthase (NOS) promoter (Ebert *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 84:5745-5749 (1987), the entirety of which is herein incorporated by reference), the octopine synthase (OCS) promoter (which are carried on tumor-inducing plasmids of *Agrobacterium tumefaciens*), the caulimovirus promoters such as the cauliflower mosaic virus (CaMV) 19S promoter (Lawton *et al.*, *Plant Mol. Biol.* 9:315-324 (1987), the entirety of which is herein incorporated by reference) and the CAMV 35S promoter (Odell *et al.*, *Nature* 313:810-812 (1985), the entirety of which is herein incorporated by reference), the figwort mosaic virus 35S-promoter, the light-inducible promoter from the small subunit of ribulose-1,5-bis-phosphate

carboxylase (ssRUBISCO), the Adh promoter (Walker *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 84:6624-6628 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase promoter (Yang *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 87:4144-4148 (1990), the entirety of which is herein incorporated by reference), the R gene complex promoter (Chandler *et al.*, *The Plant Cell* 1:1175-1183 (1989), the entirety of which is herein incorporated by reference), and the chlorophyll a/b binding protein gene promoter, etc. These promoters have been used to create DNA constructs which have been expressed in plants; *see, e.g.*, PCT publication WO 84/02913, herein incorporated by reference in its entirety.

Promoters which are known or are found to cause transcription of DNA in plant cells can be used in the present invention. Such promoters may be obtained from a variety of sources such as plants and plant viruses. It is preferred that the particular promoter selected should be capable of causing sufficient expression to result in the production of an effective amount of protein to cause the desired phenotype. In addition to promoters which are known to cause transcription of DNA in plant cells, other promoters may be identified for use in the current invention by screening a plant cDNA library for genes which are selectively or preferably expressed in the target tissues or cells.

For the purpose of expression in source tissues of the plant, such as the leaf, seed, root or stem, it is preferred that the promoters utilized in the present invention have relatively high expression in these specific tissues. For this purpose, one may choose from a number of promoters for genes with tissue- or cell-specific or -enhanced expression. Examples of such promoters reported in the literature include the chloroplast glutamine synthetase GS2 promoter from pea (Edwards *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 87:3459-3463 (1990), herein incorporated by reference in its entirety), the chloroplast fructose-1,6-biphosphatase (FBPase)

promoter from wheat (Lloyd *et al.*, *Mol. Gen. Genet.* 225:209-216 (1991), herein incorporated by reference in its entirety), the nuclear photosynthetic ST-LS1 promoter from potato (Stockhaus *et al.*, *EMBO J.* 8:2445-2451 (1989), herein incorporated by reference in its entirety), the phenylalanine ammonia-lyase (PAL) promoter and the chalcone synthase (CHS) promoter from *Arabidopsis thaliana*. Also reported to be active in photosynthetically active tissues are the ribulose-1,5-bisphosphate carboxylase (RbcS) promoter from eastern larch (*Larix laricina*), the promoter for the *cab* gene, *cab6*, from pine (Yamamoto *et al.*, *Plant Cell Physiol.* 35:773-778 (1994), herein incorporated by reference in its entirety), the promoter for the *Cab-1* gene from wheat (Fejes *et al.*, *Plant Mol. Biol.* 15:921-932 (1990), herein incorporated by reference in its entirety), the promoter for the *CAB-1* gene from spinach (Lubberstedt *et al.*, *Plant Physiol.* 104:997-1006 (1994), herein incorporated by reference in its entirety), the promoter for the *cab1R* gene from rice (Luan *et al.*, *Plant Cell.* 4:971-981 (1992), the entirety of which is herein incorporated by reference), the pyruvate, orthophosphate dikinase (PPDK) promoter from *Zea mays* (Matsuoka *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.)* 90:9586-9590 (1993), herein incorporated by reference in its entirety), the promoter for the tobacco *Lhcb1*2* gene (Cerdan *et al.*, *Plant Mol. Biol.* 33:245-255. (1997), herein incorporated by reference in its entirety), the *Arabidopsis thaliana* *SUC2* sucrose-H⁺ symporter promoter (Truernit *et al.*, *Planta.* 196:564-570 (1995), herein incorporated by reference in its entirety), and the promoter for the thylacoid membrane proteins from spinach (*psaD*, *psaF*, *psaE*, *PC*, *FNR*, *atpC*, *atpD*, *cab*, *rbcS*). Other promoters for the chlorophyll *a/b*-binding proteins may also be utilized in the present invention, such as the promoters for *Lhcb* gene and *PsbP* gene from white mustard (*Sinapis alba*; Kretsch *et al.*, *Plant Mol. Biol.* 28:219-229 (1995), the entirety of which is herein incorporated by reference).

For the purpose of expression in sink tissues of the plant, such as the tuber of the potato plant, the fruit of tomato, or the seed of *Zea mays*, wheat, rice, and barley, it is preferred that the promoters utilized in the present invention have relatively high expression in these specific tissues. A number of promoters for genes with tuber-specific or -enhanced expression are known, including the class I patatin promoter (Bevan *et al.*, *EMBO J.* 8:1899-1906 (1986); Jefferson *et al.*, *Plant Mol. Biol.* 14:995-1006 (1990), both of which are herein incorporated by reference in its entirety), the promoter for the potato tuber ADPGPP genes, both the large and small subunits, the sucrose synthase promoter (Salanoubat and Belliard, *Gene*. 60:47-56 (1987), Salanoubat and Belliard, *Gene*. 84:181-185 (1989), both of which are incorporated by reference in their entirety), the promoter for the major tuber proteins including the 22 kd protein complexes and proteinase inhibitors (Hannapel, *Plant Physiol.* 101:703-704 (1993), herein incorporated by reference in its entirety), the promoter for the granule bound starch synthase gene (GBSS) (Visser *et al.*, *Plant Mol. Biol.* 17:691-699 (1991), herein incorporated by reference in its entirety), and other class I and II patatins promoters (Koster-Topfer *et al.*, *Mol. Gen. Genet.* 219:390-396 (1989); Mignery *et al.*, *Gene*. 62:27-44 (1988), both of which are herein incorporated by reference in their entirety).

Other promoters can also be used to express a fructose 1,6 biphosphate aldolase gene in specific tissues, such as seeds or fruits. The promoter for β -conglycinin (Chen *et al.*, *Dev. Genet.* 10:112-122 (1989), herein incorporated by reference in its entirety) or other seed-specific promoters such as the napin and phaseolin promoters, can be used. The zeins are a group of storage proteins found in *Zea mays* endosperm. Genomic clones for zein genes have been isolated (Pedersen *et al.*, *Cell* 29:1015-1026 (1982), herein incorporated by reference in its entirety), and the promoters from these clones, including the 15 kD, 16 kD, 19 kD, 22 kD, 27 kD,

and gamma genes, could also be used. Other promoters known to function, for example, in *Zea mays*, include the promoters for the following genes: *waxy*, *Brittle*, *Shrunken 2*, Branching enzymes I and II, starch synthases, debranching enzymes, oleosins, glutelins, and sucrose synthases. A particularly preferred promoter for *Zea mays* endosperm expression is the promoter for the glutelin gene from rice, more particularly the Osgt-1 promoter (Zheng *et al.*, *Mol. Cell Biol.* 13:5829-5842 (1993), herein incorporated by reference in its entirety). Examples of promoters suitable for expression in wheat include those promoters for the ADPglucose pyrophosphorylase (ADPGPP) subunits, the granule bound and other starch synthases, the branching and debranching enzymes, the embryogenesis-abundant proteins, the gliadins, and the glutenins. Examples of such promoters in rice include those promoters for the ADPGPP subunits, the granule bound and other starch synthases, the branching enzymes, the debranching enzymes, sucrose synthases, and the glutelins. A particularly preferred promoter is the promoter for rice glutelin, Osgt-1. Examples of such promoters for barley include those for the ADPGPP subunits, the granule bound and other starch synthases, the branching enzymes, the debranching enzymes, sucrose synthases, the hordeins, the embryo globulins, and the aleurone specific proteins.

Root specific promoters may also be used. An example of such a promoter is the promoter for the acid chitinase gene (Samac *et al.*, *Plant Mol. Biol.* 25:587-596 (1994), the entirety of which is herein incorporated by reference). Expression in root tissue could also be accomplished by utilizing the root specific subdomains of the CaMV35S promoter that have been identified (Lam *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.)* 86:7890-7894 (1989), herein incorporated by reference in its entirety). Other root cell specific promoters include those

reported by Conkling *et al.* (Conkling *et al.*, *Plant Physiol.* 93:1203-1211 (1990), the entirety of which is herein incorporated by reference).

Additional promoters that may be utilized are described, for example, in U.S. Patent Nos. 5,378,619, 5,391,725, 5,428,147, 5,447,858, 5,608,144, 5,608,144, 5,614,399, 5,633,441, 5,633,435, and 4,633,436, all of which are herein incorporated in their entirety. In addition, a tissue specific enhancer may be used (Fromm *et al.*, *The Plant Cell* 1:977-984 (1989), the entirety of which is herein incorporated by reference).

Constructs or vectors may also include, with the coding region of interest, a nucleic acid sequence that acts, in whole or in part, to terminate transcription of that region. For example, such sequences have been isolated including the Tr7 3' sequence and the nos 3' sequence (Ingelbrecht *et al.*, *The Plant Cell* 1:671-680 (1989), the entirety of which is herein incorporated by reference; Bevan *et al.*, *Nucleic Acids Res.* 11:369-385 (1983), the entirety of which is herein incorporated by reference), or the like.

A vector or construct may also include regulatory elements. Examples of such include the Adh intron 1 (Callis *et al.*, *Genes and Develop.* 1:1183-1200 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase intron (Vasil *et al.*, *Plant Physiol.* 91:1575-1579 (1989), the entirety of which is herein incorporated by reference) and the TMV omega element (Gallie *et al.*, *The Plant Cell* 1:301-311 (1989), the entirety of which is herein incorporated by reference). These and other regulatory elements may be included when appropriate.

A vector or construct may also include a selectable marker. Selectable markers may also be used to select for plants or plant cells that contain the exogenous genetic material. Examples of such include, but are not limited to, a neo gene (Potrykus *et al.*, *Mol. Gen. Genet.* 199:183-188

(1985), the entirety of which is herein incorporated by reference) which codes for kanamycin resistance and can be selected for using kanamycin, G418, etc.; a bar gene which codes for bialaphos resistance; a mutant EPSP synthase gene (Hinchee *et al.*, *Bio/Technology* 6:915-922 (1988), the entirety of which is herein incorporated by reference) which encodes glyphosate resistance; a nitrilase gene which confers resistance to bromoxynil (Stalker *et al.*, *J. Biol. Chem.* 263:6310-6314 (1988), the entirety of which is herein incorporated by reference); a mutant acetolactate synthase gene (ALS) which confers imidazolinone or sulphonylurea resistance (European Patent Application 154,204 (Sept. 11, 1985), the entirety of which is herein incorporated by reference); and a methotrexate resistant DHFR gene (Thillet *et al.*, *J. Biol. Chem.* 263:12500-12508 (1988), the entirety of which is herein incorporated by reference).

A vector or construct may also include a transit peptide. Incorporation of a suitable chloroplast transit peptide may also be employed (European Patent Application Publication Number 0218571, the entirety of which is herein incorporated by reference). Translational enhancers may also be incorporated as part of the vector DNA. DNA constructs could contain one or more 5' non-translated leader sequences which may serve to enhance expression of the gene products from the resulting mRNA transcripts. Such sequences may be derived from the promoter selected to express the gene or can be specifically modified to increase translation of the mRNA. Such regions may also be obtained from viral RNAs, from suitable eukaryotic genes, or from a synthetic gene sequence. For a review of optimizing expression of transgenes, see Koziel *et al.*, *Plant Mol. Biol.* 32:393-405 (1996), the entirety of which is herein incorporated by reference.

A vector or construct may also include a screenable marker. Screenable markers may be used to monitor expression. Exemplary screenable markers include a β -glucuronidase or uidA

gene (GUS) which encodes an enzyme for which various chromogenic substrates are known (Jefferson, *Plant Mol. Biol. Rep.* 5:387-405 (1987), the entirety of which is herein incorporated by reference; Jefferson *et al.*, *EMBO J.* 6:3901-3907 (1987), the entirety of which is herein incorporated by reference); an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues ((Dellaporta *et al.*, *Stadler Symposium 11*:263-282 (1988), the entirety of which is herein incorporated by reference); a β -lactamase gene (Sutcliffe *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.)* 75:3737-3741 (1978), the entirety of which is herein incorporated by reference), a gene which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a luciferase gene (Ow *et al.*, *Science* 234:856-859 (1986), the entirety of which is herein incorporated by reference) a xylE gene (Zukowsky *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.)* 80:1101-1105 (1983), the entirety of which is herein incorporated by reference) which encodes a catechol dioxygenase that can convert chromogenic catechols; an α -amylase gene (Ikata *et al.*, *Bio/Technol.* 8:241-242 (1990), the entirety of which is herein incorporated by reference); a tyrosinase gene (Katz *et al.*, *J. Gen. Microbiol.* 129:2703-2714 (1983), the entirety of which is herein incorporated by reference) which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to melanin; an α -galactosidase, which will turn a chromogenic α -galactose substrate.

Included within the terms "selectable or screenable marker genes" are also genes which encode a secretable marker whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected catalytically. Secretable proteins fall into a number of classes, including small, diffusible

proteins detectable, *e.g.*, by ELISA, small active enzymes detectable in extracellular solution (*e.g.*, α -amylase, β -lactamase, phosphinothricin transferase), or proteins which are inserted or trapped in the cell wall (such as proteins which include a leader sequence such as that found in the expression unit of extension or tobacco PR-S). Other possible selectable and/or screenable marker genes will be apparent to those of skill in the art.

Methods and compositions for transforming a bacteria and other microorganisms are known in the art (see for example Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1989), the entirety of which is herein incorporated by reference).

There are many methods for introducing transforming nucleic acid molecules into plant cells. Suitable methods are believed to include virtually any method by which nucleic acid molecules may be introduced into a cell, such as by *Agrobacterium* infection or direct delivery of nucleic acid molecules such as, for example, by PEG-mediated transformation, by electroporation or by acceleration of DNA coated particles, etc. (Pottyskus, *Ann. Rev. Plant Physiol. Plant Mol. Biol.* 42:205-225 (1991), the entirety of which is herein incorporated by reference; Vasil, *Plant Mol. Biol.* 25:925-937 (1994), the entirety of which is herein incorporated by reference. For example, electroporation has been used to transform *Zea mays* protoplasts (Fromm *et al.*, *Nature* 312:791-793 (1986), the entirety of which is herein incorporated by reference).

Technology for introduction of DNA into cells is well known to those of skill in the art. Four general methods for delivering a gene into cells have been described: (1) chemical methods (Graham and van der Eb, *Virology*, 54:536-539 (1973), the entirety of which is herein incorporated by reference); (2) physical methods such as microinjection (Capecchi, *Cell* 22:479-

488 (1980), electroporation (Wong and Neumann, *Biochem. Biophys. Res. Commun.*, 107:584-587 (1982); Fromm *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.)*, 82:5824-5828 (1985); U.S. Patent No. 5,384,253; and the gene gun (Johnston and Tang, *Methods Cell Biol.* 43:353-365 (1994), all of which the entirety is herein incorporated by reference; (3) viral vectors (Clapp, *Clin. Perinatol.*, 20:155-168 (1993); Lu *et al.*, *J. Exp. Med.*, 178:2089-2096 (1993); Eglitis and Anderson, *Biotechniques*, 6:608-614 (1988), all of which the entirety is herein incorporated by reference); and (4) receptor-mediated mechanisms (Curiel *et al.*, *Hum. Gen. Ther.*, 3:147-154 (1992); Wagner *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, 89:6099-6103 (1992), all of which the entirety is herein incorporated by reference).

Acceleration methods that may be used include, for example, microprojectile bombardment and the like. One example of a method for delivering transforming nucleic acid molecules to plant cells is microprojectile bombardment. This method has been reviewed by Yang and Christou, eds., *Particle Bombardment Technology for Gene Transfer*, Oxford Press, Oxford, England (1994), the entirety of which is herein incorporated by reference). Non-biological particles (microprojectiles) that may be coated with nucleic acids and delivered into cells by a propelling force. Exemplary particles include those comprised of tungsten, gold, platinum, and the like.

A particular advantage of microprojectile bombardment, in addition to it being an effective means of reproducibly, and stably transforming monocotyledons, is that neither the isolation of protoplasts (Cristou *et al.*, *Plant Physiol.* 87:671-674 (1988), the entirety of which is herein incorporated by reference) nor the susceptibility of *Agrobacterium* infection is required. An illustrative embodiment of a method for delivering DNA into maize cells by acceleration is a biolistics-particle delivery system, which can be used to propel particles coated with DNA

through a screen, such as a stainless steel or Nytex screen, onto a filter surface covered with corn cells cultured in suspension. Gordon-Kamm *et al.*, describes the basic procedure for coating tungsten particles with DNA (Gordon-Kamm *et al.*, *Plant Cell* 2:603-618 (1990), the entirety of which is herein incorporated by reference). The screen disperses the tungsten nucleic acid particles so that they are not delivered to the recipient cells in large aggregates. A particle delivery system suitable for use with the present invention is the helium acceleration PDS-1000/He gun which is available from Bio-Rad Laboratories (Bio-Rad, Hercules, California)(Sanford *et al.*, *Technique* 3:3-16 (1991), the entirety of which is herein incorporated by reference).

For the bombardment, cells in suspension may be concentrated on filters. Filters containing the cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the gun and the cells to be bombarded.

Alternatively, immature embryos or other target cells may be arranged on solid culture medium. The cells to be bombarded are positioned at an appropriate distance below the macroprojectile stopping plate. If desired, one or more screens are also positioned between the acceleration device and the cells to be bombarded. Through the use of techniques set forth herein one may obtain up to 1000 or more foci of cells transiently expressing a marker gene. The number of cells in a focus which express the exogenous gene product 48 hours post-bombardment often range from one to ten and average one to three.

In bombardment transformation, one may optimize the prebombardment culturing conditions and the bombardment parameters to yield the maximum numbers of stable transformants. Both the physical and biological parameters for bombardment are important in

this technology. Physical factors are those that involve manipulating the DNA/microprojectile precipitate or those that affect the flight and velocity of either the macro- or microprojectiles. Biological factors include all steps involved in manipulation of cells before and immediately after bombardment, the osmotic adjustment of target cells to help alleviate the trauma associated with bombardment, and also the nature of the transforming DNA, such as linearized DNA or intact supercoiled plasmids. It is believed that pre-bombardment manipulations are especially important for successful transformation of immature embryos.

In another alternative embodiment, plastids can be stably transformed. Methods disclosed for plastid transformation in higher plants include particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination (Svab *et al. Proc. Natl. Acad. Sci. (U.S.A.)* 87:8526-8530 (1990); Svab and Maliga *Proc. Natl. Acad. Sci. (U.S.A.)* 90:913-917 (1993)); (Staub, J.M. and Maliga, P. *EMBO J.* 12:601-606 (1993), U.S. Patents 5,451,513 and 5,545,818 all of which are herein incorporated by reference in their entirety).

Accordingly, it is contemplated that one may wish to adjust various aspects of the bombardment parameters in small scale studies to fully optimize the conditions. One may particularly wish to adjust physical parameters such as gap distance, flight distance, tissue distance, and helium pressure. One may also minimize the trauma reduction factors by modifying conditions which influence the physiological state of the recipient cells and which may therefore influence transformation and integration efficiencies. For example, the osmotic state, tissue hydration and the subculture stage or cell cycle of the recipient cells may be adjusted for optimum transformation. The execution of other routine adjustments will be known to those of skill in the art in light of the present disclosure.

Agrobacterium-mediated transfer is a widely applicable system for introducing genes into plant cells because the DNA can be introduced into whole plant tissues, thereby bypassing the need for regeneration of an intact plant from a protoplast. The use of *Agrobacterium*-mediated plant integrating vectors to introduce DNA into plant cells is well known in the art. See, for example the methods described (Fraley *et al.*, *Biotechnology* 3:629-635 (1985); Rogers *et al.*, *Meth. In Enzymol.*, 153:253-277 (1987), both of which are herein incorporated by reference in their entirety. Further, the integration of the Ti-DNA is a relatively precise process resulting in few rearrangements. The region of DNA to be transferred is defined by the border sequences, and intervening DNA is usually inserted into the plant genome as described (Spielmann *et al.*, *Mol. Gen. Genet.*, 205:34 (1986), the entirety of which is herein incorporated by reference).

Modern *Agrobacterium* transformation vectors are capable of replication in *E. coli* as well as *Agrobacterium*, allowing for convenient manipulations as described (Klee *et al.*, *In: Plant DNA Infectious Agents*, T. Hohn and J. Schell, eds., Springer-Verlag, New York, pp. 179-203 (1985), the entirety of which is herein incorporated by reference. Moreover, recent technological advances in vectors for *Agrobacterium*-mediated gene transfer have improved the arrangement of genes and restriction sites in the vectors to facilitate construction of vectors capable of expressing various polypeptide coding genes. The vectors described have convenient multi-linker regions flanked by a promoter and a polyadenylation site for direct expression of inserted polypeptide coding genes and are suitable for present purposes (Rogers *et al.*, *Meth. In Enzymol.*, 153:253-277 (1987), the entirety of which is herein incorporated by reference). In addition, *Agrobacterium* containing both armed and disarmed Ti genes can be used for the transformations. In those plant strains where *Agrobacterium*-mediated transformation is efficient, it is the method of choice because of the facile and defined nature of the gene transfer.

A transgenic plant formed using *Agrobacterium* transformation methods typically contains a single gene on one chromosome. Such transgenic plants can be referred to as being heterozygous for the added gene. More preferred is a transgenic plant that is homozygous for the added structural gene; *i.e.*, a transgenic plant that contains two added genes, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) an independent segregant transgenic plant that contains a single added gene, germinating some of the seed produced and analyzing the resulting plants produced for the gene of interest.

It is also to be understood that two different transgenic plants can also be mated to produce offspring that contain two independently segregating added, exogenous genes. Selfing of appropriate progeny can produce plants that are homozygous for both added, exogenous genes that encode a polypeptide of interest. Back-crossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated, as is vegetative propagation.

Transformation of plant protoplasts can be achieved using methods based on calcium phosphate precipitation, polyethylene glycol treatment, electroporation, and combinations of these treatments. See for example (Potrykus *et al.*, *Mol. Gen. Genet.*, 205:193-200 (1986); Lorz *et al.*, *Mol. Gen. Genet.*, 199:178, (1985); Fromm *et al.*, *Nature*, 319:791,(1986); Uchimiya *et al.*, *Mol. Gen. Genet.*:204:204, (1986); Callis *et al.*, *Genes and Development*, 1183,(1987); Marcotte *et al.*, *Nature*, 335:454, (1988), all of which the entirety is herein incorporated by reference).

Application of these systems to different plant strains depends upon the ability to regenerate that particular plant strain from protoplasts. Illustrative methods for the regeneration of cereals from protoplasts are described (Fujimura *et al.*, *Plant Tissue Culture Letters*, 2:74,(1985); Toriyama *et al.*, *Theor Appl. Genet.* 205:34. (1986); Yamada *et al.*, *Plant Cell Rep.*,

4:85, (1986); Abdullah *et al.*, *Biotechnology*, 4:1087, (1986), all of which the entirety is herein incorporated by reference).

To transform plant strains that cannot be successfully regenerated from protoplasts, other ways to introduce DNA into intact cells or tissues can be utilized. For example, regeneration of cereals from immature embryos or explants can be effected as described (Vasil, *Biotechnology*, 6:397, (1988), the entirety of which is herein incorporated by reference). In addition, "particle gun" or high-velocity microprojectile technology can be utilized (Vasil *et al.*, *Bio/Technology* 10:667, (1992), the entirety of which is herein incorporated by reference).

Using the latter technology, DNA is carried through the cell wall and into the cytoplasm on the surface of small metal particles as described (Klein *et al.*, *Nature*, 328:70, (1987); Klein *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.)*, 85:8502-8505, (1988); McCabe *et al.*, *Biotechnology*, 6:923, (1988), all of which the entirety is herein incorporated by reference). The metal particles penetrate through several layers of cells and thus allow the transformation of cells within tissue explants.

Other methods of cell transformation can also be used and include but are not limited to introduction of DNA into plants by direct DNA transfer into pollen (Zhou *et al.*, *Methods in Enzymology*, 101:433, (1983); Hess *et al.*, *Intern Rev. Cytol.*, 107:367, (1987); Luo *et al.*, *Plant Mol. Biol. Reporter*, 6:165, (1988), all of which the entirety is herein incorporated by reference), by direct injection of DNA into reproductive organs of a plant (Pena *et al.*, *Nature*, 325:274, (1987), the entirety of which is herein incorporated by reference), or by direct injection of DNA into the cells of immature embryos followed by the rehydration of dessicated embryos (Neuhaus *et al.*, *Theor. Appl. Genet.*, 75:30, (1987), the entirety of which is herein incorporated by reference).

The regeneration, development, and cultivation of plants from single plant protoplast transformants or from various transformed explants is well known in the art (Weissbach and Weissbach, *In: Methods for Plant Molecular Biology*, (Eds.), Academic Press, Inc., San Diego, CA, (1988), the entirety of which is herein incorporated by reference). This regeneration and growth process typically includes the steps of selection of transformed cells, culturing those individualized cells through the usual stages of embryonic development through the rooted plantlet stage. Transgenic embryos and seeds are similarly regenerated. The resulting transgenic rooted shoots are thereafter planted in an appropriate plant growth medium such as soil.

The development or regeneration of plants containing the foreign, exogenous gene that encodes a protein of interest is well known in the art. Preferably, the regenerated plants are self-pollinated to provide homozygous transgenic plants, as discussed before. Otherwise, pollen obtained from the regenerated plants is crossed to seed-grown plants of agronomically important lines. Conversely, pollen from plants of these important lines is used to pollinate regenerated plants. A transgenic plant of the present invention containing a desired polypeptide is cultivated using methods well known to one skilled in the art.

There are a variety of methods for the regeneration of plants from plant tissue. The particular method of regeneration will depend on the starting plant tissue and the particular plant species to be regenerated.

Methods for transforming dicots, primarily by use of *Agrobacterium tumefaciens*, and obtaining transgenic plants have been published for cotton (U.S. Patent No. 5,004,863, U.S. Patent No. 5,159,135, U.S. Patent No. 5,518,908, all of which the entirety is herein incorporated by reference); soybean (U.S. Patent No. 5,569,834, U.S. Patent No. 5,416,011, McCabe *et al.*, *Biotechnology* 6:923, (1988), Christou *et al.*, *Plant Physiol.*, 87:671-674 (1988), all of which the

entirety is herein incorporated by reference); *Brassica* (U.S. Patent No. 5,463,174, the entirety of which is herein incorporated by reference); peanut (Cheng *et al.*, *Plant Cell Rep.* 15:653-657 (1996), McKently *et al.*, *Plant Cell Rep.* 14:699-703 (1995), all of which the entirety is herein incorporated by reference); papaya (Yang *et al.*, (1996), the entirety of which is herein incorporated by reference); pea (Grant *et al.*, *Plant Cell Rep.* 15:254-258, (1995), the entirety of which is herein incorporated by reference).

Transformation of monocotyledons using electroporation, particle bombardment, and *Agrobacterium* have also been reported. Transformation and plant regeneration have been achieved in asparagus (Bytebier *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.)* 84:5345, (1987), the entirety of which is herein incorporated by reference); barley (Wan and Lemaux, *Plant Physiol* 104:37, (1994), the entirety of which is herein incorporated by reference); maize (Rhodes *et al.*, *Science* 240:204, (1988), Gordon-Kamm *et al.*, *Plant Cell*, 2:603, (1990), Fromm *et al.*, *Bio/Technology* 8:833, (1990), Koziel *et al.*, *Bio/Technology* 11:194, (1993), Armstrong *et al.*, *Crop Science* 35:550-557, (1995), all of which the entirety is herein incorporated by reference); oat (Somers *et al.*, *Bio/Technology*, 10:1589, (1992), the entirety of which is herein incorporated by reference); orchardgrass (Horn *et al.*, *Plant Cell Rep.* 7:469, (1988), the entirety of which is herein incorporated by reference); rice (Toriyama *et al.*, *Theor Appl. Genet.* 205:34, (1986); Park *et al.*, *Plant Mol. Biol.*, 32:1135-1148, (1996); Abedinia *et al.*, *Aust. J. Plant Physiol.* 24:133-141, (1997); Zhang and Wu, *Theor. Appl. Genet.* 76:835, (1988); Zhang *et al.*, *Plant Cell Rep.* 7:379, (1988); Batraw and Hall, *Plant Sci.* 86:191-202, (1992); Christou *et al.*, *Bio/Technology* 9:957, (1991), all of which the entirety is herein incorporated by reference); sugarcane (Bower and Birch, *Plant J.* 2:409, (1992), the entirety of which is herein incorporated by reference); tall fescue (Wang *et al.*, *Bio/Technology* 10:691, (1992), the entirety of which is herein incorporated

by reference), and wheat (Vasil et al., Bio/Technology 10:667, (1992), the entirety of which is herein incorporated by reference; U.S. Patent No. 5,631,152, the entirety of which is herein incorporated by reference.

Assays for gene expression based on the transient expression of cloned nucleic acid constructs have been developed by introducing the nucleic acid molecules into plant cells by polyethylene glycol treatment, electroporation, or particle bombardment (Marcotte, *et al.*, *Nature*, 335:454-457 (1988), the entirety of which is herein incorporated by reference; Marcotte, *et al.*, *Plant Cell*, 1:523-532 (1989), the entirety of which is herein incorporated by reference; McCarty, *et al.*, *Cell* 66:895-905 (1991), the entirety of which is herein incorporated by reference; Hattori, *et al.*, *Genes Dev.* 6:609-618 (1992), the entirety of which is herein incorporated by reference; Goff, *et al.*, *EMBO J.* 9:2517-2522 (1990), the entirety of which is herein incorporated by reference). Transient expression systems may be used to functionally dissect gene constructs (See generally, Mailga *et al.*, *Methods in Plant Molecular Biology*, Cold Spring Harbor Press (1995)).

Any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a permanent or transient manner in combination with other genetic elements such as vectors, promoters enhancers etc. Further any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a manner that allows for over expression of the protein or fragment thereof encoded by the nucleic acid molecule.

Nucleic acid molecules of the present invention may be used in cosuppression. Cosuppression is the reduction in expression levels, usually at the level of RNA, of a particular endogenous gene or gene family by the expression of a homologous sense construct that is capable of transcribing mRNA of the same strandedness as the transcript of the endogenous gene

(Napoli *et al.*, *Plant Cell* 2:279-289 (1990), the entirety of which is herein incorporated by reference; van der Krol *et al.*, *Plant Cell* 2:291-299 (1990), the entirety of which is herein incorporated by reference). Cosuppression may result from stable transformation with a single copy nucleic acid molecule that is homologous to a nucleic acid sequence found with the cell (Prolls and Meyer, *Plant J.* 2:465-475 (1992), the entirety of which is herein incorporated by reference) or with multiple copies of a nucleic acid molecule that is homologous to a nucleic acid sequence found with the cell (Mittlesten *et al.*, *Mol. Gen. Genet.* 244: 325-330 (1994), the entirety of which is herein incorporated by reference). Genes, even though different, linked to homologous promoters may result in the cosuppression of the linked genes (Vaucheret, *C.R. Acad. Sci. III* 316: 1471-1483 (1993), the entirety of which is herein incorporated by reference).

This technique has, for example been applied to generate white flowers from red petunia and tomatoes that do not ripen on the vine. Up to 50% of petunia transformants that contained a sense copy of the chalcone synthase (CHS) gene produced white flowers or floral sectors; this was as a result of the post-transcriptional loss of mRNA encoding CHS (Flavell, *Proc. Natl. Acad. Sci. (U.S.A.)* 91:3490-3496 (1994)), the entirety of which is herein incorporated by reference). Cosuppression may require the coordinate transcription of the transgene and the endogenous gene, and can be reset by a developmental control mechanism (Jorgensen, *Trends Biotechnol.* 8:340344 (1990), the entirety of which is herein incorporated by reference; Meins and Kunz, In: *Gene Inactivation and Homologous Recombination in Plants* (Paszkowski, J., ed.), pp. 335-348. Kluwer Academic, Netherlands (1994), the entirety of which is herein incorporated by reference).

It is understood that one or more of the nucleic acids of the present invention, including nucleic acid molecules having a nucleic acid sequence selected from the group consisting of SEQ

ID NO:1 or complement thereof through SEQ ID NO:20082 or complement thereof or fragments thereof, may be introduced into a plant cell and transcribed using an appropriate promoter with such transcription resulting in the co-suppression of an endogenous protein.

Nucleic acid molecules of the present invention may be used to reduce gene function. Antisense approaches are a way of preventing or reducing gene function by targeting the genetic material (Mol *et al.*, *FEBS Lett.* 268:427-430 (1990), the entirety of which is herein incorporated by reference). The objective of the antisense approach is to use a sequence complementary to the target gene to block its expression and create a mutant cell line or organism in which the level of a single chosen protein is selectively reduced or abolished. Antisense techniques have several advantages over other 'reverse genetic' approaches. The site of inactivation and its developmental effect can be manipulated by the choice of promoter for antisense genes or by the timing of external application or microinjection. Antisense can manipulate its specificity by selecting either unique regions of the target gene or regions where it shares homology to other related genes (Hiatt *et al.*, *In Genetic Engineering*, Setlow (ed.), Vol. 11, New York: Plenum 49-63 (1989), the entirety of which is herein incorporated by reference).

The principle of regulation by antisense RNA is that RNA that is complementary to the target mRNA is introduced into cells, resulting in specific RNA:RNA duplexes being formed by base pairing between the antisense substrate and the target mRNA (Green *et al.*, *Annu. Rev. Biochem.* 55:569-597 (1986), the entirety of which is herein incorporated by reference). Under one embodiment, the process involves the introduction and expression of an antisense gene sequence. Such a sequence is one in which part or all of the normal gene sequences are placed under a promoter in inverted orientation so that the 'wrong' or complementary strand is transcribed into a noncoding antisense RNA that hybridizes with the target mRNA and interferes

with its expression (Takayama and Inouye, *Crit. Rev. Biochem. Mol. Biol.* 25:155-184 (1990), the entirety of which is herein incorporated by reference). An antisense vector is constructed by standard procedures and introduced into cells by transformation, transfection, electroporation, microinjection, or by infection, etc. The type of transformation and choice of vector will determine whether expression is transient or stable. The promoter used for the antisense gene may influence the level, timing, tissue, specificity, or inducibility of the antisense inhibition.

It is understood that protein synthesis activity in a plant cell may be reduced or depressed by growing a transformed plant cell containing a nucleic acid molecule of the present invention.

Antibodies have been expressed in plants (Hiatt *et al.*, *Nature* 342:76-78 (1989), the entirety of which is herein incorporated by reference; Conrad and Fielder, *Plant Mol. Biol.* 26:1023-1030 (1994), the entirety of which is herein incorporated by reference). Cytoplasmic expression of a scFv (single-chain Fv antibodies) has been reported to delay infection by artichoke mottled crinkle virus. Transgenic plants that express antibodies directed against endogenous proteins may exhibit a physiological effect (Philips *et al.*, *EMBO J.* 16:4489-4496 (1997), the entirety of which is herein incorporated by reference; Marion-Poll, *Trends in Plant Science* 2:447-448 (1997), the entirety of which is herein incorporated by reference). For example, expressed anti-abscisic antibodies reportedly result in a general perturbation of seed development (Philips *et al.*, *EMBO J.* 16:4489-4496 (1997)).

Nucleic acid molecules of the present invention may be used as antibodies. Antibodies that are catalytic may also be expressed in plants (abzymes). The principle behind abzymes is that since antibodies may be raised against many molecules, this recognition ability can be directed toward generating antibodies that bind transition states to force a chemical reaction forward (Persidas, *Nature Biotechnology* 15:1313-1315 (1997), the entirety of which is herein

incorporated by reference; Baca *et al.*, *Ann. Rev. Biophys. Biomol. Struct.* 26:461-493 (1997), the entirety of which is herein incorporated by reference). The catalytic abilities of abzymes may be enhanced by site directed mutagenesis. Examples of abzymes are, for example, set forth in U.S. Patent No. 5,658,753; U.S. Patent No. 5,632,990; U.S. Patent No. 5,631,137; U.S. Patent 5,602,015; U.S. Patent No. 5,559,538; U.S. Patent No. 5,576,174; U.S. Patent No. 5,500,358; U.S. Patent 5,318,897; U.S. Patent No. 5,298,409; U.S. Patent No. 5,258,289 and U.S. Patent No. 5,194,585, all of which are herein incorporated in their entirety.

It is understood that any of the antibodies of the present invention may be expressed in plants and that such expression can result in a physiological effect. It is also understood that any of the expressed antibodies may be catalytic.

In addition to the above discussed procedures, practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of macromolecules (e.g., DNA molecules, plasmids, etc.), generation of recombinant organisms and the screening and isolating of clones, (see for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989); Mailga *et al.*, *Methods in Plant Molecular Biology*, Cold Spring Harbor Press (1995), the entirety of which is herein incorporated by reference; Birren *et al.*, *Genome Analysis: Analyzing DNA*, 1, Cold Spring Harbor, New York, the entirety of which is herein incorporated by reference).

The nucleotide sequence provided in SEQ ID NO:1, through SEQ ID NO:20082 or fragment thereof, or complement thereof, or a nucleotide sequence at least 90% identical, preferably 95%, identical even more preferably 99% or 100% identical to the sequence provided in SEQ ID NO:1 through SEQ ID NO:20082 or fragment thereof, or complement thereof, can be

"provided" in a variety of mediums to facilitate use fragment thereof. Such a medium can also provide a subset thereof in a form that allows a skilled artisan to examine the sequences.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc, storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate media comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt

any number of data processor structuring formats (e.g., text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing one or more of nucleotide sequences of the present invention, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem.* 17:203-207 (1993), the entirety of which is herein incorporated by reference) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding fragments within the sequences of the present invention and are useful in producing commercially important proteins such as enzymes used in amino acid biosynthesis, metabolism, transcription, translation, RNA processing, nucleic acid and a protein degradation, protein modification, and DNA replication, restriction, modification, recombination, and repair.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the nucleic acid molecule of the present invention. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled

artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequence of the present invention that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available and can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTIN and BLASTIX (NCBIA). One of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that during searches for commercially important fragments of the nucleic acid molecules of the present invention, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, *cis* elements, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequences of the present invention sequence identified using a search means as described above, and an output means for outputting the identified homologous sequences. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the sequence of the present invention by varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments sequence of the present invention. For example, implementing software which implement the BLAST and BLAZE algorithms (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) can be used to identify open frames within the nucleic acid molecules of the present invention. A skilled artisan can readily recognize that any

one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Example 1

BACs are stable, non-chimeric cloning systems having genomic fragment inserts (100-300 kb) and their DNA can be prepared for most types of experiments including DNA sequencing. BAC vector, pBeloBAC11, is derived from the endogenous *E. coli* F-factor plasmid, which contains genes for strict copy number control and unidirectional origin of DNA replication. Additionally, pBeloBAC11 has three unique restriction enzyme sites (*Hind* III, *Bam* HI and *Sph* I) located within the *LacZ* gene which can be used as cloning sites for megabase-size plant DNA. Indigo, another BAC vector contains *Hind* III and *Eco* RI cloning sites. This vector also contains a random mutation in the *LacZ* gene that allows for darker blue colonies.

As an alternative, the P1-derived artificial chromosome (PAC) can be used as a large DNA fragment cloning vector (Ioannou, *et al.*, *Nature Genet.* 6:84-89 (1994), the entirety of which is herein incorporated by reference; Suzuki, *et al.*, *Gene* 199:133-137 (1997), the entirety of which is herein incorporated by reference). The PAC vector has most of the features of the BAC system, but also contains some of the elements of the bacteriophage P1 cloning system.

BAC libraries are generated by ligating size-selected restriction digested DNA with pBeloBAC11 followed by electroporation into *E. coli*. BAC library construction and characterization is extremely efficient when compared to YAC (yeast artificial chromosome)

library construction and analysis, particularly because of the chimerism associated with YACs and difficulties associated with extracting YAC DNA.

There are two general methods for preparing megabase-size DNA from plants. The protoplast method yields megabase-size DNA of high quality with minimal breakage. The process involves preparing young leaves which are manually feathered with a razor-blade before being incubated for four to five hours with cell-wall-degrading enzymes. The second method developed by Zhange *et al.*, *Plant J.* 7:175-184 (1995) the entirety of which is herein incorporated by reference is a universal nuclei method that works well for several divergent plant taxa. Fresh or frozen tissue is homogenized with a blender or mortar and pestle. Nuclei are then isolated and embedded. DNA is prepared by the nucleic method often more concentrated and is reported to contain lower amounts of chloroplast DNA than the protoplast method.

Once protoplasts or nuclei are produced, they are embedded in an agarose matrix as plugs or microbeads. The agarose provides a support matrix to prevent shearing of the DNA while allowing enzymes and buffers to diffuse into the DNA. The DNA is purified and manipulated in the agarose and is stable for more than one year at 4°C.

Once high molecular weight DNA has been prepared, it is fragmented to the desired size range. In general, DNA fragmentation utilizes two general approaches, 1) physical shearing and 2) partial digestion with a restriction enzyme that cuts relatively frequently within the genome. Since physical shearing is not dependent upon the frequency and distribution of particular restriction enzymes sites, this method should yield the most random distribution of DNA fragments. However, the ends of the sheared DNA fragments must be repaired and cloned directly or restriction enzyme sites added by the addition of synthetic linkers. Because of the subsequent steps required to clone DNA fragmented by shearing, most protocols fragment DNA

by partial restriction enzyme digestion. The advantage of partial restriction enzyme digestion is that no further enzymatic modification of the ends of the restriction fragments are necessary. Four common techniques that can be used to achieve reproducible partial digestion of megabase-size DNA are 1) varying the concentration of the restriction enzyme, 2) varying the time of incubation with the restriction enzyme 3) varying the concentration of an enzyme cofactor (e.g., Mg^{2+}) and 4) varying the ratio of endonuclease to methylase.

There are three cloning sites in pBeloBAC11, but only *Hind* III and *Bam* HI produce 5' overhangs for easy vector dephosphorylation. These two restriction enzymes are primarily used to construct BAC libraries. The optimal partial digestion conditions for megabase-size DNA are determined by wide and narrow window digestions. To optimize the optimum amount of *Hind* III, 1, 2, 3, 10, and 5- units of enzyme are each added to 50 ml aliquots of microbeads and incubated at 37 °C for 20 minutes

After partial digestion of megabase-size DNA, the DNA is run on a pulsed-field gel, and DNA in a size range of 100-500 kb is excised from the gel. This DNA is ligated to the BAC vector or subjected to a second size selection on a pulsed field gel under different running conditions. Studies have previously reported that two rounds of size selection can eliminate small DNA fragments co-migrating with the selected range in the first pulse-field fractionation. Such a strategy results in an increase in insert sizes and a more uniform insert size distribution. A practical approach to performing size selections is to first test for the number of clones/microliter of ligation and insert size from the first size selected material. If the numbers are good (500 to 2000 white colony/microliter of ligation) and the size range is also good (50 to 300 kb) then a second size selection is practical. When performing a second size selection one expects a 80 to 95% decrease in the number of recombinant clones per transformation.

Twenty to two hundred nanograms of the size-selected DNA is ligated to dephosphorylated BAC vector (molar ratio of 10 to 1 in BAC vector excess). Most BAC libraries use a molar ratio of 5 to 15 : 1 (size selected DNA:BAC vector).

Transformation is carried out by electroporation and the transformation efficiency for BACs is about 40 to 1,500 transformants from one microliter of ligation product or 20 to 1000 transformants/ng DNA.

Several tests can be carried out to determine the quality of a BAC library. Three basic tests to evaluate the quality include: the genome coverage of a BAC library-average insert size, average number of clones hybridizing with single copy probes and chloroplast DNA content.

The determination of the average insert size of the library is assessed in two ways. First, during library construction every ligation is tested to determine the average insert size by assaying 20-50 BAC clones per ligation. DNA is isolated from recombinant clones using a standard mini preparation protocol, digested with *Not* I to free the insert from the BAC vector and then sized using pulsed field gel electrophoresis (Maule, *Molecular Biotechnology* 9:107-126 (1998), the entirety of which is herein incorporated by reference).

To determine the genome coverage of the library, it is screened with single copy RFLP markers distributed randomly across the genome by hybridization. Microtiter plates containing BAC clones are spotted onto Hybond membranes. Bacteria from 48 or 72 plates are spotted twice onto one membrane resulting in 18,000 to 27,648 unique clones on each membrane in either a 4X4 or 5X5 orientation. Since each clone is present twice, false positives are easily eliminated and true positives are easily recognized and identified.

Finally, the chloroplast DNA content in the BAC library is estimated by hybridizing three chloroplast genes spaced evenly across the chloroplast genome to the library on high density hybridization filters.

There are strategies for isolating rare sequences within the genome. For example, higher plant genomes can range in size from 100 Mb/1C (*Arabidopsis*) to 15,966 Mb/C (*Triticum aestivum*), (Arumuganathan and Earle, *Plant Mol Bio Rep.* 9:208-219 (1991), the entirety of which is herein incorporated by reference). The number of clones required to achieve a given probability that any DNA sequence will be represented in a genomic library is $N = (\ln(1-P))/(\ln(1-L/G))$ where N is the number of clones required, P is the probability desired to get the target sequence, L is the length of the average clone insert in base pairs and G is the haploid genome length in base pairs (Clarke *et al.*, *Cell* 9:91-100 (1976) the entirety of which is herein incorporated by reference).

The soybean BAC library of the present invention is constructed in the pBeloBAC11 or similar vector. Inserts are generated by partial *Eco* RI or other enzymatic digestion of DNA from the cultivar A3244. The library provides approximately twenty fold coverage of the soybean genome.

Example 2

Nucleic acid sequences are identified using a cascade of BLASTX, followed by BLASTN if no BLASTX hit is found.. Default BLAST parameters are used. BLASTX compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database. BLASTN compares a nucleotide query sequence against a nucleotide

sequence database. Matches found with BLAST P-values equal or less than $1E-8$ (probability) are classified as hits.

Example 3

Two basic methods can be used for DNA sequencing, the chain termination method of Sanger *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.)* 74:5463-5467 (1977), the entirety of which is herein incorporated by reference and the chemical degradation method of Maxam and Gilbert, *Proc. Natl. Acad. Sci.(U.S.A.)* 74:560-564 (1977), the entirety of which is herein incorporated by reference. Automation and advances in technology such as the replacement of radioisotopes with fluorescence-based sequencing have reduced the effort required to sequence DNA (Craxton, *Methods*, 2:20-26 (1991), the entirety of which is herein incorporated by reference; Ju *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.)* 92:4347-4351 (1995), the entirety of which is herein incorporated by reference; Tabor and Richardson, *Proc. Natl. Acad. Sci.(U.S.A.)* 92:6339-6343 (1995), the entirety of which is herein incorporated by reference). Automated sequencers are available from, for example, Pharmacia Biotech, Inc., Piscataway, New Jersey (Pharmacia ALF), LI-COR, Inc., Lincoln, Nebraska (LI-COR 4,000) and Millipore, Bedford, Massachusetts (Millipore BaseStation).

In addition, advances in capillary gel electrophoresis have also reduced the effort required to sequence DNA and such advances provide a rapid high resolution approach for sequencing DNA samples (Swerdlow and Gesteland, *Nucleic Acids Res.* 18:1415-1419 (1990); Smith, *Nature* 349:812-813 (1991); Luckey *et al.*, *Methods Enzymol.* 218:154-172 (1993); Lu *et al.*, *J. Chromatog. A.* 680:497-501 (1994); Carson *et al.*, *Anal. Chem.* 65:3219-3226 (1993); Huang *et*

al., *Anal. Chem.* 64:2149-2154 (1992); Kheterpal *et al.*, *Electrophoresis* 17:1852-1859 (1996); Quesada and Zhang, *Electrophoresis* 17:1841-1851 (1996); Baba, *Yakugaku Zasshi* 117:265-281 (1997), all of which are herein incorporated by reference in their entirety).

A number of sequencing techniques are known in the art, including fluorescence-based sequencing methodologies. These methods have the detection, automation and instrumentation capability necessary for the analysis of large volumes of sequence data. Currently, the 377 DNA Sequencer (Perkin-Elmer Corp., Applied Biosystems Div., Foster City, CA) allows the most rapid electrophoresis and data collection. With these types of automated systems, fluorescent dye-labeled sequence reaction products are detected and data entered directly into the computer, producing a chromatogram that is subsequently viewed, stored, and analyzed using the corresponding software programs. These methods are known to those of skill in the art and have been described and reviewed (Birren *et al.*, *Genome Analysis: Analyzing DNA*, 1, Cold Spring Harbor, New York, the entirety of which is herein incorporated by reference).

Example 4

To identify sequences containing microsatellites or simple sequence repeats (SSR), a SSR repeat pattern library is generated by using a Perl program, *SSR_generator.pl*, developed at Monsanto. The library contains repeat patterns of di-, tri-, tetra-, penta- and hexa- nucleotide repeats, a total of 5421 patterns. The length of di-, tri-, tetra-, penta- and hexa- nucleotide repeat units were 18, 12, 9, 5 and 4, respectively. These repeat patterns are used to search against the BAC-end sequence databases by the BLASTN program. If the search is performed on both strands, complementary and replicated patterns of an SSR library are removed from the library to avoid redundancy of SSRs. For di-nucleotide repeats, there are four unique patterns, i.e. (CA)_n.

The SSR-containing sequences identified from BAC ends are searched against each other as well as the existing SSR collections by using BLASTN, and clustering of the sequences is performed by using CLUSTER2, a tool developed at Monsanto. The minimal match-length is set to 100 base pairs. Any redundant sequences are removed and the unique ones are then passed through a visible inspection to further remove those with not enough flanking sequences for primer design and those with substantial ambiguous nucleotides.

primers are designed from good quality unique sequences. A public available primer design software program, PRIMER 3, (Cambridge, MA) is used. PRIMER 3 can be accessed through the internet at (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>). Default parameters are used except those for product size and primer size are changed. Product Size is Min: 80, Opt: 100, Max: 120, while Primer Size is Min: 18, Opt: 22 and Max: 27. Oligos are synthesized by Genosis Biotechnologies, Inc (Houston, Texas).

The above protocols are used to develop primers from Sequence id

GM_M02_A2_B07_MR_MR containing the following nucleotide composition:

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ATTGAGACTTTGACGCANAGTCAGATGGTGCGTCATGCTCTTTCATTACATTGGAC
ATCATNTACTACCCTTTGAAGACCCTCGATCCATGGAAGGGTTAATTGGTG

This sequence contains CTT dinucleotide repeats with a repeat unit of 11. Using the Primer 3 program, two primers are selected: SER157F GTGTCTTTCGGATGCTTCTTCT and SER157R CACCATTTTGCACCTAAGTTGA. When these two primers are used to amplify genomic DNAs from eight different varieties, Minsoy, Noir, PIC, HS-1, A3244, H6686, A0868 and H5088, three alleles are detected. Sizes of these alleles ranged from 80 to 110 bp. The size variation in the PCR products result from repeat numbers in different varieties.

PCR reaction conditions

Genomic DNA is isolated from young leaves of *Glycine max* or *Glycine soja* plants. Two leaf discs are collected (approximately 40 mg) from a healthy leaf and stored on wet ice or at 4°C. Tissue samples are then freeze-dried and stored at -20°C or -80°C. The frozen samples are kept as dry as possible and sealed from contact with the atmosphere. The freeze-dried samples from -20°C or -80°C, are allowed to warm up to room temperature prior to unscaling or opening. One leaflet (or 2 leaf discs) is inserted into an 1.5ml Eppendorf tube, placed on dry ice, and crushed with a wooden dowel. Approximately 200 µl of microprep buffer (25 ml extraction buffer (350 mM sorbitol, 100 mM Tris-base, 5 mM EDTA-Na₂), 25 ml nuclei lysis buffer (1M Tris/HCl, 0.5 M EDTA, 5 M NaCl, 2% CTAB), 10ml 5% sarkosyl, 0.1g Na bisulfite) is added to each sample. The sample is then homogenized. An additional 550 µl of microprep buffer is added, vortexed for about 30-60 seconds, and incubated at 65°C for about 60 minutes. About 700 µl chloroform/isoamyl (24:1) is added, mixed well for about 10-30 seconds. Centrifugation of the tubes is performed at approximately 10,000 rpm for 5 minutes in a microcentrifuge. The aqueous phase is transferred into a new tube and RNA is removed from the extract by the

addition of 30 μ l of RNase (10mg/ml) to the aqueous phase and incubated for 1 hour at room temperature. Approximately 500 μ l ice-cold isopropanol is added to the aqueous extract, and the tubes inverted until the DNA precipitated. The precipitated solution is kept at 4°C for about 1 hour or overnight. Centrifugation of the tubes is performed at approximately 10,000 rpm for 5 minutes in a microcentrifuge. The supernatant is discarded and the pellet washed 1-3 times with 200 μ l 70% ethanol. The ethanol is removed using a micropipette and pellet dried at 37°C for 10 minutes. The DNA is dissolved in 50 μ l TE (10 mM Tris-HCl pH8.0, 0.1 mM EDTA), then kept overnight at 4°C. Centrifugation of the tubes is performed at approximately 10,000 rpm for 5 minutes and then the supernatant is transferred into new tubes. Using this method, approximately 2 μ g of DNA per mg of fresh leaf tissue is extracted.

DNA concentration is measured by a Spectrometry (Molecular Devices, Sunnyvale, California) and adjusted to proper concentration for use as template. The total volume for PCR reaction is 20 μ l. The reaction mixture contains: Template DNA at a concentration of 15 ng, 0.15 μ M of primer, .03 unit of Taq DNA polymerase (Perkin Elmer), 50 μ M of dNTP, the Reaction buffer contains, 10 mM Tris.HCl pH8.5, 1.5 mM MgCl₂, 50 mM KCl and water is added to a total volume of 20 μ l.

The PCR is performed on a Perkin Elmer DNA Thermal Cycler 9700 using the following cycle profile: hold at 94 °C for 3 min, 32 cycles of 94°C for 25 second, 47 °C for 25 second and 72 °C for 25 second, and 72 °C for 3min of final extension.

An acrylamide gel is prepared using 56.5 ml water, 3.5 ml 10x TAE buffer, 10.5 ml 40 acrylamide stock solution, 50 μ l TEMED, 0.06 g ammonium persulfate. To each PCR, sample 20 μ l of formamide loading dye is added to each sample and the samples are denatured at 90°C

for 3 minutes with a 4°C hold in a thermocycler. 1.5 µl of each sample is loaded onto the gel. Gels are run at constant wattage to give a constant heat development during electrophoresis at 40 to 50 Volt/cm of the gel length. Gels should be run at approximately 50°C during electrophoresis. Electrophoresis is stopped when the Bromophenol blue dye is at the bottom of the gel. After electrophoresis, the gel is stained in 1 x SYBR solution for 15 to 20 minutes with vigorous shaking. A Gel image is recorded using an Alpha-InnoTech imager.

Example 5

In order to create a file containing complex repeats, the GCG (Madison, WI) REPEAT program is used to determine initial internal repeats. Stringency is defined as 19 matched bases out of every contiguous 20 bases in the repeated diagonals part of the REPEAT program algorithm. After the REPEAT program is run on the STCs, a REPEAT output file is processed with the UNIX utilities grep, sort, uniq and sed to produce a GCG pattern file. The GCG pattern file is broken into size groups: <20, 20-39, 40-59, 60-79, 80-89, 100-119, 120-139, 140-159, 160-179, 180-199, 200-219, and >220. Each pattern group is compared against the entire STC library using the GCG FINDPATTERNS program. Sequences of size 1-19 are allowed no mismatches. The 20-39 group are allowed one mismatch. A pattern of size n is allowed floor (n/20) mismatches. Patterns that occurred in at least 100 STCs are selected in this step. The results of the FINDPATTERNS program is post-processed with the UNIX utilities grep, sort and uniq and with the GCG REFORMAT program to produce GCG sequence files. Each sequence file is derived from a selected pattern and placed in a subdirectory that corresponds to its size group. GELSTART, GELENTER, GELMERGE and GELASSEMBLE are used to coalesce similar sequences of each size group. Patterns are 90% similar before they are aligned and the

patterns overlap by at least two thirds of the modal length in their length group. The GELSTART program creates a subdirectory which contains the individual and the coalesced consensus sequences. The consensus sequences are placed into a single directory and a FASTA style sequence library is constructed from it. The REPEAT-MASKER program is used to mask the original STCs. The unmasked sequences that remain afterward are concatenated into 100 KB pseudo-sequences. The pseudo-sequences are fed back into this algorithm and the new repeat patterns that result are added to the repeat library. The algorithm is iterated 3 times.

The repeat library is compared to the STCs using NCBI BLASTN version 2.0. HSPs are reported if they satisfied the criteria of:

"observed fractional match" \geq "allowed fractional match"

where "observed fractional match" is defined as:

"fraction of HSP similarity" \times "fraction of query sequence in HSP"

and "allowed fractional match" is defined as:

$$(\text{"repeat length"} - \text{"floor (repeat length/20)}) / \text{"repeat length"}$$

Table 1

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
1	GM_49_B2_A03_T7	g4063760	BLASTX	332	6e-28	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2	GM_49_B2_A04_MR	g3142328	BLASTN	1418	2e-57	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3	GM_49_B2_A06_T7	g2995405	BLASTX	167	2e-10	43	(Y12432) polyprotein [Ananas comosus]
4	GM_49_B2_B02_MR	g1769898	BLASTX	253	5e-20	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5	GM_49_B2_C01_MR	g2961390	BLASTX	199	3e-19	89	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]
6	GM_49_B2_C02_MR	g2995405	BLASTX	478	6e-44	55	(Y12432) polyprotein [Ananas comosus]
7	GM_49_B2_C03_MR	g587603	BLASTN	362	2e-09	64	P.falciapum gene for beta subunit RNA polymerase
8	GM_49_B2_C06_MR	g4063760	BLASTX	193	3e-14	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9	GM_49_B2_C07_MR	g2995405	BLASTX	356	8e-31	48	(Y12432) polyprotein [Ananas comosus]
10	GM_49_B2_C07_T7	g4063760	BLASTX	207	1e-14	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11	GM_49_B2_D02_T7	g2500724	BLASTX	277	3e-22	98	PREPROTEIN TRANSLOCASE SECA SUBUNIT PRECURSOR gi 1122325 2129894 pir S72453 secA protein precursor - garden pea gi 1122325 (X82404) chloroplast SecA protein [Pisum sativum]
12	GM_49_B2_D03_MR	g1769898	BLASTX	245	4e-19	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13	GM_49_B2_D08_MR	g18559	BLASTN	1100	7e-43	75	G.max gene for catalase
14	GM_49_B2_D11_T7	g4092470	BLASTN	412	1e-11	67	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
15	GM_49_B2_D12_MR	g18559	BLASTN	1055	8e-41	75	G.max gene for catalase
16	GM_49_B2_F02_MR	g2160694	BLASTX	162	3e-10	56	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
17	GM_49_B2_E02_T7	g2462058	BLASTX	302	4e-26	57	(Y13389) reverse transcriptase [Antirrhinum majus]
18	GM_49_B2_E03_MR	g2982431	BLASTX	224	2e-16	37	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
19	GM_49_B2_F03_T7	g3097320	BLASTN	830	1e-30	79	Glycine max gene for Bd 30K, complete cds
20	GM_49_B2_F04_MR	g1769898	BLASTX	245	4e-19	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
21	GM_49_B2_E09_MR	g477068	BLASTX	138	1e-08	39	reverse transcriptase (copa-like retrotransposon) - Pinus coulteri=pine (fragment) >gi 169382 (M94488) reverse transcriptase [Pinus coulteri]
22	GM_49_B2_E11_MR	g2346988	BLASTX	160	3e-10	70	(AB006606) ZPT4-4 [Petunia x hybrida]
23	GM_49_B2_F02_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
24	GM_49_B2_F02_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
25	GM_49_B2_F04_T7	g1666236	BLASTX	198	8e-15	30	(U76261) unknown [Hordeum vulgare]
26	GM_49_B2_F07_T7	g3075399	BLASTX	136	2e-10	50	(AC004484) SF16-like protein [Arabidopsis thaliana]
27	GM_49_B2_F09_T7	g1236920	BLASTN	375	5e-10	64	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and VarIp (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
28	GM_49_B2_F10_T7	g3142303	BLASTX	257	7e-20	44	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana] (U22103) gag-protease polypeptide [Glycine max] (AC005396) putative En/Spm transposon protein. 5' partial [Arabidopsis thaliana] Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22 (ESSAII project) Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds (Y08010) lectin receptor kinase [Arabidopsis thaliana] (AC005561) putative POL3 protein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. Athila hypothetical protein 1 - Arabidopsis thaliana retrotransposon gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] Petunia vein clearing virus, complete genome hypothetical protein - garden snapdragon (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana] Myrmecia pilosula H187.145 mitochondrion cytochrome b gene, partial cds.
29	GM_49_B2_F11_MR	g905361	BLASTX	624	3e-60	97	(X01380) ORF1 [Zea mays]
30	GM_49_B2_G04_T7	g3650039	BLASTX	206	7e-15	43	(AJ000387) protease [Drosophila melanogaster] (AB007466) reverse transcriptase-like protein [Vicia faba] (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana] hypothetical protein 82 - common tobacco chloroplast gi 225200 prf 1211235AE ORF 82 [Nicotiana tabacum]
31	GM_49_B2_G08_T7	g3402747	BLASTN	376	6e-10	64	G.max chloroplast DNA for tRNA (Arg) Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. Saccharomyces cerevisiae complete mitochondrial genome (AF069298) No definition line found [Arabidopsis thaliana] (U22103) gag-protease polypeptide [Glycine max] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
32	GM_49_B2_G09_MR	g3193221	BLASTN	373	7e-10	67	
33	GM_49_B2_G12_MR	g1769897	BLASTX	198	3e-14	49	
34	GM_49_B2_H06_MR	g4063760	BLASTX	281	2e-22	55	
35	GM_49_B2_H06_T7	g507910	BLASTN	697	7e-25	86	
36	GM_49_B2_H10_MR	g2129618	BLASTX	213	2e-15	44	
37	GM_51_A1_A05_MR	g2463654	BLASTN	450	2e-13	62	
38	GM_51_A1_A12_MR	g100484	BLASTX	211	2e-15	47	
39	GM_51_A1_B05_MR	g3319362	BLASTX	197	1e-13	41	
40	GM_51_A1_B09_MR	g576762	BLASTN	364	8e-10	62	
41	GM_51_A1_C03_MR	g22490	BLASTX	186	7e-14	41	
42	GM_51_A1_C04_MR	g2791289	BLASTX	129	5e-09	41	
43	GM_51_A1_C05_T7	g2522228	BLASTX	187	3e-13	71	
44	GM_51_A1_D08_MR	g3319362	BLASTX	286	4e-26	46	
45	GM_51_A1_D09_MR	g82231	BLASTX	157	8e-11	93	
46	GM_51_A1_D09_T7	g11575	BLASTN	1003	5e-39	95	
47	GM_51_A1_D11_MR	g3142328	BLASTN	471	3e-14	70	
48	GM_51_A1_E02_T7	g4063760	BLASTX	164	4e-10	41	
49	GM_51_A1_E07_T7	g507910	BLASTN	491	1e-15	76	
50	GM_51_A1_E12_MR	g4160362	BLASTN	439	9e-13	64	
51	GM_51_A1_F07_T7	g3193284	BLASTX	264	5e-21	64	
52	GM_51_A1_F08_MR	g905361	BLASTX	252	7e-20	39	
53	GM_51_A1_F10_T7	g3142328	BLASTN	704	7e-25	81	

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
54	GM_51_A1_G06_T7	g2995405	BLASTX	212	2e-15	50	(Y12432) polyprotein [Ananas comosus]
55	GM_51_A1_H04_T7	g100484	BLASTX	242	1e-18	52	hypothetical protein - garden snapdragon
56	GM_51_A1_H07_MR	g3142330	BLASTX	597	2e-57	84	(U96295) envelope-like [Glycine max]
57	GM_51_A1_H09_MR	g130582	BLASTX	213	3e-15	33	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
							(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
58	GM_51_A1_H10_MR	g3142379	BLASTX	204	1e-16	60	(AF053008) envelope-like [Glycine max]
59	GM_51_A2_A08_MR	g3097320	BLASTN	421	5e-12	66	Glycine max gene for Bd 30K, complete cds
60	GM_51_A2_A09_MR	g4063760	BLASTX	209	8e-15	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
61	GM_51_A2_A11_MR	g1785739	BLASTX	159	6e-11	39	(Y08502) orf240b [Arabidopsis thaliana]
62	GM_51_A2_A12_MR	g4063760	BLASTX	249	1e-20	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
63	GM_51_A2_C01_MR	g2995405	BLASTX	105	2e-10	54	(Y12432) polyprotein [Ananas comosus]
64	GM_51_A2_C05_MR	g3142328	BLASTN	587	1e-19	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
65	GM_51_A2_C12_MR	g2522227	BLASTX	205	7e-16	52	(AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]
66	GM_51_A2_D02_MR	g2829133	BLASTX	170	7e-12	66	Glycine max (Rab1p) mRNA, complete cds.
67	GM_51_A2_F02_MR	g414831	BLASTN	354	1e-09	97	Glycine max BSR-101 satellite SB92 genomic sequence.
68	GM_51_A2_F12_MR	g507910	BLASTN	686	2e-24	86	Glycine max gene for Bd 30K, complete cds
69	GM_51_A2_F03_T7	g3097320	BLASTN	465	5e-14	83	Glycine max 5' end not determined experimentally [Zea mays]
70	GM_51_A2_F12_MR	g3645899	BLASTX	164	1e-18	42	(U68408) 5' end not determined experimentally [Zea mays]
71	GM_51_A2_G01_MR	g3406033	BLASTN	381	4e-10	64	Homo sapiens 12p13.3 RPC14-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence [Homo sapiens]
72	GM_51_A2_G09_MR	g3142328	BLASTN	706	5e-25	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence CYTOCHROME P450 LXXIA3 (P-450EG3) gi 480397 pir S36807 cytochrome P450 71A3 - eggplant (fragment) gi 408142 (X70982)
73	GM_51_A2_G10_MR	g584862	BLASTX	301	5e-26	62	p450 hydroxylase [Solanum melongena]
74	GM_51_A2_H01_MR	g3777527	BLASTX	159	2e-09	49	(AF053008) gag-pol polyprotein [Glycine max]
75	GM_51_A2_H07_MR	g3021696	BLASTN	374	7e-10	62	Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, complete sequence [Homo sapiens]
76	GM_51_B2_A08_MR	g505129	BLASTN	402	3e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
77	GM_51_B2_A09_MR	g4063760	BLASTX	197	1e-13	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
78	GM_51_B2_A11_MR	g3845293	BLASTN	365	2e-09	61	Plasmodium falciparum chromosome 2, section 58 of 73 of the complete sequence
79	GM_51_B2_A12_MR	g2827717	BLASTX	148	1e-08	75	(AL021684) phosphoenolpyruvate carboxykinase (ATP) - like protein [Arabidopsis thaliana]
80	GM_51_B2_B03_MR	g3377848	BLASTX	166	7e-17	48	(AF076274) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
81	GM_51_B2_B04_MR	g2160155	BLASTN	364	1e-20	69	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
82	GM_51_B2_C03_MR	g905361	BLASTX	437	3e-40	97	(U22103) gag-protease polypeptide [Glycine max]
83	GM_51_B2_C05_MR	g2443320	BLASTX	343	5e-29	48	(D85597) polypeptide [Oryza australiensis]
84	GM_51_B2_C06_MR	g507910	BLASTN	393	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
85	GM_51_B2_C07_MR	g18695	BLASTN	464	4e-14	91	Soybean nodulin 22 gene
86	GM_51_B2_D04_MR	g4063760	BLASTX	237	2e-31	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
87	GM_51_B2_D07_MR	g18559	BLASTN	349	9e-09	69	G max gene for catalase
88	GM_51_B2_D08_MR	g2244915	BLASTX	171	7e-11	34	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
89	GM_51_B2_D09_MR	g3695395	BLASTX	246	3e-19	35	(AF096372) contains similarity to reverse transcriptase (PFam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
90	GM_51_B2_D12_MR	g505267	BLASTX	151	2e-09	49	(X77111) chitinase, class V [Nicotiana tabacum]
91	GM_51_B2_F01_MR	g14222	BLASTN	458	1e-14	65	Saccharomyces cerevisiae mitochondrial gene aap1 for mitochondrial ATPase subunit 8
92	GM_51_B2_F06_MR	g130582	BLASTX	157	3e-09	34	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE; (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
93	GM_51_B2_F07_MR	g3269290	BLASTX	254	6e-20	38	(AL030978) putative receptor like kinase [Arabidopsis thaliana]
94	GM_51_B2_F08_MR	g2827635	BLASTX	184	6e-26	70	(AL021636) predicted protein [Arabidopsis thaliana]
95	GM_51_B2_F11_MR	g3319351	BLASTX	289	5e-26	56	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
96	GM_51_B2_G09_MR	g18559	BLASTN	938	2e-35	79	G max gene for catalase
97	GM_51_B2_G12_MR	g3695412	BLASTX	368	4e-33	65	(AF096373) contains similarity to group 1 glycosyl transferases (PFam: PF00534, E=2.1e-11) [Arabidopsis thaliana]
98	GM_51_B2_H02_MR	g1142702	BLASTN	404	9e-12	77	Glycine max satellite STR120-A.4.
99	GM_51_B2_H05_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
100	GM_51_B2_H07_MR	g4063756	BLASTN	492	3e-15	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
101	GM_51_B2_H09_MR	g507910	BLASTN	392	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
102	GM_51_B2_H10_MR	g3928086	BLASTX	305	2e-26	55	(AC005770) unknown protein [Arabidopsis thaliana]
103	GM_52_A1_A04_MR	g4063760	BLASTX	160	1e-09	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
104	GM_52_A1_A04_T7	g3645899	BLASTX	328	1e-27	53	(U68408) 5' end not determined experimentally [Zea mays]
105	GM_52_A1_A05_MR	g905361	BLASTX	409	5e-37	90	(U22103) gag-protease polypeptide [Glycine max]
106	GM_52_A1_A12_MR	g2384675	BLASTX	150	7e-17	71	(AF012659) putative potassium transporter AtKT4p [Arabidopsis thaliana]
107	GM_52_A1_B04_MR	g18559	BLASTN	596	5e-20	72	G.max gene for catalase
108	GM_52_A1_B06_MR	g2583130	BLASTX	234	2e-17	41	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
109	GM_52_A1_B07_MR	g3645899	BLASTX	199	8e-14	51	(U68408) 5' end not determined experimentally [Zea mays]
110	GM_52_A1_B08_MR	g100484	BLASTX	303	3e-25	55	hypothetical protein - garden snapdragon
111	GM_52_A1_B10_MR	g2995405	BLASTX	260	2e-20	52	(Y12432) polypeptide [Ananas comosus]
112	GM_52_A1_C07_MR	g18559	BLASTN	719	1e-25	73	G.max gene for catalase
113	GM_52_A1_D02_MR	g4063760	BLASTX	228	2e-21	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
114	GM_52_A1_D02_T7	g4063760	BLASTX	502	4e-46	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
115	GM_52_A1_D07_MR	g4063760	BLASTX	261	4e-22	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
116	GM_52_A1_D10_MR	g2085783	BLASTN	408	2e-11	68	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
117	GM_52_A1_D11_MR	g3645899	BLASTX	317	2e-26	52	(U68408) 5' end not determined experimentally [Zea mays]
118	GM_52_A1_E01_T7	g3639087	BLASTX	393	7e-35	71	(AF090444) phospholipase D2 [Brassica oleracea]
119	GM_52_A1_F02_T7	g3319351	BLASTX	338	2e-28	45	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
120	GM_52_A1_F04_MR	g2832304	BLASTX	130	5e-18	59	(AF044489) receptor-like protein kinase [Oryza sativa]
121	GM_52_A1_F08_MR	g3810596	BLASTX	134	1e-14	60	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
122	GM_52_A1_F02_T7	g2245107	BLASTX	108	6e-11	62	(Z97343) thioesterase homolog [Arabidopsis thaliana]
123	GM_52_A1_F03_T7	g100484	BLASTX	362	1e-31	56	hypothetical protein - garden snapdragon
124	GM_52_A1_F12_MR	g507910	BLASTN	339	1e-08	71	Glycine max BSR-101 satellite SB92 genomic sequence
125	GM_52_A1_F12_T7	g3777526	BLASTN	1004	2e-38	87	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polypeptide (pol) gene, complete cds; and envelope-like gene, partial cds
126	GM_52_A1_G02_MR	g3097320	BLASTN	427	3e-12	71	Glycine max gene for Bd 30K, complete cds
127	GM_52_A1_G04_T7	g2764526	BLASTN	410	7e-19	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
128	GM_52_A1_G06_T7	g4038056	BLASTX	323	3e-27	48	(AC005897) putative transposon [Arabidopsis thaliana]
129	GM_52_A1_G08_T7	g4063760	BLASTX	347	2e-29	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
130	GM_52_A2_A04_MR	g2429543	BLASTX	164	4e-10	32	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans])
131	GM_52_A2_A05_MR	g3033389	BLASTX	191	5e-13	39	(AC004238) Cf-2, 1-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
132	GM_52_A2_A08_T7	g4063760	BLASTX	524	2e-48	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
133	GM_52_A2_A11_MR	g4038056	BLASTX	181	3e-20	46	(AC005897) putative transposon [Arabidopsis thaliana]
134	GM_52_A2_B08_MR	g3687234	BLASTX	113	5e-13	40	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
135	GM_52_A2_C01_MR	g3063460	BLASTX	154	6e-10	48	(AC003981) F22O13.22 [Arabidopsis thaliana]
136	GM_52_A2_C01_T7	g1480927	BLASTN	1266	1e-51	93	Glycine max cdc2 protein kinase (cdc2(1)) nonprocessed pseudogene
137	GM_52_A2_C08_MR	g3820757	BLASTN	345	9e-09	61	Caenorhabditis elegans cosmid Y53C12D, complete sequence
138	GM_52_A2_D05_T7	g507910	BLASTN	377	2e-10	81	[Caenorhabditis elegans]
139	GM_52_A2_D09_T7	g905361	BLASTX	436	4e-40	96	Glycine max BSR-101 satellite SB92 genomic sequence.
140	GM_52_A2_E02_MR	g3097320	BLASTN	451	2e-13	68	(U22103) gag-protease polyprotein [Glycine max]
141	GM_52_A2_E02_T7	g4063760	BLASTX	485	5e-50	68	Glycine max gene for Bd 30K, complete cds
142	GM_52_A2_E03_MR	g3777527	BLASTX	191	8e-13	77	(AC005561) putative POL3 protein [Arabidopsis thaliana]
143	GM_52_A2_E05_T7	g3510339	BLASTN	495	2e-15	71	(AF053008) gag-pol polyprotein [Glycine max]
144	GM_52_A2_E10_MR	g3777526	BLASTN	389	1e-10	87	(AF053008) gag-pol polyprotein [Glycine max]
145	GM_52_A2_E12_T7	g3779026	BLASTX	341	9e-29	50	Arabidopsis thaliana genome DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]
146	GM_52_A2_F07_MR	g4063760	BLASTX	270	2e-21	55	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
147	GM_52_A2_F07_T7	g507910	BLASTN	529	3e-17	79	(AC005171) putative retrotransposon [Arabidopsis thaliana]
148	GM_52_A2_F11_T7	g3513747	BLASTX	173	7e-11	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
149	GM_52_A2_G03_T7	g3402704	BLASTX	142	6e-09	33	Glycine max BSR-101 satellite SB92 genomic sequence.
150	GM_52_A2_G05_MR	g4038056	BLASTX	374	1e-32	52	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
151	GM_52_A2_G05_T7	g1142701	BLASTN	1375	8e-56	86	terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
152	GM_52_A2_G07_T7	g3097836	BLASTN	389	2e-10	60	(AC004261) hypothetical protein [Arabidopsis thaliana]
153	GM_52_A2_G11_T7	g3738339	BLASTX	227	3e-17	80	(AC005897) putative transposon [Arabidopsis thaliana]
154	GM_52_A2_H03_T7	g2558655	BLASTX	221	2e-16	61	Glycine max satellite STR120-A.3.
155	GM_52_A2_H05_MR	g2129618	BLASTX	167	2e-10	35	Glycine max satellite STR120-A.3.
156	GM_52_A2_H07_MR	g3097320	BLASTN	450	2e-13	72	Homo sapiens chromosome 5, PAC clone 17e19 (LBNI, H148), complete sequence [Homo sapiens]
157	GM_52_B1_A07_MR	g3319362	BLASTX	308	2e-25	64	(AC005170) putative kinase [Arabidopsis thaliana]
158	GM_52_B1_A08_MR	g3327392	BLASTX	171	6e-11	38	(AC002354) No definition line found [Arabidopsis thaliana]
159	GM_52_B1_A09_MR	g507910	BLASTN	382	1e-10	72	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
							Glycine max gene for Bd 30K, complete cds
							Glycine max contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
							(AC004483) reverse-transcriptase-like protein [Arabidopsis thaliana]
							Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
160	GM_52_B1_B02_T7	g905361	BLASTX	170	5e-11	32	(U22103) gag-protease polyprotein [Glycine max]
161	GM_52_B1_B11_MR	g2760830	BLASTX	391	2e-35	70	(AC003105) putative beta-ketacyl-CoA synthase [Arabidopsis thaliana]
162	GM_52_B1_C01_MR	g3777527	BLASTX	448	4e-40	83	(AF053008) gag-pol polyprotein [Glycine max]
163	GM_52_B1_C02_T7	g1769898	BLASTX	173	3e-26	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
164	GM_52_B1_C08_MR	g18559	BLASTN	435	1e-12	67	G.max gene for catalase
165	GM_52_B1_C12_MR	g3319345	BLASTX	252	1e-19	38	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
166	GM_52_B1_C12_T7	g18559	BLASTN	947	6e-36	77	G.max gene for catalase
167	GM_52_B1_D04_MR	g2522230	BLASTX	305	2e-26	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
168	GM_52_B1_D08_MR	g99922	BLASTX	487	1e-45	63	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
169	GM_52_B1_D11_MR	g1142702	BLASTN	361	8e-10	75	Glycine max satellite STR120-A.4.
170	GM_52_B1_D12_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
171	GM_52_B1_D12_T7	g507910	BLASTN	388	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
172	GM_52_B1_E06_MR	g3688328	BLASTX	141	5e-09	54	(AJ228325) reverse transcriptase [Ginkgo biloba]
173	GM_52_B1_E06_T7	g1177046	BLASTX	153	3e-10	64	(AJ228325) reverse transcriptase [Ginkgo biloba]
174	GM_52_B1_E12_MR	g3142328	BLASTN	1676	4e-69	92	14 KD ZINC-BINDING PROTEIN (PROTEIN KINASE C INHIBITOR) (PKC1) gi 493053 (U09406) putative protein kinase C inhibitor [Brassica juncea]
175	GM_52_B1_F03_T7	g99922	BLASTX	118	8e-10	67	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
176	GM_52_B1_F04_MR	g1061040	BLASTX	160	2e-10	53	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
177	GM_52_B1_F04_T7	g4063760	BLASTX	175	3e-11	56	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] gi 1587694 prf 2207220A sterol C-methyltransferase [Arabidopsis thaliana]
178	GM_52_B1_F05_MR	g2262155	BLASTN	332	2e-09	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
179	GM_52_B1_F07_T7	g2462134	BLASTX	155	1e-09	29	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]
180	GM_52_B1_F09_T7	g130582	BLASTX	417	6e-37	57	(Y13368) reverse transcriptase [Beta vulgaris]

Seq No.	C'loncID	NCBI gi	Method	Score	P-value	% Ident	Description
181	GM_52_B1_G02_T7	g130582	BLASTX	246	3e-22	52	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE+; REVERSE TRANSCRIPTASE+; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum] Zea mays Ty3/gypsy-type retrotransposon reverse transcriptase/integrase polyprotein pseudogene, partial sequence. (U76261) unknown [Hordeum vulgare] (AC005561) putative POL3 protein [Arabidopsis thaliana] (D85597) polyprotein [Oryza australiensis] (AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana] (U22103) gag-protease polyprotein [Glycine max] (AF089084) putative auxin efflux carrier protein; AtPIN1 [Arabidopsis thaliana] (AC005957) reverse transcriptase-like protein [Arabidopsis thaliana] Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene HEAT SHOCK 70 KD PROTEIN gi 99913 pir S14992 heat shock protein, 70K - soybean gi 18663 (X62799) Heat Shock 70kD protein [Glycine max] Glycine max gene for Bd 30K, complete cds Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; MAH20 (AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense] Glycine max BSR-101 satellite SB92 genomic sequence. (AC005561) putative POL3 protein [Arabidopsis thaliana] (AF053008) gag-pol polyprotein [Glycine max] (AB007466) reverse transcriptase-like protein [Vicia faba] Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] (U72725) receptor kinase-like protein [Oryza longistaminata] Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. (U68408) 5' end not determined experimentally [Zea mays] (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 33.26) [Arabidopsis thaliana]
182	GM_52_B1_G07_T7	g2655227	BLASTN	345	9e-09	67	
183	GM_52_B1_G09_MR	g1666236	BLASTX	158	1e-18	40	
184	GM_52_B1_H02_MR	g4063760	BLASTX	380	5e-33	50	
185	GM_52_B1_H05_T7	g2443320	BLASTX	246	9e-19	59	
186	GM_52_B1_H09_T7	g3810596	BLASTX	201	4e-14	53	
187	GM_52_B2_A02_T7	g905361	BLASTX	215	7e-16	39	
188	GM_52_B2_A07_T7	g4151319	BLASTX	144	3e-16	83	
189	GM_52_B2_A09_MR	g4115365	BLASTX	231	4e-17	35	
190	GM_52_B2_A10_T7	g1480927	BLASTN	1660	2e-69	90	
191	GM_52_B2_A11_T7	g123601	BLASTX	250	4e-22	53	
192	GM_52_B2_A12_T7	g3097320	BLASTN	379	4e-10	70	
193	GM_52_B2_B01_T7	g2351062	BLASTN	389	1e-10	63	
194	GM_52_B2_B02_T7	g2688839	BLASTX	134	2e-15	69	
195	GM_52_B2_B04_MR	g507910	BLASTN	577	2e-19	82	
196	GM_52_B2_B04_T7	g4063760	BLASTX	310	1e-25	57	
197	GM_52_B2_B07_MR	g3777527	BLASTX	741	2e-71	93	
198	GM_52_B2_B09_MR	g2522228	BLASTX	255	7e-32	60	
199	GM_52_B2_B11_T7	g3142328	BLASTN	835	4e-59	89	
200	GM_52_B2_C04_MR	g2129618	BLASTX	275	5e-22	44	
201	GM_52_B2_C07_MR	g2586083	BLASTX	161	1e-12	42	
202	GM_52_B2_D01_MR	g507910	BLASTN	613	4e-21	83	
203	GM_52_B2_D01_T7	g507910	BLASTN	552	2e-18	78	
204	GM_52_B2_D06_MR	g3645899	BLASTX	141	9e-17	60	
205	GM_52_B2_D06_T7	g3319363	BLASTX	154	6e-19	39	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
206	GM_52_B2_D08_MR	g1142701	BLASTN	1376	7e-56	86	Glycine max satellite STR120-A.3.
207	GM_52_B2_D09_MR	g100484	BLASTX	296	2e-24	53	hypothetical protein - garden snapdragon (AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]
208	GM_52_B2_D11_MR	g2829133	BLASTX	179	8e-20	73	Plasmodium falciparum MAl3P4, complete sequence [Plasmodium falciparum]
209	GM_52_B2_D11_T7	g3763998	BLASTN	325	2e-09	63	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence.
210	GM_52_B2_E01_MR	g3142328	BLASTN	740	2e-26	90	Glycine max BSR-101 satellite SB92 genomic sequence.
211	GM_52_B2_E08_T7	g507910	BLASTN	370	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
212	GM_52_B2_E10_MR	g3777527	BLASTX	561	3e-52	92	(AF053008) gag-pol polyprotein [Glycine max]
213	GM_52_B2_F02_MR	g1518540	BLASTX	515	1e-48	88	(U53418) UDP-glucose dehydrogenase [Glycine max]
214	GM_52_B2_F12_MR	g507910	BLASTN	657	4e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
215	GM_52_B2_G02_T7	g3645899	BLASTX	214	2e-18	51	(U68408) 5' end not determined experimentally [Zea mays]
216	GM_52_B2_G05_MR	g3097320	BLASTN	739	2e-26	77	Glycine max gene for Bd 30K, complete cds
217	GM_52_B2_H08_MR	g3645899	BLASTX	260	2e-32	58	(U68408) 5' end not determined experimentally [Zea mays]
218	GM_52_B2_H09_T7	g2443320	BLASTX	167	3e-10	33	(D85597) polyprotein [Oryza australiensis]
219	GM_52_B2_H10_T7	g3777527	BLASTX	137	2e-12	39	(AF053008) gag-pol polyprotein [Glycine max]
220	GM_53_A1_A01_T7	g3142328	BLASTN	1897	3e-79	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
221	GM_53_A1_A03_T7	g2969943	BLASTN	353	7e-09	60	Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS
222	GM_53_A1_B02_MR	g3097320	BLASTN	1331	3e-53	82	Glycine max gene for Bd 30K, complete cds
223	GM_53_A1_B04_MR	g130582	BLASTX	185	3e-12	33	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
224	GM_53_A1_B08_MR	g2655098	BLASTX	215	6e-16	37	(TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
225	GM_53_A1_B10_MR	g1666236	BLASTX	144	9e-09	27	(AF023472) peptide transporter [Hordeum vulgare]
226	GM_53_A1_C01_T7	g2245043	BLASTX	103	1e-11	55	(U76261) unknown [Hordeum vulgare]
227	GM_53_A1_C04_T7	g170065	BLASTN	348	9e-09	70	(Z97342) resistance gene [Arabidopsis thaliana]
228	GM_53_A1_C09_MR	g100484	BLASTX	300	6e-25	47	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds.
229	GM_53_A1_C11_T7	g3421384	BLASTX	201	1e-14	46	hypothetical protein - garden snapdragon (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
230	GM_53_A1_C12_MR	g3645899	BLASTX	220	4e-16	46	(U68408) 5' end not determined experimentally [Zea mays]
231	GM_53_A1_D02_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
232	GM_53_A1_D11_MR	g505129	BLASTN	374	6e-10	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
233	GM_53_A1_E01_MR	g3142328	BLASTN	2046	3e-86	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
234	GM_53_A1_F07_T7	g99729	BLASTX	195	8e-15	47	hypothetical protein 2 - Arabidopsis thaliana retrotransposon T.a1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
235	GM_53_A1_F12_MR	g857392	BLASTN	462	4e-14	68	Soybean mRNA for mitotic cyclin a1-type, complete cds
236	GM_53_A1_G05_MR	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
237	GM_53_A1_G08_T7	g2443320	BLASTX	223	3e-16	41	(D85597) polyprotein [Oryza australiensis]
238	GM_53_A1_G12_T7	g3810596	BLASTX	310	9e-26	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
239	GM_53_B1_A05_T7	g18559	BLASTN	767	9e-28	75	G.max gene for catalase
240	GM_53_B1_B04_T7	g2995405	BLASTX	408	2e-36	54	(Y12432) polyprotein [Ananas comosus]
241	GM_53_B1_B08_MR	g13767	BLASTN	249	2e-10	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
242	GM_53_B1_B10_T7	g3777527	BLASTX	172	9e-11	33	(AF053008) gag-pol polyprotein [Glycine max]
243	GM_53_B1_C02_T7	g507910	BLASTN	429	9e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
244	GM_53_B1_C04_MR	g22447	BLASTN	360	3e-09	65	Zea mays ZMPMS2 gene for 19 kDa zein protein.
245	GM_53_B1_C08_MR	g507910	BLASTN	595	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
246	GM_53_B1_C09_T7	g130406	BLASTX	97	1e-10	42	RETROVIRUS-RELATED POL POLYPROTEIN (ENDONUCLEASE) gi 91265 pir A26621 retrovirus-related endonuclease (EC 3.1.-.-) - mouse (fragment) gi 61659 (X05165) endonuclease (39) AA [Murine leukemia virus] gi 222106 gnl PID d1000518 (D00121) endonuclease [Murine leukemia virus]
247	GM_53_B1_C11_MR	g507910	BLASTN	562	9e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
248	GM_53_B1_C12_MR	g226407	BLASTX	162	9e-10	45	retrotransposon del1-46 [Lilium henryi]
249	GM_53_B1_D01_MR	g2443320	BLASTX	198	1e-13	41	(D85597) polyprotein [Oryza australiensis]
250	GM_53_B1_D05_MR	g2463568	BLASTN	363	1e-09	85	Glycine max mRNA for squalene synthase, complete cds
251	GM_53_B1_D09_MR	g245316	BLASTX	183	1e-13	81	reverse transcriptase [Petunia hybrida=petunias, cv. nana compacta, Peptide Transposon Partial, 76 aa]
252	GM_53_B1_E04_MR	g3777527	BLASTX	204	3e-14	39	(AF053008) gag-pol polyprotein [Glycine max]
253	GM_53_B1_E05_MR	g2129618	BLASTX	115	2e-12	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
254	GM_53_B1_E09_MR	g507910	BLASTN	492	1e-15	79	Glycine max BSR-101 satellite SB92 genomic sequence.
255	GM_53_B1_E11_T7	g3845268	BLASTN	386	2e-10	63	Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
256	GM_53_B1_E12_MR	g507910	BLASTN	540	8e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
257	GM_53_B1_F10_MR	g1171591	BLASTN	361	3e-09	61	P.falciparum complete gene map of plastid-like DNA (IR-B)
258	GM_53_B1_G01_T7	g3493214	BLASTX	169	1e-10	33	(AF056940) pol polyprotein [Drosophila virilis]
259	GM_53_B1_G02_T7	g282881	BLASTX	207	7e-15	51	receptor-like protein kinase precursor - Arabidopsis thaliana gi 166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
260	GM_53_B1_G07_MR	g18559	BLASTN	1348	4e-54	80	G.max gene for catalase
261	GM_53_B1_G10_MR	g3142328	BLASTN	1760	5e-73	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
262	GM_53_B1_G11_MR	g3283026	BLASTX	187	9e-13	33	putative transposase [Ananas comosus]
263	GM_53_B1_H10_T7	g2995405	BLASTX	208	6e-15	44	(Y12432) polyprotein [Ananas comosus]
264	GM_53_B2_A02_T7	g1142703	BLASTN	292	3e-16	78	Glycine max satellite STR120-B.1.
265	GM_53_B2_A12_MR	g3097836	BLASTN	396	7e-11	69	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148).
266	GM_53_B2_B10_MR	g4063760	BLASTX	392	2e-34	66	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148).
267	GM_53_B2_B11_MR	g2879886	BLASTN	384	2e-10	61	complete sequence [Homo sapiens]
268	GM_53_B2_C03_MR	g2522228	BLASTX	462	5e-43	62	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
269	GM_53_B2_C05_MR	g3142328	BLASTN	1045	2e-40	88	Saccharomyces cerevisiae mitochondrial tRNA-Tyr. tRNA-Asn. & tRNA-Met genes
270	GM_53_B2_D02_T7	g2264320	BLASTN	653	2e-22	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
271	GM_53_B2_E01_MR	g4115373	BLASTX	178	1e-11	35	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
272	GM_53_B2_E02_MR	g3097320	BLASTN	384	2e-10	74	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: Arabidopsis thaliana
273	GM_53_B2_E02_T7	g4063756	BLASTN	416	9e-12	61	MX110, complete sequence [Arabidopsis thaliana]
274	GM_53_B2_E04_MR	g3513747	BLASTX	247	5e-20	46	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]
275	GM_53_B2_E06_T7	g3097320	BLASTN	394	8e-11	66	Glycine max gene for Bd 30K, complete cds
276	GM_53_B2_E07_T7	g3184508	BLASTN	393	1e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
277	GM_53_B2_E09_MR	g3142328	BLASTN	1844	7e-77	94	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
278	GM_53_B2_E10_T7	g3449327	BLASTN	468	4e-14	72	Glycine max gene for Bd 30K, complete cds
279	GM_53_B2_F01_MR	g3377855	BLASTX	512	2e-48	68	Homo sapiens chromosome 17, clone HRP41C23, complete sequence [Homo sapiens]
280	GM_53_B2_F04_MR	g4151066	BLASTX	243	2e-27	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
							Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]
							(AF076274) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
							(Y10861) ribonucleotide reductase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
281	GM_53_B2_F05_T7	g18559	BLASTN	349	9e-09	77	G.max gene for catalase (AC005561) putative POL3 protein [Arabidopsis thaliana]
282	GM_53_B2_F10_MR	g4063760	BLASTX	512	4e-47	60	Glycine max BSR-101 satellite SB92 genomic sequence.
283	GM_53_B2_F10_T7	g507910	BLASTN	542	7e-18	80	(AB007466) reverse transcriptase-like protein [Vicia faba]
284	GM_53_B2_G01_MR	g2522228	BLASTX	469	8e-44	62	Phoebe sennae large subunit ribosomal RNA gene, partial sequence;
285	GM_53_B2_G04_MR	g2895630	BLASTN	398	3e-11	61	tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
286	GM_53_B2_G09_MR	g3402703	BLASTX	145	9e-09	77	(AC004261) hypothetical protein [Arabidopsis thaliana]
287	GM_53_B2_G09_T7	g1769898	BLASTX	419	3e-38	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
288	GM_53_B2_G11_MR	g1167523	BLASTX	191	8e-13	39	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
289	GM_53_B2_H02_MR	g2555572	BLASTN	1740	2e-72	96	small auxin up RNA gene cluster: orf 15A [Glycine max=soybeans, cv. Wayne, Genomic, 637 nt]
290	GM_54_A1_A02_MR	g1165321	BLASTN	378	4e-10	69	Glycine max extensin (SbHRGP3) gene, complete cds
291	GM_54_A1_A04_MR	g629693	BLASTX	136	1e-11	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
292	GM_54_A1_A05_MR	g507910	BLASTN	660	3e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
293	GM_54_A1_A07_T7	g507910	BLASTN	445	2e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
294	GM_54_A1_A09_MR	g905361	BLASTX	195	1e-13	33	(U22103) gag-protease polypeptide [Glycine max]
295	GM_54_A1_B01_MR	g4063756	BLASTN	498	2e-15	72	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
296	GM_54_A1_B12_MR	g1785699	BLASTX	124	4e-12	44	(Y08501) orf145a [Arabidopsis thaliana]
297	GM_54_A1_C08_MR	g2760839	BLASTX	298	8e-25	48	(AC003105) putative receptor kinase [Arabidopsis thaliana]
298	GM_54_A1_D04_MR	g3142328	BLASTN	386	2e-10	92	Glycine max partial SIRE-1 sequence ribonuclease II and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
299	GM_54_A1_D06_MR	g4063760	BLASTX	167	2e-10	40	Glycine max gene for Bd 30K, complete cds
300	GM_54_A1_D09_T7	g3097320	BLASTN	405	3e-11	74	(U76261) unknown [Hordeum vulgare]
301	GM_54_A1_D10_MR	g1666236	BLASTX	179	1e-12	31	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
302	GM_54_A1_D11_MR	g3687234	BLASTX	192	4e-13	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
303	GM_54_A1_D12_MR	g4063760	BLASTX	251	3e-19	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
304	GM_54_A1_E07_T7	g100484	BLASTX	248	2e-19	55	hypothetical protein - garden snapdragon
305	GM_54_A1_F07_MR	g507910	BLASTN	416	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
306	GM_54_A1_F08_MR	g4092471	BLASTN	441	7e-13	71	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
307	GM_54_A1_F09_MR	g1769897	BLASTX	217	3e-16	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
308	GM_54_A1_G03_MR	g4063760	BLASTX	184	4e-12	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
309	GM_54_A1_G04_MR	g18695	BLASTN	346	9e-09	67	Soybean nodulin 22 gene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
310	GM_54_A1_G10_MR	g2388834	BLASTN	388	2e-10	65	Human DNA sequence from PAC 341110 on chromosome 6q22.2-22.33. Contains 60S ribosomal protein L5 like (pseudo)gene, EST's and STSs
311	GM_54_A1_G11_MR	g2095405	BLASTX	371	2e-32	51	(Y12432) polyprotein [Ananas comosus]
312	GM_54_A2_A12_T7	g4063760	BLASTX	245	1e-18	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
313	GM_54_A2_B05_MR	g3777527	BLASTX	216	2e-15	73	(AF053008) gag-pol polyprotein [Glycine max]
314	GM_54_A2_C03_T7	g4063760	BLASTX	160	1e-09	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
315	GM_54_A2_C04_T7	g3645899	BLASTX	128	1e-09	36	(U68408) 5' end not determined experimentally [Zea mays]
316	GM_54_A2_D12_T7	g4115365	BLASTX	156	4e-09	37	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
317	GM_54_A2_E01_T7	g18559	BLASTN	628	2e-21	76	G.max gene for catalase
318	GM_54_A2_E02_T7	g3645899	BLASTX	313	5e-26	50	(U68408) 5' end not determined experimentally [Zea mays]
319	GM_54_A2_E04_MR	g170606	BLASTN	700	4e-25	67	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
320	GM_54_A2_E06_T7	g1142700	BLASTN	698	5e-25	78	Glycine max satellite STR120-A.2.
321	GM_54_A2_E12_T7	g1658457	BLASTX	348	6e-31	75	(U75248) reverse transcriptase [Gossypium barbadense]
322	GM_54_A2_G11_T7	g3249073	BLASTX	123	4e-09	36	(AC004473) Contains similarity to reverse transcriptase-like protein gb 2244803 from A. thaliana chromosome 4 contig gb Z97336.
323	GM_54_A2_H01_MR	g3142328	BLASTN	536	3e-17	86	[Arabidopsis thaliana]
324	GM_54_A2_H01_T7	g100484	BLASTX	386	3e-34	59	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
325	GM_54_A2_H02_T7	g99922	BLASTX	342	5e-32	74	hypothetical protein - garden snapdragon
326	GM_54_B1_A02_MR	g2342725	BLASTX	193	1e-14	67	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
327	GM_54_B1_A03_MR	g507910	BLASTN	426	1e-12	75	(AC002341) hypothetical protein [Arabidopsis thaliana]
328	GM_54_B1_A06_MR	g507910	BLASTN	414	4e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
329	GM_54_B1_B03_T7	g3142328	BLASTN	624	3e-21	75	Glycine max BSR-101 satellite SB92 genomic sequence.
330	GM_54_B1_B09_T7	g4063760	BLASTX	285	5e-23	56	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
331	GM_54_B1_B10_T7	g18768	BLASTN	374	1e-10	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
332	GM_54_B1_B11_MR	g1769897	BLASTX	178	5e-12	27	Soybean Tgm6 transposable element 3' end
333	GM_54_B1_C01_MR	g19274	BLASTN	374	5e-10	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
334	GM_54_B1_C03_MR	g3319362	BLASTX	343	3e-29	48	L.esculentum mRNA for protein with leucine zipper.
335	GM_54_B1_C05_MR	g3746069	BLASTX	157	3e-09	35	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
336	GM_54_B1_C05_T7	g2443320	BLASTX	380	5e-33	53	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
337	GM_54_B1_D01_T7	g905361	BLASTX	689	4e-67	95	(D85597) polyprotein [Oryza australiensis]
338	GM_54_B1_D03_T7	g3687234	BLASTX	214	2e-15	40	(U22103) gag-protease polyprotein [Glycine max]
							(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
339	GM_54_B1_D08_T7	g18559	BLASTN	1789	3e-74	93	G.max gene for catalase
340	GM_54_B1_D10_MR	g1755186	BLASTX	405	5e-37	53	(U75204) germin-like protein [Arabidopsis thaliana]
341	GM_54_B1_D12_MR	g3777527	BLASTX	636	3e-60	91	(AF053008) gag-pol polyprotein [Glycine max]
342	GM_54_B1_E02_T7	g4038056	BLASTX	359	4e-31	54	(AC005897) putative transposon [Arabidopsis thaliana]
343	GM_54_B1_E05_T7	g2264312	BLASTN	503	1e-15	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
344	GM_54_B1_F02_MR	g4063760	BLASTX	277	4e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
345	GM_54_B1_F02_T7	g507910	BLASTN	747	4e-27	90	Glycine max BSR-101 satellite SB92 genomic sequence.
346	GM_54_B1_F04_MR	g1236949	BLASTX	273	7e-22	91	(U50075) lipoxigenase L-5 [Glycine max]
347	GM_54_B1_F11_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
348	GM_54_B1_F11_T7	g507910	BLASTN	379	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
349	GM_54_B1_G01_MR	g3068705	BLASTX	183	1e-13	62	(AF049236) unknown [Arabidopsis thaliana]
350	GM_54_B1_G02_MR	g4063760	BLASTX	303	7e-25	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
351	GM_54_B1_G02_T7	g507910	BLASTN	729	3e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
352	GM_54_B1_G08_MR	g421955	BLASTX	199	9e-33	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
353	GM_54_B1_G08_T7	g4115365	BLASTX	237	9e-18	39	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
354	GM_54_B1_G09_MR	g2443320	BLASTX	177	2e-11	35	(D85597) polyprotein [Oryza australiensis]
355	GM_54_B1_H01_MR	g507910	BLASTN	552	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
356	GM_54_B1_H01_T7	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
357	GM_54_B1_H02_MR	g905361	BLASTX	272	5e-22	39	(U22103) gag-protease polyprotein [Glycine max]
358	GM_54_B1_H03_T7	g18559	BLASTN	1712	1e-70	92	G.max gene for catalase
359	GM_54_B1_H05_MR	g3478665	BLASTN	350	9e-09	68	Homo sapiens PAC clone DJ0870F17 from 7q33-q36, complete sequence [Homo sapiens]
360	GM_54_B1_H11_MR	g507910	BLASTN	575	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
361	GM_54_B2_A01_T7	g3645899	BLASTX	339	9e-29	49	(U68408) 5' end not determined experimentally [Zea mays]
362	GM_54_B2_A03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
363	GM_54_B2_A03_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
364	GM_54_B2_A06_MR	g2315153	BLASTX	165	6e-11	70	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
365	GM_54_B2_A08_T7	g4038056	BLASTX	352	7e-33	41	(AC005897) putative transposon [Arabidopsis thaliana]
366	GM_54_B2_A10_MR	g2522228	BLASTX	475	2e-44	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
367	GM_54_B2_B05_MR	g1402881	BLASTX	199	6e-14	48	(X98130) non-ltr retrotransposon reverse transcriptase-like protein [Arabidopsis thaliana]
368	GM_54_B2_B06_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
369	GM_54_B2_B06_T7	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
370	GM_54_B2_B07_T7	g2879929	BLASTX	198	4e-15	31	(AB010897) secretory, endostyle (zone2) [Ciona intestinalis]
371	GM_54_B2_B08_MR	g3894391	BLASTX	237	4e-18	42	(AF053997) Hcr2-5B [Lycopersicon esculentum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
372	GM_54_B2_C02_T7	g2895866	BLASTX	175	3e-15	68	(AF045770) methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]
373	GM_54_B2_C06_T7	g132770	BLASTX	183	1e-13	88	CHLOROPLAST 50S RIBOSOMAL PROTEIN L20 gi 71275 pir R5NT20 ribosomal protein L20 - common tobacco chloroplast gi 11852 (Z00044) ribosomal protein L20 [Nicotiana tabacum] 225221 prf 1211235BC ribosomal protein L20 [Nicotiana tabacum] Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
374	GM_54_B2_C08_MR	g505129	BLASTN	352	6e-09	65	Glycine max gene for Bd 30K, complete cds (Y15295) L-ascorbate oxidase [Medicago truncatula] (AF053008) envelope-like [Glycine max]
375	GM_54_B2_C09_MR	g3097320	BLASTN	1734	2e-71	83	Glycine max BSR-101 satellite SB92 genomic sequence.
376	GM_54_B2_C12_T7	g2598579	BLASTX	240	1e-18	68	G.max gene for catalase
377	GM_54_B2_D01_MR	g3142379	BLASTN	174	2e-13	54	(AL031394) putative protein [Arabidopsis thaliana]
378	GM_54_B2_D01_T7	g507910	BLASTN	390	5e-11	73	Arabidopsis thaliana chromosome II BAC F41.23 genomic sequence, complete sequence [Arabidopsis thaliana]
379	GM_54_B2_D09_MR	g18559	BLASTN	390	1e-10	68	Arabidopsis thaliana chromosome II BAC F41.23 genomic sequence, complete sequence [Arabidopsis thaliana]
380	GM_54_B2_D12_MR	g3549664	BLASTX	212	9e-17	51	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) gi 72709 pir F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast gi 225285 prf 121235W photosystem II 44KD protein [Nicotiana tabacum]
381	GM_54_B2_F02_T7	g2583106	BLASTN	433	2e-12	72	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP. 47 PROTEIN) gi 72708 pir QJLV6A photosystem II chlorophyll a-binding protein psbB - liverwort (Marchantia polymorpha) chloroplast gi 11700 (X04465) psbB gene product [Marchantia polymorpha]
382	GM_54_B2_F03_MR	g131289	BLASTX	509	5e-48	85	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] (AC005561) putative POL3 protein [Arabidopsis thaliana] (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
383	GM_54_B2_E03_T7	g131269	BLASTX	277	7e-23	79	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
384	GM_54_B2_E05_MR	g2129618	BLASTX	204	2e-14	42	A.thaliana constans gene.
385	GM_54_B2_F09_MR	g4063760	BLASTX	540	3e-50	72	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
386	GM_54_B2_E09_T7	g3319362	BLASTX	212	3e-15	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
387	GM_54_B2_E11_MR	g4126312	BLASTN	444	5e-13	61	
388	GM_54_B2_E11_T7	g2695704	BLASTN	456	1e-13	66	
389	GM_54_B2_F05_MR	g1431738	BLASTN	410	1e-11	67	
390	GM_54_B2_F09_MR	g3810596	BLASTX	165	2e-17	39	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
391	GM_54_B2_I09_T7	g2414348	BLASTN	377	5e-10	65	Caenorhabditis elegans cosmid Y37A1A, complete sequence [Caenorhabditis elegans] (AC003671) Similar to serine/threonine kinase gb Y12531 from Brassica oleracea. [Arabidopsis thaliana] (U76261) unknown [Hordeum vulgare] Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana] Arabidopsis thaliana genomic DNA, chromosome 5, p1 clone: MUI.8 Arabidopsis thaliana BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. J-domain protein - Arabidopsis thaliana gi 928936 (Z49238) J- domain protein [Arabidopsis thaliana] gi 1585434 prf 2124427A diamide resistance gene [Arabidopsis thaliana] (AC005561) putative POL3 protein [Arabidopsis thaliana] G.max gene for catalase Pisum sativum S-adenosylmethionine decarboxylase mRNA, complete cds. (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana] (AB007466) reverse transcriptase-like protein [Vicia faba] (Y08010) lectin receptor kinase [Arabidopsis thaliana] (Y12321) open reading frame 2 [Brassica oleracea] (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana] (AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score 12.22) [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score 11.19) [Arabidopsis thaliana] Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana] (AL031986) putative protein [Arabidopsis thaliana] Arabidopsis thaliana BAC T9E19 (AL031187) putative transposable element [Arabidopsis thaliana] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U68408) 5' end not determined experimentally [Zea mays] (AJ001200) reverse transcriptase [Alstroemeria aurea]
392	GM_54_B2_F12_MR	g3176673	BLASTX	222	1e-17	44	
393	GM_54_B2_G02_T7	g1666236	BLASTX	154	3e-23	33	
394	GM_54_B2_G03_MR	g3873174	BLASTN	452	2e-13	67	
395	GM_54_B2_G05_MR	g2656030	BLASTN	827	3e-30	68	
396	GM_54_B2_G09_MR	g507910	BLASTN	405	1e-11	74	
397	GM_54_B2_G09_T7	g507910	BLASTN	408	8e-12	75	
398	GM_54_B2_G10_MR	g2129626	BLASTX	173	9e-21	47	
399	GM_54_B2_G12_T7	g4063760	BLASTX	311	1e-25	55	
400	GM_54_B2_H01_MR	g18559	BLASTN	989	8e-38	77	
401	GM_54_B2_H02_T7	g1421750	BLASTN	383	2e-10	83	
402	GM_54_B2_H04_MR	g3319362	BLASTX	262	1e-20	47	
403	GM_54_B2_H07_MR	g2522228	BLASTX	304	2e-43	59	
404	GM_54_B2_H09_MR	g1769897	BLASTX	348	2e-34	65	
405	GM_54_B2_H09_T7	g2462936	BLASTX	235	7e-32	60	
406	GM_54_B2_H12_MR	g3319362	BLASTX	187	9e-27	55	
407	GM_55_A1_A02_T7	g3377848	BLASTX	195	4e-14	37	
408	GM_55_A1_A03_T7	g507910	BLASTN	387	7e-11	78	
409	GM_55_A1_A05_T7	g3513747	BLASTX	404	2e-35	53	
410	GM_55_A1_A08_MR	g4092471	BLASTN	443	6e-13	66	
411	GM_55_A1_A11_T7	g3805845	BLASTX	226	9e-17	63	
412	GM_55_A1_B03_MR	g3859610	BLASTN	862	6e-32	67	
413	GM_55_A1_B04_MR	g3402755	BLASTX	230	6e-28	47	
414	GM_55_A1_B06_MR	g3142328	BLASTN	2136	2e-90	97	
415	GM_55_A1_B10_T7	g3645899	BLASTX	157	2e-09	41	
416	GM_55_A1_C03_MR	g2791937	BLASTX	315	2e-27	64	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
417	GM_55_A1_C05_MR	g3777527	BLASTX	770	2e-74	97	(AF053008) gag-pol polyprotein [Glycine max]
418	GM_55_A1_C07_MR	g18559	BLASTN	1346	5e-54	87	G.max gene for catalase
419	GM_55_A1_C08_MR	g3142328	BLASTN	651	2e-22	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
420	GM_55_A1_C11_MR	g2522230	BLASTX	288	1e-24	40	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976)
421	GM_55_A1_D03_T7	g99726	BLASTX	169	5e-12	47	orf 3 [Arabidopsis thaliana]
422	GM_55_A1_D05_MR	g2522228	BLASTX	416	3e-38	71	(AB007466) reverse transcriptase-like protein [Vicia faba]
423	GM_55_A1_D12_T7	g1707642	BLASTX	205	1e-14	33	(Y07748) TMK [Oryza sativa]
424	GM_55_A1_E02_T7	g3097320	BLASTN	928	5e-35	81	Glycine max gene for Bd 30K, complete cds
425	GM_55_A1_E06_T7	g3142328	BLASTN	951	4e-36	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
426	GM_55_A1_E09_MR	g130582	BLASTX	422	2e-37	55	REVERSE TRANSCRIPTASE ; ENDONUCLEASE (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
427	GM_55_A1_E11_T7	g3650039	BLASTX	258	2e-20	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
428	GM_55_A1_F01_MR	g3142328	BLASTN	1169	5e-46	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975)
429	GM_55_A1_F02_T7	g99730	BLASTX	256	1e-20	56	orf 3 [Arabidopsis thaliana]
430	GM_55_A1_F04_T7	g3859610	BLASTN	586	2e-19	66	Arabidopsis thaliana BAC T9E19
431	GM_55_A1_F10_MR	g99922	BLASTX	460	8e-43	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
432	GM_55_A1_G03_MR	g2656031	BLASTN	496	2e-15	72	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; MXC20
433	GM_55_A1_G08_T7	g3287695	BLASTX	153	5e-09	60	(AC003979) Similar to hypothetical protein C34B7.2 gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis thaliana]
434	GM_55_A1_G10_T7	g130582	BLASTX	154	7e-09	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
435	GM_55_A1_H01_T7	g4063760	BLASTX	464	4e-42	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
436	GM_55_A1_H02_T7	g1769898	BLASTX	295	1e-24	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
437	GM_55_A1_H05_MR	g3142328	BLASTN	1163	9e-46	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
438	GM_55_A1_H10_MR	g3097320	BLASTN	430	2e-12	72	Glycine max gene for Bd 30K, complete cds
439	GM_55_A1_H11_MR	g3334667	BLASTX	212	8e-16	77	(Y10493) putative cytochrome P450 [Glycine max]
440	GM_55_A1_H12_MR	g3777527	BLASTX	699	6e-67	94	(AF053008) gag-pol polyprotein [Glycine max]
441	GM_55_A2_A02_MR	g2522228	BLASTX	264	6e-22	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
442	GM_55_A2_A03_T7	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence
443	GM_55_A2_A05_MR	g507910	BLASTN	630	7e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence
444	GM_55_A2_A05_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence
445	GM_55_A2_A10_MR	g665934	BLASTX	130	8e-13	39	(U20341) ORF III [Cassava vein mosaic virus] gi 1399884 (U59751) ORF 3 [Cassava vein mosaic virus]
446	GM_55_A2_B01_T7	g4038056	BLASTX	295	3e-24	43	(AC005897) putative transposon [Arabidopsis thaliana]
447	GM_55_A2_B03_MR	g505129	BLASTN	378	4e-10	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
448	GM_55_A2_B10_T7	g2865437	BLASTX	219	8e-16	53	(AF039376) polyprotein [Arabidopsis arenosa]
449	GM_55_A2_B12_MR	g507910	BLASTN	351	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence
450	GM_55_A2_B12_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence
451	GM_55_A2_C01_MR	g905361	BLASTX	690	3e-67	92	(U22103) gag-protease polyprotein [Glycine max]
452	GM_55_A2_C02_MR	g905361	BLASTX	303	2e-44	85	(U22103) gag-protease polyprotein [Glycine max]
453	GM_55_A2_C05_MR	g1568664	BLASTX	216	1e-16	38	(U70873) O-methyltransferase [Pinus radiata]
454	GM_55_A2_C08_T7	g3930515	BLASTX	121	4e-12	47	(AF059674) putative gag protein [Nicotiana tabacum]
455	GM_55_A2_C09_T7	g1666236	BLASTX	160	1e-10	30	(U76261) unknown [Hordeum vulgare]
456	GM_55_A2_C12_T7	g522302	BLASTX	171	3e-14	48	(L35053) endonuclease [Magnaporthe grisea]
457	GM_55_A2_D05_MR	g100484	BLASTX	115	4e-09	63	hypothetical protein - garden snapdragon
458	GM_55_A2_D09_T7	g1708314	BLASTX	532	2e-50	76	HEAT SHOCK PROTEIN 83 gi 169296 (M99431) heat shock protein 83 [Pharbitis nil] gi 445625 prf 1909372A heat shock protein 83 [Ipomoea nil]
459	GM_55_A2_E02_MR	g507910	BLASTN	393	4e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence
460	GM_55_A2_E09_MR	g3687234	BLASTX	170	1e-10	34	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
461	GM_55_A2_E10_MR	g507910	BLASTN	348	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence
462	GM_55_A2_E10_T7	g507910	BLASTN	467	2e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence
463	GM_55_A2_F02_MR	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence
464	GM_55_A2_F03_MR	g3831457	BLASTX	349	4e-31	64	(AC005700) putative ion channel protein [Arabidopsis thaliana]
465	GM_55_A2_F04_MR	g2522228	BLASTX	417	3e-38	73	(AB007466) reverse transcriptase-like protein [Vicia faba]
466	GM_55_A2_F06_MR	g3645899	BLASTX	144	7e-20	50	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
467	GM_55_A2_F08_T7	g2073447	BLASTN	416	9e-12	67	L-japonicus gln1, pgl & krm genes (Z97341) similarity to a membrane-associated salt-inducible protein [Arabidopsis thaliana]
468	GM_55_A2_F12_MR	g2244996	BLASTX	385	5e-34	59	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Y13368) reverse transcriptase [Beta vulgaris]
469	GM_55_A2_G02_MR	g3142328	BLASTN	797	4e-29	78	(U22103) gag-protease polyprotein [Glycine max]
470	GM_55_A2_G04_T7	g2462134	BLASTX	328	1e-28	47	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
471	GM_55_A2_G09_MR	g905361	BLASTX	171	4e-11	29	(Y12432) polyprotein [Ananas comosus]
472	GM_55_A2_H03_T7	g2583130	BLASTX	156	7e-13	32	(U76261) unknown [Hordeum vulgare]
473	GM_55_A2_H05_MR	g2995405	BLASTX	450	6e-41	64	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
474	GM_55_A2_H06_T7	g1666236	BLASTX	180	9e-13	28	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
475	GM_55_A2_H08_T7	g130582	BLASTX	358	1e-30	61	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
476	GM_55_A2_H11_T7	g13767	BLASTN	441	9e-14	63	DIHYDROFOLATE REDUCTASE / THYMIDYLATE SYNTHASE (DHFR-TS) gi 1362048 pir S55683 dihydrofolate reductase-thymidylate synthase - soybean gi 999190 bbs 166832 (S78087) dihydrofolate reductase-thymidylate synthase, DHFR-TS=bifunctional enzyme (EC 1.5.1.3) [Glycine max. seedling. Peptide, 530 aa] [Glycine max] gi 1096144 prf 2111237A dihydrofolate reductase-thymidylate synthase [Glycine max] (AC005169) putative copia-like transposable element [Arabidopsis thaliana]
477	GM_55_B1_A03_T7	g1706522	BLASTX	206	2e-31	87	(U76261) unknown [Hordeum vulgare]
478	GM_55_B1_A04_MR	g3687234	BLASTX	172	5e-19	55	Saccharomyces douglasii mtDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
479	GM_55_B1_A04_T7	g1666236	BLASTX	170	1e-11	27	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence [Plasmodium falciparum]
480	GM_55_B1_A05_MR	g13619	BLASTN	503	1e-16	65	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
481	GM_55_B1_A12_MR	g2982576	BLASTN	353	5e-14	62	Caenorhabditis elegans cosmid Y38H8A, complete sequence [Caenorhabditis elegans]
482	GM_55_B1_B05_MR	g2194136	BLASTX	344	4e-29	51	Glycine max gene for Bd 30K, complete cds
483	GM_55_B1_B05_T7	g2815075	BLASTN	470	3e-14	62	
484	GM_55_B1_B06_MR	g3097320	BLASTN	545	1e-17	81	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
485	GM_55_B1_B11_MR	g4140712	BLASTX	197	2e-20	48	(AF110183) putative integrase [Oryza sativa]
486	GM_55_B1_B12_MR	g4063760	BLASTX	492	5e-45	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
487	GM_55_B1_B12_T7	g4063760	BLASTX	458	2e-41	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
488	GM_55_B1_C02_T7	g507910	BLASTN	424	2e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
489	GM_55_B1_C03_MR	g2760832	BLASTX	170	6e-12	43	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]
490	GM_55_B1_C05_T7	g18767	BLASTN	424	7e-23	83	Soybean Tgm6 transposable element 5' end
491	GM_55_B1_C06_MR	g18559	BLASTN	452	2e-13	75	G.max gene for catalase
492	GM_55_B1_C09_MR	g170029	BLASTN	389	1e-10	80	Glycine max cv. Dare nodulin 26 gene fragment.
493	GM_55_B1_C10_MR	g3097320	BLASTN	776	4e-28	80	Glycine max gene for Bd 30K, complete cds
494	GM_55_B1_C11_T7	g3176768	BLASTN	372	9e-11	62	Homo sapiens allele 1 fragile site locus (FRA10B) minisatellite. 3' sequence
495	GM_55_B1_D05_T7	g2708743	BLASTX	191	8e-13	39	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
496	GM_55_B1_D09_T7	g342952	BLASTN	348	1e-09	60	paramecium species 1.168 mt dna dimer: replication init. region.
497	GM_55_B1_D11_MR	g4063760	BLASTX	390	4e-34	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
498	GM_55_B1_D11_T7	g507910	BLASTN	565	6e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
499	GM_55_B1_D12_MR	g2121303	BLASTN	471	3e-14	60	Homo sapiens cosmid Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
500	GM_55_B1_E05_T7	g1167523	BLASTX	417	6e-37	52	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
501	GM_55_B1_E07_MR	g4063760	BLASTX	411	2e-36	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
502	GM_55_B1_F05_T7	g4115942	BLASTX	152	3e-09	84	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=238.4, E= 1e-67, N=1) and EF hand domains (Pfam: PF00036, score=109.0, E=8.9e-29, N=5) [Arabidopsis thaliana]
503	GM_55_B1_F09_MR	g1076286	BLASTX	534	7e-51	82	amidophosphoribosyltransferase - Arabidopsis thaliana gi 469193.gnl PID d1006574 (D28868) amidophosphoribosyltransferase [Arabidopsis thaliana]
504	GM_55_B1_F12_T7	g3645899	BLASTX	146	2e-09	63	(U68408) 5' end not determined experimentally [Zea mays]
505	GM_55_B1_G02_T7	g3097320	BLASTN	1585	9e-65	83	Glycine max gene for Bd 30K, complete cds
506	GM_55_B1_G03_MR	g2522230	BLASTX	151	4e-10	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
507	GM_55_B1_G04_MR	g3831457	BLASTX	340	3e-30	63	(AC005700) putative ion channel protein [Arabidopsis thaliana]
508	GM_55_B1_G08_MR	g2982291	BLASTX	195	7e-22	82	(AF051230) heat shock protein [Picea mariana]
509	GM_55_B1_H06_MR	g2244915	BLASTX	293	6e-24	42	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
510	GM_55_B1_H09_MR	g1666236	BLASTX	219	3e-17	32	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
511	GM_55_B1_H10_MR	g2522230	BLASTX	270	1e-22	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
512	GM_55_B2_A02_MR	g2780996	BLASTX	160	5e-10	54	Chain A, Crystal Structure Of A Eukaryotic (Pea Seedling) Copper-Containing Amine Oxidase At 2.2a Resolution Oxidase, Copper, Pea Seedling, Oxidoreductase Mol_id: 1; Molecule: Copper Amine Oxidase; Chain: A, B; Ec: 1.4.3.6; Biolog... gi 2780997 pdb 1KSI B Chain B, Crystal Structure Of A Eukaryotic (Pea Seedling) Copper-Containing Amine Oxidase At 2.2a Resolution Oxidase, Copper, Pea Seedling, Oxidoreductase Mol_id: 1; Molecule: Copper Amine Oxidase; Chain: A, B; Ec: 1.4.3.6; Biolog...
513	GM_55_B2_A07_T7	g507910	BLASTN	351	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
514	GM_55_B2_B05_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
515	GM_55_B2_B06_T7	g18767	BLASTN	340	5e-09	65	Soybean Tgm6 transposable element 5' end
516	GM_55_B2_B09_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
517	GM_55_B2_C04_MR	g4063760	BLASTX	226	1e-16	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
518	GM_55_B2_C09_T7	g3426334	BLASTN	439	7e-13	61	Pisum sativum pectin methylesterase (repmel) gene, complete cds
519	GM_55_B2_C12_T7	g1142701	BLASTN	734	7e-27	85	Glycine max satellite STR120-A.3.
520	GM_55_B2_D06_T7	g4063760	BLASTX	490	8e-45	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
521	GM_55_B2_D07_T7	g507910	BLASTN	456	5e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
522	GM_55_B2_D08_MR	g402616	BLASTN	401	3e-11	93	G, max satellite DNA
523	GM_55_B2_E06_T7	g4050011	BLASTN	471	3e-14	62	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
524	GM_55_B2_F03_T7	g2997694	BLASTX	158	3e-20	36	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
525	GM_55_B2_F10_T7	g3845197	BLASTN	395	8e-11	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
526	GM_55_B2_G04_MR	g2462058	BLASTX	148	9e-10	46	(Y13389) reverse transcriptase [Antirrhinum majus]
527	GM_55_B2_G05_MR	g2462056	BLASTX	178	6e-13	48	(Y13388) reverse transcriptase [Antirrhinum majus]
528	GM_55_B2_H12_MR	g507910	BLASTN	501	5e-16	84	Glycine max BSR-101 satellite SB92 genomic sequence.
529	GM_56_A1_A02_MR	g1769898	BLASTX	520	3e-49	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
530	GM_56_A1_A03_MR	g507910	BLASTN	340	9e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
531	GM_56_A1_A03_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
532	GM_56_A1_A05_T7	g81869	BLASTX	313	2e-27	62	hydroxyproline-rich glycoprotein (clone Hyp2.13) - kidney bean (fragment) gi 169349 (M18095) hydroxyproline-rich glycoprotein [Phaseolus vulgaris]
533	GM_56_A1_A06_MR	g2656031	BLASTN	354	6e-09	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20
534	GM_56_A1_B02_MR	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
535	GM_56_A1_B03_MR	g3059060	BLASTN	386	2e-10	58	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
536	GM_56_A1_B04_MR	g3142328	BLASTN	968	7e-37	70	Glycine max partial cds, and long terminal repeat, complete sequence like genes, partial cds, and long terminal repeat, complete sequence (AC005897) putative transposon [Arabidopsis thaliana]
537	GM_56_A1_B06_MR	g4038056	BLASTX	241	2e-18	51	Glycine max BSR-101 satellite SB92 genomic sequence.
538	GM_56_A1_C01_MR	g507910	BLASTN	564	7e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence. Ta1-2
539	GM_56_A1_C01_T7	g507910	BLASTN	617	3e-21	83	hypothetical protein 2 - Arabidopsis thaliana retrotransposon (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975)
540	GM_56_A1_C04_T7	g99729	BLASTX	238	3e-19	42	orf 2 [Arabidopsis thaliana]
541	GM_56_A1_D05_MR	g2191182	BLASTX	353	6e-31	44	orf 2 [Arabidopsis thaliana] similar to N. tabacum membrane-associated salt-inducible protein (PID:g473874) [Arabidopsis thaliana]
542	GM_56_A1_D06_T7	g2982243	BLASTX	163	2e-11	47	inducible protein (PID:g473874) [Arabidopsis thaliana]
543	GM_56_A1_D07_MR	g475599	BLASTN	320	3e-11	71	(AF051204) hypothetical protein [Picea mariana]
544	GM_56_A1_D08_MR	g1167523	BLASTX	665	2e-63	64	Glycine max Century 84 BIP isoform B mRNA, complete cds.
545	GM_56_A1_D12_MR	g4063760	BLASTX	111	8e-11	47	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
546	GM_56_A1_E02_MR	g3687828	BLASTN	376	6e-10	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
547	GM_56_A1_E02_T7	g1619602	BLASTX	134	3e-10	53	Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence [Homo sapiens]
548	GM_56_A1_E03_MR	g3834324	BLASTX	145	4e-09	83	(Y08726) MtN3 [Medicago truncatula]
549	GM_56_A1_E03_T7	g1171583	BLASTN	321	9e-12	67	(AC005679) Similar to gb X92762 tafazzins protein from Homo sapiens. [Arabidopsis thaliana]
550	GM_56_A1_E07_MR	g4063760	BLASTX	646	1e-61	57	P.falciparum complete gene map of plastid-like DNA (IR-A)
551	GM_56_A1_E09_MR	g507910	BLASTN	384	9e-11	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
552	GM_56_A1_E10_T7	g4063760	BLASTX	687	6e-66	77	Glycine max BSR-101 satellite SB92 genomic sequence.
553	GM_56_A1_F11_MR	g1666236	BLASTX	259	2e-24	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
554	GM_56_A1_F12_T7	g2335061	BLASTN	397	7e-11	63	(U76261) unknown [Hordeum vulgare]
555	GM_56_A1_G02_MR	g1931642	BLASTX	162	1e-14	47	Homo sapiens chromosome 16 BAC clone CTT987SK-334D11 complete sequence [Homo sapiens]
556	GM_56_A1_G07_MR	g507910	BLASTN	600	2e-20	82	complete sequence [Homo sapiens]
557	GM_56_A1_G07_T7	g507910	BLASTN	570	4e-19	81	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
558	GM_56_A1_G08_MR	g995751	BLASTN	519	1e-16	66	Glycine max BSR-101 satellite SB92 genomic sequence.
559	GM_56_A1_G08_T7	g2661071	BLASTX	218	2e-35	74	Glycine max BSR-101 satellite SB92 genomic sequence.
560	GM_56_A1_G10_MR	g3319351	BLASTX	310	2e-25	34	Glycine max BSR-101 satellite SB92 genomic sequence. encoding Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence (AF035309) similar to 26S proteasome subunit p45 [Homo sapiens] (AF077407) contains similarity to reverse transcriptases (PF:am:rvt.hmm, score: 116.22) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
561	GM_56_A1_G12_T7	g13581	BLASTN	472	4e-15	63	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTUCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
562	GM_56_A1_H01_MR	g2979597	BLASTN	520	2e-16	64	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
563	GM_56_A1_H05_MR	g2688839	BLASTX	128	2e-14	78	(AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense]
564	GM_56_A1_H06_T7	g2995405	BLASTX	321	5e-27	56	(Y12432) polyprotein [Ananas comosus]
565	GM_56_A1_H08_MR	g3097320	BLASTN	1007	1e-38	76	Glycine max gene for Bd 30K, complete cds
566	GM_56_A1_H09_MR	g3695395	BLASTX	224	7e-17	38	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
567	GM_56_A1_H10_T7	g18559	BLASTN	542	2e-17	71	G-max gene for catalase
568	GM_56_A2_A04_T7	g507910	BLASTN	352	3e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
569	GM_56_A2_A08_T7	g3845197	BLASTN	475	2e-14	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
570	GM_56_A2_B01_MR	g4063760	BLASTX	251	3e-19	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
571	GM_56_A2_B02_T7	g3193221	BLASTN	407	2e-11	73	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
572	GM_56_A2_B06_MR	g1666236	BLASTX	205	3e-18	37	(U76261) unknown [Hordeum vulgare]
573	GM_56_A2_B07_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
574	GM_56_A2_B09_T7	g4038056	BLASTX	313	4e-26	45	(AC005897) putative transposon [Arabidopsis thaliana]
575	GM_56_A2_B10_T7	g21376	BLASTN	352	5e-09	70	Sesbania rostrata Srgb3 gene for leghemoglobin
576	GM_56_A2_B11_MR	g905361	BLASTX	408	6e-37	91	(U22103) gag-protease polyprotein [Glycine max]
577	GM_56_A2_B12_T7	g99727	BLASTX	173	2e-11	31	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345510 gnl PID e73213 (X53975) orf 1 [Arabidopsis thaliana]
578	GM_56_A2_C07_MR	g3097320	BLASTN	437	9e-13	69	Glycine max gene for Bd 30K, complete cds
579	GM_56_A2_C11_MR	g1769897	BLASTX	304	9e-26	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
580	GM_56_A2_D01_MR	g4063760	BLASTX	256	9e-21	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
581	GM_56_A2_D01_T7	g4063760	BLASTX	343	4e-29	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
582	GM_56_A2_D07_MR	g3142328	BLASTN	621	4e-21	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence.
583	GM_56_A2_E05_T7	g507910	BLASTN	593	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
584	GM_56_A2_E07_MR	g2522227	BLASTX	152	8e-10	46	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
585	GM_56_A2_E09_T7	g2995405	BLASTX	364	9e-44	63	(Y12432) polyprotein [Ananas comosus]
586	GM_56_A2_E11_MR	g505129	BLASTN	348	9e-09	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
587	GM_56_A2_E12_MR	g3914449	BLASTX	204	5e-15	75	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica]
588	GM_56_A2_F02_T7	g3097320	BLASTN	1265	3e-50	80	Glycine max gene for Bd 30K, complete cds
589	GM_56_A2_F06_T7	g507910	BLASTN	483	3e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
590	GM_56_A2_G02_T7	g1669680	BLASTN	507	7e-16	63	Human DNA sequence from PAC 293E14 contains ESTs, STS (AB007466) reverse transcriptase-like protein [Vicia faba]
591	GM_56_A2_G07_T7	g2522228	BLASTX	398	2e-36	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
592	GM_56_A2_G08_MR	g4063760	BLASTX	372	3e-32	54	(D85597) polyprotein [Oryza australiensis]
593	GM_56_A2_G09_T7	g2443320	BLASTX	292	1e-23	43	Glycine max BSR-101 satellite SB92 genomic sequence.
594	GM_56_A2_G12_MR	g507910	BLASTN	453	7e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
595	GM_56_A2_G12_T7	g507910	BLASTN	509	2e-16	77	(AF053008) gag-pol polyprotein [Glycine max]
596	GM_56_A2_H01_T7	g3777527	BLASTX	144	3e-25	42	Glycine max BSR-101 satellite SB92 genomic sequence.
597	GM_56_A2_H02_MR	g507910	BLASTN	409	7e-12	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC002294) Similar to transcription factor gb Z46606 1658307 and others [Arabidopsis thaliana]
598	GM_56_A2_H04_MR	g3142328	BLASTN	2184	1e-92	95	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MW109, complete sequence [Arabidopsis thaliana]
599	GM_56_A2_H05_T7	g2443887	BLASTX	187	2e-12	59	(AC004238) hypothetical protein [Arabidopsis thaliana]
600	GM_56_A2_H06_MR	g2564051	BLASTN	515	3e-16	64	Glycine max BSR-101 satellite SB92 genomic sequence.
601	GM_56_A2_H07_T7	g3033399	BLASTX	246	3e-19	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
602	GM_56_A2_H08_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
603	GM_56_A2_H08_T7	g4063760	BLASTX	371	4e-32	54	Glycine max BSR-101 satellite SB92 genomic sequence.
604	GM_56_B1_A04_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
605	GM_56_B1_A04_T7	g507910	BLASTN	374	3e-10	72	Glycine max ferritin gene, nuclear gene encoding chloroplast protein, complete cds
606	GM_56_B1_A05_MR	g968986	BLASTN	365	1e-09	73	(AF049236) unknown [Arabidopsis thaliana]
607	GM_56_B1_A05_T7	g3068704	BLASTX	411	1e-43	87	Human DNA sequence from clone 101G11 on chromosome 22q12.
608	GM_56_B1_A06_T7	g3820976	BLASTN	427	3e-12	65	Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complet...
609	GM_56_B1_A07_MR	g1171583	BLASTN	376	6e-10	63	P.falciparum complete gene map of plastid-like DNA (IR-A)
610	GM_56_B1_A10_MR	g2801676	BLASTN	755	6e-28	72	Glycine max telomere-associated sequence STAS5
611	GM_56_B1_B02_T7	g280411	BLASTX	178	7e-16	54	hypothetical protein - rice transposon Tos1 (fragment) gi 218244 gnl PID d1002752 (D12825) reverse transcriptase [Oryza sativa]
612	GM_56_B1_B03_T7	g4092471	BLASTN	471	3e-14	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
613	GM_56_B1_B05_MR	g1666236	BLASTX	154	7e-13	30	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
614	GM_56_B1_B07_T7	g1769896	BLASTN	563	2e-18	75	A.thaliana lectin receptor kinase gene
615	GM_56_B1_C01_MR	g100484	BLASTX	166	4e-17	54	hypothetical protein - garden snapdragon
616	GM_56_B1_C08_MR	g2337888	BLASTN	406	3e-11	75	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]
617	GM_56_B1_C09_MR	g507910	BLASTN	633	5e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
618	GM_56_B1_C12_MR	g18559	BLASTN	647	3e-22	71	G-max gene for catalase
619	GM_56_B1_D02_MR	g2129618	BLASTX	225	1e-16	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
620	GM_56_B1_E01_T7	g3319345	BLASTX	209	5e-15	36	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
621	GM_56_B1_E02_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
622	GM_56_B1_E03_MR	g3645899	BLASTX	322	6e-27	56	(U68408) 5' end not determined experimentally [Zea mays]
623	GM_56_B1_E03_T7	g4063760	BLASTX	559	3e-52	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
624	GM_56_B1_E04_T7	g3142328	BLASTN	1287	2e-51	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
625	GM_56_B1_E05_MR	g507910	BLASTN	389	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
626	GM_56_B1_E05_T7	g507910	BLASTN	402	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
627	GM_56_B1_E06_MR	g2443320	BLASTX	117	7e-13	48	(D85597) polyprotein [Oryza australiensis]
628	GM_56_B1_E07_T7	g3426334	BLASTN	554	4e-18	61	Pisum sativum pectin methyltransferase (rcpme1) gene, complete cds
629	GM_56_B1_E08_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
630	GM_56_B1_E08_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
631	GM_56_B1_E12_T7	g2245104	BLASTX	174	5e-11	44	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
632	GM_56_B1_F02_T7	g3142328	BLASTN	1088	2e-42	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
633	GM_56_B1_F04_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
634	GM_56_B1_F05_MR	g3930515	BLASTX	113	1e-11	42	(AF059674) putative gag protein [Nicotiana tabacum]
635	GM_56_B1_F08_T7	g507910	BLASTN	454	7e-14	81	Glycine max BSR-101 satellite SB92 genomic sequence.
636	GM_56_B1_F10_MR	g99922	BLASTX	612	5e-59	86	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
637	GM_56_B1_G01_T7	g3142328	BLASTN	1303	4e-52	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
638	GM_56_B1_G08_MR	g3777527	BLASTX	149	2e-09	30	(AF053008) gag-pol polyprotein [Glycine max]
639	GM_56_B1_G09_MR	g3777527	BLASTX	243	3e-18	44	(AF053008) gag-pol polyprotein [Glycine max]
640	GM_56_B1_G12_MR	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
641	GM_56_B1_H04_T7	g226407	BLASTX	298	3e-24	52	retrotransposon dell-46 [Lilium henryi]
642	GM_56_B1_H06_MR	g507910	BLASTN	394	3e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
643	GM_56_B1_H06_T7	g3142328	BLASTN	2037	9e-86	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
644	GM_56_B1_H08_T7	g3142328	BLASTN	1999	5e-84	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
645	GM_56_B2_A05_MR	g3869068	BLASTN	359	3e-09	59	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]
646	GM_56_B2_A06_MR	g2924729	BLASTN	697	2e-24	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
647	GM_56_B2_A08_MR	g3873182	BLASTN	600	5e-20	70	Homo sapiens chromosome 17, clone HRPK.235.1_10, complete sequence [Homo sapiens]
648	GM_56_B2_B01_MR	g507910	BLASTN	401	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
649	GM_56_B2_B01_T7	g4063760	BLASTX	105	1e-11	69	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
650	GM_56_B2_B04_MR	g18559	BLASTN	1035	6e-40	75	G-max gene for catalase
651	GM_56_B2_B04_T7	g3142328	BLASTN	1755	9e-73	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
652	GM_56_B2_B11_T7	g4063760	BLASTX	210	1e-35	65	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
653	GM_56_B2_B12_T7	g1769899	BLASTX	190	3e-14	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
654	GM_56_B2_C06_T7	g4063760	BLASTX	290	4e-26	61	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
655	GM_56_B2_C10_T7	g3377855	BLASTX	473	3e-44	72	(AF076274) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
656	GM_56_B2_D04_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
657	GM_56_B2_D04_T7	g507910	BLASTN	555	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
658	GM_56_B2_D06_T7	g2522228	BLASTX	336	1e-29	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
659	GM_56_B2_D10_MR	g2129618	BLASTX	276	4e-22	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
660	GM_56_B2_D12_T7	g3777527	BLASTX	201	7e-14	38	(AF053008) gag-pol polyprotein [Glycine max]
661	GM_56_B2_E02_MR	g3142328	BLASTN	538	2e-17	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
662	GM_56_B2_E03_T7	g3777527	BLASTX	413	2e-36	58	(AF053008) gag-pol polyprotein [Glycine max]
663	GM_56_B2_E08_T7	g505129	BLASTN	398	5e-11	63	Winged bean DNA, Kuntz chymotrypsin inhibitor-3 gene homologous region
664	GM_56_B2_E09_MR	g2894612	BLASTX	153	3e-15	56	(AL021889) putative protein [Arabidopsis thaliana]
665	GM_56_B2_E10_MR	g3377816	BLASTX	114	4e-09	35	(AF076275) contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]
666	GM_56_B2_E11_T7	g507910	BLASTN	436	4e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
667	GM_56_B2_E12_T7	g130582	BLASTX	299	2e-24	42	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE : REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum] Arabidopsis thaliana chromosome IV from 19 cM, complete sequence [Arabidopsis thaliana] (AL022140) LTR retrotransposon like protein [Arabidopsis thaliana] and Saccharomyces cerevisiae mitochondrial Tyr-tRNA, Asn-tRNA and Met-tRNA genes probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum] Glycine max gene for Bd 30K, complete cds hypothetical protein - garden snapdragon (Z97341) similarity to membrane transport protein [Arabidopsis thaliana] Soybean Tgm6 transposable element 3' end (AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana] paramecium species 5,87 mt dna dimer: replication init. region. Human fragile site locus (FRA16B) minisatellite repeat hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana] (AC005311) putative reverse transcriptase [Arabidopsis thaliana] (AF053008) gag-pol polyprotein [Glycine max] (Y08010) lectin receptor kinase [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (AL022223) receptor protein kinase - like protein [Arabidopsis thaliana] (AC002339) unknown protein [Arabidopsis thaliana] Glycine max gene for Bd 30K, complete cds (Y12432) polyprotein [Ananas comosus] Glycine max BSR-101 satellite SB92 genomic sequence. Pisum sativum pectin methylesterase (cpme1) gene, complete cds (AC002391) putative serine/threonine protein kinase [Arabidopsis thaliana] (Y13368) reverse transcriptase [Beta vulgaris]
668	GM_56_B2_F04_T7	g3241935	BLASTN	517	3e-16	64	
669	GM_56_B2_F06_MR	g2961349	BLASTX	279	2e-22	44	
670	GM_56_B2_G01_MR	g2924341	BLASTN	478	8e-15	63	
671	GM_56_B2_G03_T7	g629693	BLASTX	305	2e-26	48	
672	GM_56_B2_G10_MR	g3097320	BLASTN	632	1e-21	86	
673	GM_56_B2_G12_T7	g100484	BLASTX	248	2e-19	57	
674	GM_56_B2_H02_T7	g2245004	BLASTX	283	2e-23	53	
675	GM_56_B2_H04_T7	g18768	BLASTN	408	4e-12	68	
676	GM_56_B2_H05_MR	g3319351	BLASTX	271	2e-21	43	
677	GM_56_B2_H08_T7	g342963	BLASTN	479	3e-15	67	
678	GM_56_B2_H12_MR	g1840106	BLASTN	396	1e-11	62	
679	GM_57_A1_A02_T7	g99726	BLASTX	138	1e-08	52	
680	GM_57_A1_A05_MR	g3746069	BLASTX	237	9e-18	33	
681	GM_57_A1_B03_T7	g3777527	BLASTX	237	1e-17	93	
682	GM_57_A1_B05_MR	g1769897	BLASTX	257	1e-20	57	
683	GM_57_A1_C04_MR	g507910	BLASTN	555	2e-18	79	
684	GM_57_A1_C05_T7	g2982452	BLASTX	211	4e-15	68	
685	GM_57_A1_D02_MR	g2335100	BLASTX	465	9e-43	59	
686	GM_57_A1_D05_MR	g3097320	BLASTN	1148	6e-45	81	
687	GM_57_A1_D05_T7	g2995405	BLASTX	230	3e-17	67	
688	GM_57_A1_D11_MR	g507910	BLASTN	438	4e-13	75	
689	GM_57_A1_E06_MR	g3426334	BLASTN	367	1e-09	69	
690	GM_57_A1_E07_MR	g2642445	BLASTX	87	5e-10	55	
691	GM_57_A1_F08_MR	g2462134	BLASTX	190	2e-13	28	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
692	GM_57_A1_E08_T7	g1167523	BLASTX	211	6e-15	64	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
693	GM_57_A1_F10_MR	g2129618	BLASTX	257	2e-21	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
694	GM_57_A1_G09_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
695	GM_57_A1_G11_MR	g1707007	BLASTX	256	3e-20	32	(U78721) hypothetical protein [Arabidopsis thaliana]
696	GM_57_A1_H01_MR	g3097320	BLASTN	707	6e-25	73	Glycine max gene for Bd 30K, complete cds
697	GM_57_A1_H10_MR	g2853072	BLASTX	453	4e-42	61	(AL021768) putative protein [Arabidopsis thaliana]
698	GM_57_A2_A01_MR	g130582	BLASTX	315	3e-28	57	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
699	GM_57_A2_A02_T7	g2996647	BLASTN	509	6e-16	66	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
700	GM_57_A2_A03_MR	g4063760	BLASTX	460	1e-41	70	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
701	GM_57_A2_A03_T7	g507910	BLASTN	608	7e-21	83	(AC005561) putative POL3 protein [Arabidopsis thaliana]
702	GM_57_A2_A05_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
703	GM_57_A2_A05_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
704	GM_57_A2_B01_T7	g3319362	BLASTX	101	6e-09	30	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
705	GM_57_A2_B03_MR	g507910	BLASTN	407	9e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
706	GM_57_A2_B03_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
707	GM_57_A2_B04_MR	g18559	BLASTN	1043	3e-40	75	G.max gene for catalase
708	GM_57_A2_B05_MR	g18559	BLASTN	865	3e-32	75	G.max gene for catalase
709	GM_57_A2_B08_MR	g421955	BLASTX	325	1e-28	48	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
710	GM_57_A2_B08_T7	g3063465	BLASTX	224	9e-17	51	(AC003981) F22O13.27 [Arabidopsis thaliana]
711	GM_57_A2_B10_MR	g3241854	BLASTX	542	2e-51	62	(AB006009) thaumatin-like protein precursor [Pyrus pyrifolia]
712	GM_57_A2_B10_T7	g1769897	BLASTX	142	1e-10	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
713	GM_57_A2_B11_MR	g99922	BLASTX	270	1e-22	53	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
714	GM_57_A2_B12_MR	g2462058	BLASTX	290	7e-25	50	(Y13389) reverse transcriptase [Antirrhinum majus]
715	GM_57_A2_C01_MR	g99922	BLASTX	442	6e-41	64	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
716	GM_57_A2_C05_MR	g1663549	BLASTX	300	8e-30	52	(U55809) disease resistance protein homolog [Glycine max]
717	GM_57_A2_C05_T7	g3935164	BLASTX	101	1e-11	57	(AC004557) F17L21.7 [Arabidopsis thaliana]
718	GM_57_A2_C07_MR	g387902	BLASTX	244	4e-26	53	(L23524) ORF [Hordeum vulgare]
719	GM_57_A2_C08_MR	g3426334	BLASTN	374	7e-10	65	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
720	GM_57_A2_C08_T7	g170606	BLASTN	879	2e-33	68	Broad bean (V.faba) BamHI repetitive element. 1750 bp family.
721	GM_57_A2_C09_MR	g170080	BLASTN	358	3e-09	67	Soybean seed lectin gene transposable element tgm1.
722	GM_57_A2_C09_T7	g13767	BLASTN	344	2e-09	64	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
723	GM_57_A2_C12_T7	g1619956	BLASTX	120	5e-13	71	(U72151) voltage-gated chloride channel [Arabidopsis thaliana]
724	GM_57_A2_D01_MR	g2465923	BLASTX	194	2e-15	55	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
725	GM_57_A2_D06_T7	g507910	BLASTN	498	7e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
726	GM_57_A2_D07_MR	g3142328	BLASTN	1916	3e-80	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB004906) transposase [Ipomoea purpurea]
727	GM_57_A2_D07_T7	g4063770	BLASTX	130	5e-14	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
728	GM_57_A2_E03_MR	g3319362	BLASTX	345	2e-29	49	(Y12321) open reading frame 2 [Brassica oleracea]
729	GM_57_A2_E04_T7	g2462936	BLASTX	236	4e-24	56	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5
730	GM_57_A2_E07_T7	g3250673	BLASTN	381	4e-10	68	(ESSAII project)
731	GM_57_A2_E09_T7	g3451066	BLASTX	333	2e-29	60	(AL031326) hypothetical protein [Arabidopsis thaliana]
732	GM_57_A2_E10_T7	g3097320	BLASTN	458	1e-13	69	Glycine max gene for Bd 30K, complete cds
733	GM_57_A2_F11_T7	g3097320	BLASTN	506	7e-16	70	Glycine max gene for Bd 30K, complete cds
734	GM_57_A2_F04_MR	g507910	BLASTN	500	6e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
735	GM_57_A2_F08_T7	g2895628	BLASTN	343	9e-09	67	Pteris rapae large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
736	GM_57_A2_F11_MR	g3777527	BLASTX	199	2e-18	92	(AF053008) gag-pol polyprotein [Glycine max]
737	GM_57_A2_F11_T7	g507910	BLASTN	623	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
738	GM_57_A2_G02_MR	g3335341	BLASTX	254	2e-20	43	(AC004512) T8F5.10 [Arabidopsis thaliana]
739	GM_57_A2_G04_MR	g507910	BLASTN	565	6e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
740	GM_57_A2_G04_T7	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
741	GM_57_A2_G06_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
742	GM_57_A2_G06_T7	g4063760	BLASTX	298	6e-48	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
743	GM_57_A2_H01_MR	g3599418	BLASTN	353	6e-09	83	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
744	GM_57_A2_H03_MR	g3135962	BLASTN	457	1e-13	64	Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
745	GM_57_A2_H04_MR	g1171591	BLASTN	269	8e-09	63	P.falciparum complete gene map of plastid-like DNA (IR-B) (Y08502) orf158 [Arabidopsis thaliana]
746	GM_57_A2_H08_MR	g1785744	BLASTX	359	4e-32	57	Glycine max gene for Bd 30K, complete cds
747	GM_57_A2_H08_T7	g3097320	BLASTN	402	4e-11	71	Helianthus annuus homeodomain containing protein (HAHIB-1) mRNA, partial cds.
748	GM_57_A2_H10_MR	g349378	BLASTN	237	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
749	GM_57_A2_H12_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
750	GM_57_A2_H12_T7	g507910	BLASTN	390	5e-11	73	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]
751	GM_57_B1_A04_T7	g2660670	BLASTX	100	2e-14	64	Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1
752	GM_57_B1_A08_T7	g2764525	BLASTN	483	6e-15	65	Glycine max BSR-101 satellite SB92 genomic sequence.
753	GM_57_B1_A10_T7	g507910	BLASTN	368	5e-10	73	(AL022347) putative protein [Arabidopsis thaliana]
754	GM_57_B1_B02_MR	g3021268	BLASTX	234	6e-25	63	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
755	GM_57_B1_B03_T7	g3695387	BLASTX	225	1e-16	64	(AC002387) hypothetical protein [Arabidopsis thaliana]
756	GM_57_B1_B08_MR	g2583128	BLASTX	152	2e-09	66	Glycine max gene for Bd 30K, complete cds
757	GM_57_B1_C03_MR	g3097320	BLASTN	419	6e-12	78	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
758	GM_57_B1_C03_T7	g2522230	BLASTX	162	3e-11	32	(U95973) hypothetical protein [Arabidopsis thaliana]
759	GM_57_B1_C06_T7	g2252634	BLASTX	172	3e-11	41	Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence
760	GM_57_B1_D02_MR	g3845314	BLASTN	430	2e-12	61	(AF053008) gag-pol polyprotein [Glycine max]
761	GM_57_B1_D06_MR	g3777527	BLASTX	612	1e-57	85	(AC005897) putative transposon [Arabidopsis thaliana]
762	GM_57_B1_E01_MR	g4038056	BLASTX	163	3e-20	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
763	GM_57_B1_E03_MR	g4063760	BLASTX	196	2e-13	44	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
764	GM_57_B1_E09_T7	g3695387	BLASTX	222	3e-16	64	Glycine max BSR-101 satellite SB92 genomic sequence.
765	GM_57_B1_E10_MR	g507910	BLASTN	624	1e-21	83	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB
766	GM_57_B1_F05_T7	g3059060	BLASTN	385	2e-10	63	Escort protein 1 (REP-1, RAB proteins geranyltransferase component A 1, Choroideraemia protein, T...
767	GM_57_B1_F06_T7	g18559	BLASTN	710	4e-25	72	G.max gene for catalase
768	GM_57_B1_F10_MR	g18559	BLASTN	464	5e-14	70	G.max gene for catalase
769	GM_57_B1_F10_T7	g2522228	BLASTX	398	3e-36	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
770	GM_57_B1_G06_MR	g4063760	BLASTX	227	9e-17	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
771	GM_57_B1_G06_T7	g507910	BLASTN	583	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
772	GM_57_B1_G07_MR	g18700	BLASTN	683	4e-24	77	Soybean nodulin-23 gene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
773	GM_57_B1_G09_MR	g2462936	BLASTX	166	1e-11	40	(Y12321) open reading frame 2 [Brassica oleracea]
774	GM_57_B1_G09_T7	g3319362	BLASTX	185	4e-28	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
775	GM_57_B1_G10_T7	g1167523	BLASTX	193	5e-23	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
776	GM_57_B1_H01_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
777	GM_57_B1_H01_T7	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
778	GM_57_B2_A01_MR	g2633727	BLASTX	200	1e-14	58	(Z99111) ykrT [Bacillus subtilis]
779	GM_57_B2_A04_T7	g226407	BLASTX	203	4e-14	39	retrotransposon del1-46 [Lilium henryi]
780	GM_57_B2_A05_T7	g3947437	BLASTN	366	2e-09	64	Homo sapiens BAC clone NH0342K06 from 2, complete sequence [Homo sapiens]
781	GM_57_B2_A10_T7	g507910	BLASTN	495	9e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
782	GM_57_B2_A12_MR	g3097320	BLASTN	942	1e-35	78	Glycine max gene for Bd 30K, complete cds
783	GM_57_B2_B07_MR	g3367534	BLASTX	533	2e-49	83	(AC004392) Strong similarity to coater alpha subunit (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis thaliana]
784	GM_57_B2_B08_MR	g3930515	BLASTX	121	4e-13	47	(AF059674) putative gag protein [Nicotiana tabacum]
785	GM_57_B2_B09_MR	g18559	BLASTN	947	6e-36	74	G.max gene for catalase
786	GM_57_B2_B12_T7	g3319362	BLASTX	103	4e-09	32	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
787	GM_57_B2_C03_T7	g4063756	BLASTN	377	5e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
788	GM_57_B2_C05_MR	g2160155	BLASTN	374	7e-10	64	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome I, complete sequence [Arabidopsis thaliana]
789	GM_57_B2_C10_MR	g18559	BLASTN	744	1e-26	73	G.max gene for catalase
790	GM_57_B2_C10_T7	g3777527	BLASTX	334	5e-28	49	(AF053008) gag-pol polypeptide [Glycine max]
791	GM_57_B2_D02_MR	g2367675	BLASTX	169	1e-10	31	(AF017040) Pol [Dictyostelium discoideum]
792	GM_57_B2_D02_T7	g100484	BLASTX	252	1e-21	50	hypothetical protein - garden snapdragon
793	GM_57_B2_D04_MR	g173088	BLASTX	180	1e-11	35	has homology to retroviral pol genes; ORF2 TYB3-2 (5' end of coding region not precisely determined)
794	GM_57_B2_D05_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
795	GM_57_B2_D06_MR	g3510505	BLASTX	234	2e-17	36	(AF030881) pol polypeptide [Fugu rubripes]
796	GM_57_B2_D06_T7	g2129618	BLASTX	159	1e-09	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
797	GM_57_B2_D07_T7	g3930515	BLASTX	120	2e-12	47	(AF059674) putative gag protein [Nicotiana tabacum]
798	GM_57_B2_D08_MR	g2494115	BLASTX	98	2e-13	100	(AC002376) Strong similarity to Arabidopsis ATHSAR1 (gb M90418). ESTs gb T44122.gb N65276.gb AA041135 come from this gene. [Arabidopsis thaliana]
799	GM_57_B2_D09_MR	g3785992	BLASTN	411	2e-11	64	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
800	GM_57_B2_E03_MR	g1871190	BLASTX	307	1e-26	52	(U90439) Ser/Thr kinase isolog [Arabidopsis thaliana]
801	GM_57_B2_E05_T7	g3935164	BLASTX	157	9e-11	43	(AC004557) F17L21.7 [Arabidopsis thaliana]
802	GM_57_B2_E06_T7	g2522230	BLASTX	246	4e-20	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
803	GM_57_B2_E09_T7	g18559	BLASTN	936	2e-35	76	G-max gene for catalase
804	GM_57_B2_F02_MR	g2642661	BLASTX	204	1e-14	63	(AF034545) copalyl pyrophosphate synthase [Stevia rebaudiana]
805	GM_57_B2_F05_T7	g3645899	BLASTX	209	7e-15	52	(U68408) 5' end not determined experimentally [Zea mays]
806	GM_57_B2_F08_MR	g2462134	BLASTX	115	5e-15	36	(Y13368) reverse transcriptase [Beta vulgaris]
807	GM_57_B2_F12_T7	g3599418	BLASTN	723	9e-26	83	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
808	GM_57_B2_G01_T7	g4063760	BLASTX	323	3e-30	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
809	GM_57_B2_G06_T7	g3142328	BLASTN	1038	4e-40	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
810	GM_57_B2_G08_MR	g3702324	BLASTX	209	1e-15	39	(AC005397) hypothetical protein [Arabidopsis thaliana]
811	GM_57_B2_G09_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
812	GM_57_B2_G09_T7	g507910	BLASTN	398	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
813	GM_57_B2_H01_T7	g1277164	BLASTX	287	1e-24	98	(U51853) cysteine proteinase inhibitor [Glycine max]
814	GM_57_B2_H02_MR	g2367675	BLASTX	169	1e-10	31	(AF017040) Pol [Dictyostelium discoideum]
815	GM_57_B2_H02_T7	g100484	BLASTX	260	1e-23	51	hypothetical protein - garden snapdragon
816	GM_57_B2_H05_T7	g1769897	BLASTX	315	2e-34	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
817	GM_57_B2_H06_MR	g421954	BLASTX	160	6e-10	50	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
818	GM_57_B2_H08_T7	g4038056	BLASTX	350	4e-30	51	(AC005897) putative transposon [Arabidopsis thaliana]
819	GM_57_B2_H09_MR	g2246449	BLASTN	352	7e-09	64	Lycopersicon esculentum copia-like retrotransposon ToRTL1.3-hydroxy-3-methylglutaryl CoA reductase 2 (HMG2) gene, complete cds.
820	GM_57_B2_H11_T7	g3645899	BLASTX	233	2e-26	53	(U68408) 5' end not determined experimentally [Zea mays]
821	GM_58_A1_A03_T7	g3142328	BLASTN	1374	2e-55	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
822	GM_58_A1_A04_MR	g505129	BLASTN	413	1e-11	64	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
823	GM_58_A1_A04_T7	g3142328	BLASTN	1681	2e-69	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
824	GM_58_A1_A05_MR	g3758836	BLASTN	372	9e-10	60	Plasmodium falci-parum MAL3P6, complete sequence [Plasmodium falci-parum]
825	GM_58_A1_A08_T7	g2982529	BLASTN	374	7e-10	60	Plasmodium falci-parum DNA *** SEQUENCING IN PROGRESS *** from contig 3-09, complete sequence [Plasmodium falci-parum]
826	GM_58_A1_A09_MR	g18559	BLASTN	1299	6e-52	74	G-max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
827	GM_58_A1_A10_T7	g2618684	BLASTX	184	6e-13	85	(AC002510) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase [Arabidopsis thaliana] gi 3241947 (AC004625) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase [Arabidopsis thaliana]
828	GM_58_A1_A12_MR	g4160362	BLASTN	269	6e-09	63	Saccharomyces cerevisiae complete mitochondrial genome
829	GM_58_A1_A12_T7	g3810596	BLASTX	124	7e-12	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
830	GM_58_A1_B01_MR	g507910	BLASTN	553	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
831	GM_58_A1_B04_MR	g3142328	BLASTN	1112	2e-43	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF053008) envelope-like [Glycine max]
832	GM_58_A1_B08_MR	g3142379	BLASTX	308	1e-26	65	Glycine max BSR-101 satellite SB92 genomic sequence.
833	GM_58_A1_B08_T7	g507910	BLASTN	348	4e-09	71	Soybean nodulin 22 gene
834	GM_58_A1_B09_MR	g18695	BLASTN	392	1e-13	72	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
835	GM_58_A1_B11_MR	g2708743	BLASTX	183	2e-13	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
836	GM_58_A1_B11_T7	g4063760	BLASTX	164	5e-10	25	Glycine max gene for Bd 30K, complete cds
837	GM_58_A1_C01_T7	g3097320	BLASTN	758	3e-27	71	(AC005546) R29425_1 [Homo sapiens]
838	GM_58_A1_C04_MR	g3478637	BLASTX	154	3e-09	57	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
839	GM_58_A1_C05_MR	g2961349	BLASTX	321	8e-27	44	G.max gene for catalase
840	GM_58_A1_C05_T7	g18559	BLASTN	1427	1e-57	76	(AL022580) cytochrome P450 [Arabidopsis thaliana]
841	GM_58_A1_C08_T7	g3080353	BLASTX	165	4e-11	66	(AF053008) gag-pol polyprotein [Glycine max]
842	GM_58_A1_C09_MR	g3777527	BLASTX	821	5e-80	81	(U68408) 5' end not determined experimentally [Zea mays]
843	GM_58_A1_C10_MR	g3645899	BLASTX	395	9e-35	44	(AC004238) Cf-2, 1-like protein [Arabidopsis thaliana]
844	GM_58_A1_C11_T7	g3033389	BLASTX	233	2e-17	40	(U68408) 5' end not determined experimentally [Zea mays]
845	GM_58_A1_D01_T7	g3645899	BLASTX	479	9e-44	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
846	GM_58_A1_D06_T7	g1769898	BLASTX	302	2e-33	39	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
847	GM_58_A1_D07_MR	g3758836	BLASTN	362	3e-09	61	Leishmania tarentolae maxicircle DNA fragment
848	GM_58_A1_D07_T7	g13096	BLASTN	442	5e-13	65	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ;
849	GM_58_A1_D09_T7	g130582	BLASTX	141	2e-13	42	REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
850	GM_58_A1_E02_T7	g3142328	BLASTN	1673	5e-69	94	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
851	GM_58_A1_E04_T7	g1666236	BLASTX	183	3e-25	31	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
852	GM_58_A1_E05_MR	g3176803	BLASTN	506	9e-17	62	Homo sapiens allele 15 fragile site locus (FRA10B) minisatellite sequence
853	GM_58_A1_E06_MR	g3831469	BLASTX	154	3e-09	26	(AC005700) hypothetical protein [Arabidopsis thaliana]
854	GM_58_A1_E09_MR	g1076414	BLASTX	401	7e-36	47	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) gi 757534 (X85974) subtilisin-like protease [Arabidopsis thaliana]
855	GM_58_A1_E10_MR	g1840106	BLASTN	473	2e-15	61	Human fragile site locus (FRA16B) minisatellite repeat
856	GM_58_A1_E12_T7	g3645899	BLASTX	522	2e-48	60	(U68408) 5' end not determined experimentally [Zea mays]
857	GM_58_A1_F03_T7	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
858	GM_58_A1_F06_T7	g18559	BLASTN	1075	1e-41	75	G.max gene for catalase
859	GM_58_A1_F08_T7	g3142328	BLASTN	775	5e-57	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
860	GM_58_A1_F09_T7	g3777527	BLASTX	896	5e-88	95	(AF053008) gag-pol polyprotein [Glycine max]
861	GM_58_A1_F12_MR	g1171583	BLASTN	602	4e-20	63	P.falci-parum complete gene map of plastid-like DNA (IR-A)
862	GM_58_A1_G01_T7	g3492889	BLASTN	396	7e-11	61	Homo sapiens chromosome 17, clone hRPK.746_E_8, complete sequence [Homo sapiens]
863	GM_58_A1_G04_MR	g4150930	BLASTN	496	2e-15	61	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
864	GM_58_A1_G07_MR	g2827715	BLASTX	263	1e-20	47	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
865	GM_58_A1_G10_MR	g4063760	BLASTX	254	1e-19	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
866	GM_58_A1_G10_T7	g507910	BLASTN	738	1e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
867	GM_58_A1_G12_MR	g4063770	BLASTX	231	2e-17	39	(AB004906) transposase [Ipomoea purpurea]
868	GM_58_A1_H01_MR	g2462134	BLASTX	272	2e-28	43	(Y13368) reverse transcriptase [Beta vulgaris]
869	GM_58_A1_H05_MR	g2104683	BLASTX	201	3e-14	56	(X97908) transcription factor [Vicia faba]
870	GM_58_A1_H06_MR	g576756	BLASTN	488	1e-15	63	Myrmecia pilosula H187-133 mitochondrion cytochrome b gene, partial cds.
871	GM_58_A1_H07_T7	g3281868	BLASTX	484	2e-45	63	(AL031004) putative protein [Arabidopsis thaliana]
872	GM_58_A1_H08_MR	g2129618	BLASTX	215	1e-15	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
873	GM_58_A1_H08_T7	g2129618	BLASTX	187	1e-12	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
874	GM_58_A1_H10_MR	g3142328	BLASTN	1181	1e-46	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
875	GM_58_A2_A01_MR	g4063760	BLASTX	516	1e-47	65	Glycine max gene for Bd 30K, complete cds
876	GM_58_A2_A04_T7	g3097320	BLASTN	707	6e-25	77	Glycine max gene for POL3 protein [Arabidopsis thaliana]
877	GM_58_A2_A07_T7	g4063760	BLASTX	310	1e-25	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
878	GM_58_A2_A10_MR	g507910	BLASTN	629	8e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
879	GM_58_A2_A10_T7	g507910	BLASTN	405	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
880	GM_58_A2_B03_T7	g2342686	BLASTX	179	2e-19	46	(AC00106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209). ESTs gb T44436.gb 42252 come from this gene. [Arabidopsis thaliana]
881	GM_58_A2_B04_MR	g3461840	BLASTX	299	3e-24	38	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
882	GM_58_A2_B04_T7	g3599418	BLASTN	360	3e-09	81	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
883	GM_58_A2_B11_T7	g531389	BLASTX	224	3e-16	46	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
884	GM_58_A2_B12_MR	g130582	BLASTX	207	1e-14	40	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
885	GM_58_A2_C02_T7	g4063760	BLASTX	613	5e-58	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
886	GM_58_A2_C06_MR	g3097320	BLASTN	636	9e-22	77	Glycine max gene for Bd 30K, complete cds
887	GM_58_A2_D01_MR	g3097320	BLASTN	914	2e-34	79	Glycine max gene for Bd 30K, complete cds
888	GM_58_A2_D03_T7	g3777527	BLASTX	786	3e-76	96	(AF053008) gag-pol polyprotein [Glycine max]
889	GM_58_A2_D08_MR	g2829923	BLASTX	153	2e-09	67	(AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]
890	GM_58_A2_E03_T7	g2522228	BLASTX	197	2e-14	51	(AB007466) reverse transcriptase-like protein [Vicia faba]
891	GM_58_A2_E04_MR	g18559	BLASTN	679	2e-38	79	G, max gene for catalase
892	GM_58_A2_E04_T7	g905361	BLASTX	411	3e-37	91	(U22103) gag-protease polyprotein [Glycine max]
893	GM_58_A2_E11_T7	g2564750	BLASTN	359	3e-09	69	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
894	GM_58_A2_F02_T7	g3337395	BLASTN	351	8e-09	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
895	GM_58_A2_F03_MR	g2995405	BLASTX	145	3e-24	63	(Y12432) polyprotein [Ananas comosus]
896	GM_58_A2_F04_T7	g2522228	BLASTX	217	1e-16	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
897	GM_58_A2_F06_MR	g632992	BLASTN	421	5e-12	64	Homo sapiens interleukin 9 receptor precursor (IL9R) gene, complete cds
898	GM_58_A2_F07_MR	g4063760	BLASTX	493	3e-45	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
899	GM_58_A2_F07_T7	g507910	BLASTN	367	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
900	GM_58_A2_F08_MR	g3452140	BLASTX	416	3e-38	78	(AJ004901) resistance protein [Glycine max]
901	GM_58_A2_F09_MR	g665934	BLASTX	204	1e-14	35	(U20341) ORF III [Cassava vein mosaic virus] gi 1399884 (U59751) ORF 3 [Cassava vein mosaic virus]
902	GM_58_A2_F09_T7	g3097320	BLASTN	404	3e-11	68	Glycine max gene for Bd 30K, complete cds
903	GM_58_A2_G01_MR	g1899158	BLASTN	560	1e-18	65	Saccharomyces cerevisiae synthetic green fluorescent protein (cox3: GFPm) gene, mitochondrial gene construct, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
904	GM_58_A2_G02_MR	g529353	BLASTX	224	6e-17	47	(U12757) diphenol oxidase [Acer pseudoplatanus]
905	GM_58_A2_G03_MR	g3334663	BLASTX	244	3e-19	95	(Y10491) putative cytochrome P450 [Glycine max]
906	GM_58_A2_G04_MR	g2995405	BLASTX	325	2e-27	53	(Y12432) polypeptide [Ananas comosus]
907	GM_58_A2_G05_MR	g4063756	BLASTN	455	2e-13	71	Arabidopsis thaliana chromosome II BAC T918 genomic sequence, complete sequence [Arabidopsis thaliana]
908	GM_58_A2_G07_MR	g3097320	BLASTN	1445	2e-58	82	Glycine max gene for Bd 30K, complete cds
909	GM_58_A2_G09_MR	g4160362	BLASTN	313	7e-10	60	Saccharomyces cerevisiae complete mitochondrial genome
910	GM_58_A2_G12_T7	g629693	BLASTX	146	7e-09	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
911	GM_58_A2_H02_MR	g529353	BLASTX	289	5e-24	48	(U12757) diphenol oxidase [Acer pseudoplatanus]
912	GM_58_A2_H08_MR	g2281092	BLASTX	236	4e-19	72	(AC002333) hypothetical protein [Arabidopsis thaliana]
913	GM_58_A2_H09_T7	g18559	BLASTN	354	5e-09	75	G max gene for catalase
914	GM_58_B1_A04_T7	g2522230	BLASTX	255	4e-21	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
915	GM_58_B1_A05_MR	g100484	BLASTX	349	3e-30	55	hypothetical protein - garden snapdragon
916	GM_58_B1_A10_MR	g507910	BLASTN	540	8e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
917	GM_58_B1_A10_T7	g4063760	BLASTX	412	2e-36	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
918	GM_58_B1_B01_MR	g3319362	BLASTX	154	4e-09	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
919	GM_58_B1_B03_MR	g3810596	BLASTX	274	6e-22	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
920	GM_58_B1_B05_MR	g3033389	BLASTX	185	2e-12	32	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
921	GM_58_B1_B08_MR	g3979928	BLASTN	413	1e-11	67	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
922	GM_58_B1_B09_MR	g3097320	BLASTN	765	1e-27	72	Glycine max gene for Bd 30K, complete cds
923	GM_58_B1_B11_MR	g4140712	BLASTX	138	2e-21	59	(AF110183) putative integrase [Oryza sativa]
924	GM_58_B1_C02_MR	g3097320	BLASTN	903	7e-34	78	Glycine max gene for Bd 30K, complete cds
925	GM_58_B1_C06_MR	g3097320	BLASTN	1222	3e-48	81	Glycine max gene for Bd 30K, complete cds
926	GM_58_B1_C08_T7	g4140712	BLASTX	303	3e-26	59	(AF110183) putative integrase [Oryza sativa]
927	GM_58_B1_D10_MR	g507910	BLASTN	342	7e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
928	GM_58_B1_D10_T7	g507910	BLASTN	346	5e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
929	GM_58_B1_E01_T7	g3097320	BLASTN	1191	6e-47	77	Glycine max gene for Bd 30K, complete cds
930	GM_58_B1_E02_T7	g18559	BLASTN	1085	3e-42	78	G max gene for catalase
931	GM_58_B1_E04_MR	g507910	BLASTN	433	6e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
932	GM_58_B1_E04_T7	g3142379	BLASTX	422	7e-41	64	(AF053008) envelope-like [Glycine max]
933	GM_58_B1_E06_T7	g18559	BLASTN	726	7e-26	73	G max gene for catalase
934	GM_58_B1_E07_MR	g905361	BLASTX	421	2e-38	95	(U22103) gag-protease polypeptide [Glycine max]
935	GM_58_B1_F01_MR	g507910	BLASTN	444	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
936	GM_58_B1_F01_T7	g3142330	BLASTX	467	1e-43	67	(U96295) envelope-like [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
937	GM_58_B1_F07_MR	g18559	BLASTN	950	5e-36	76	G.max gene for catalase
938	GM_58_B1_F08_T7	g3097320	BLASTN	589	1e-19	73	Glycine max gene for Bd 30K, complete cds
939	GM_58_B1_G04_MR	g309940	BLASTX	328	4e-46	100	MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR gi 100004 pir S25005 heat shock protein, 70K - kidney bean gi 22636 (X66874) 70 kDa heat shock protein [Phaseolus vulgaris] (U68408) 5' end not determined experimentally [Zea mays] Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
940	GM_58_B1_G05_T7	g3045899	BLASTX	172	5e-11	50	G.max gene for catalase
941	GM_58_B1_G09_MR	g3426334	BLASTN	404	3e-11	61	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila
942	GM_58_B1_G09_T7	g18559	BLASTN	866	3e-32	85	gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
943	GM_58_B1_H01_T7	g2129618	BLASTX	204	2e-14	38	(D85597) polyprotein [Oryza australiensis] Tobacco chloroplast genome DNA
944	GM_58_B1_H02_T7	g2443320	BLASTX	292	1e-23	50	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
945	GM_58_B1_H04_MR	g2924257	BLASTN	478	1e-14	82	(AC005561) putative POL3 protein [Arabidopsis thaliana]
946	GM_58_B1_H07_T7	g3426334	BLASTN	432	2e-12	62	Glycine max gene for Bd 30K, complete cds
947	GM_58_B2_A01_T7	g4063760	BLASTX	181	8e-12	42	(U22103) gag-protease polyprotein [Glycine max]
948	GM_58_B2_A06_MR	g3097320	BLASTN	1197	3e-47	81	Glycine max gene for Bd 30K, complete cds
949	GM_58_B2_A07_MR	g905361	BLASTX	172	3e-11	37	hypothetical protein 2 - silk worm transposon mag
950	GM_58_B2_A10_MR	g3097320	BLASTN	857	9e-32	73	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like
951	GM_58_B2_A10_T7	g84801	BLASTX	252	2e-19	36	retroelement Cyclops-2
952	GM_58_B2_B02_T7	g2764526	BLASTN	531	6e-17	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like
953	GM_58_B2_B03_T7	g2764526	BLASTN	528	8e-17	65	retroelement Cyclops-2
954	GM_58_B2_B04_T7	g629693	BLASTX	370	2e-33	58	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
955	GM_58_B2_B12_T7	g2522228	BLASTX	262	1e-21	50	(AB007466) reverse transcriptase-like protein [Vicia faba]
956	GM_58_B2_C01_T7	g1144551	BLASTN	337	6e-09	60	Anopheles melas 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
957	GM_58_B2_C02_T7	g1666236	BLASTX	163	7e-11	27	(U76261) unknown [Hordeum vulgare]
958	GM_58_B2_C04_MR	g2656026	BLASTN	371	1e-09	77	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20
959	GM_58_B2_C05_MR	g3283026	BLASTX	223	5e-19	40	putative transposase [Arabidopsis thaliana]
960	GM_58_B2_C05_T7	g3820757	BLASTN	452	1e-13	66	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
961	GM_58_B2_C07_MR	g507910	BLASTN	499	6e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
962	GM_58_B2_C07_T7	g3097320	BLASTN	348	1e-08	72	Glycine max gene for Bd 30K, complete cds
963	GM_58_B2_C11_T7	g507910	BLASTN	355	2e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
964	GM_58_B2_E01_T7	g3777527	BLASTX	150	9e-21	45	(AF053008) gag-pol polyprotein [Glycine max]

Seq No	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
965	GM_58_B2_E03_MR	g4063760	BLASTX	249	9e-33	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
966	GM_58_B2_E03_T7	g4063760	BLASTX	115	2e-12	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
967	GM_58_B2_E04_MR	g170605	BLASTN	542	7e-18	65	Broad bean (V faba) BamHI repetitive element, 1500 bp family.
968	GM_58_B2_E05_T7	g3645899	BLASTX	211	4e-15	33	(U68408) 5' end not determined experimentally [Zea mays]
969	GM_58_B2_E06_MR	g1666236	BLASTX	177	2e-12	35	(U76261) unknown [Hordeum vulgare]
970	GM_58_B2_E08_MR	g3142328	BLASTN	1115	1e-43	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
971	GM_58_B2_E08_T7	g2655309	BLASTN	344	8e-09	66	Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence
972	GM_58_B2_E11_MR	g507910	BLASTN	635	4e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
973	GM_58_B2_E12_MR	g2522227	BLASTX	150	1e-09	38	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
974	GM_58_B2_F01_MR	g2264320	BLASTN	543	2e-17	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
975	GM_58_B2_F04_MR	g3033389	BLASTX	172	5e-11	32	(AC004238) Cf-2, 1-like protein [Arabidopsis thaliana]
976	GM_58_B2_F05_T7	g2809247	BLASTX	122	1e-10	36	(AC002560) F21B7.16 [Arabidopsis thaliana]
977	GM_58_B2_F07_T7	g3176804	BLASTN	378	6e-11	62	Homo sapiens allele 15 fragile site locus (FRA10B) minisatellite, 3' sequence
978	GM_58_B2_F08_MR	g507910	BLASTN	380	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
979	GM_58_B2_F08_T7	g507910	BLASTN	349	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
980	GM_58_B2_F09_T7	g2129618	BLASTX	233	2e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
981	GM_58_B2_F11_T7	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
982	GM_58_B2_G04_MR	g507910	BLASTN	491	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
983	GM_58_B2_G04_T7	g507910	BLASTN	481	4e-15	79	Glycine max BSR-101 satellite SB92 genomic sequence.
984	GM_58_B2_G09_MR	g905361	BLASTX	223	9e-17	37	Glycine max BSR-101 satellite SB92 genomic sequence.
985	GM_58_B2_G09_T7	g3650039	BLASTX	250	6e-25	56	(U22103) gag-protease polyprotein [Glycine max]
986	GM_58_B2_G12_MR	g1666236	BLASTX	147	4e-09	30	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
987	GM_59_A1_A03_T7	g3834313	BLASTX	220	2e-17	76	(U76261) unknown [Hordeum vulgare]
988	GM_59_A1_A06_MR	g18559	BLASTN	655	1e-22	72	(AC005679) Strong similarity to T16B12.3 gi 3746060 unknown protein from Arabidopsis thaliana BAC gb AC005311. [Arabidopsis thaliana]
989	GM_59_A1_A11_MR	g4115365	BLASTX	157	3e-09	30	G-max gene for catalase
990	GM_59_A1_A11_T7	g861155	BLASTX	169	5e-11	40	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
991	GM_59_A1_B04_T7	g2462134	BLASTX	192	1e-13	41	(Z35162) beta-fructofuranosidase; cell wall invertase I; fructosidase [Vicia faba]
992	GM_59_A1_B10_MR	g4063760	BLASTX	263	2e-22	49	(Y13368) reverse transcriptase [Beta vulgaris]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
993	GM_59_A1_C02_MR	g1785699	BLASTX	162	3e-11	34	(Y08501) orf145a [Arabidopsis thaliana]
994	GM_59_A1_C07_MR	g507910	BLASTN	480	4e-15	79	Glycine max BSR-101 satellite SB92 genomic sequence.
995	GM_59_A1_C07_T7	g507910	BLASTN	352	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
996	GM_59_A1_C09_T7	g3142328	BLASTN	920	1e-34	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence.
997	GM_59_A1_D05_T7	g507910	BLASTN	352	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
998	GM_59_A1_D07_MR	g2522228	BLASTX	154	1e-09	56	(AB007466) reverse transcriptase-like protein [Vicia faba]
999	GM_59_A1_D08_MR	g629693	BLASTX	258	2e-21	45	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1000	GM_59_A1_D09_T7	g3024450	BLASTX	102	2e-11	57	(PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 2143323 gnl PID e319087 (Y13328) 51kDa chlorophyll a protein [Populus deltoides]
1001	GM_59_A1_D11_MR	g3128166	BLASTN	364	2e-09	70	Arabidopsis thaliana chromosome II BAC F411 genomic sequence, complete sequence [Arabidopsis thaliana]
1002	GM_59_A1_F01_T7	g2465923	BLASTX	235	6e-22	72	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
1003	GM_59_A1_F05_T7	g3142379	BLASTX	242	3e-19	66	(AF053008) envelope-like [Glycine max]
1004	GM_59_A1_F10_T7	g422418	BLASTX	112	5e-12	42	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
1005	GM_59_A1_G01_T7	g1709970	BLASTX	308	1e-26	81	60S RIBOSOMAL PROTEIN L10A
1006	GM_59_A1_G07_MR	g1769897	BLASTX	202	7e-25	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1007	GM_59_A1_H03_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
1008	GM_59_A1_H05_T7	g3650039	BLASTX	179	5e-12	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
1009	GM_59_A1_H11_T7	g3834313	BLASTX	191	2e-14	63	(AC005679) Strong similarity to T16B12.3 gi 3746060 unknown protein from Arabidopsis thaliana BAC gb AC005311. [Arabidopsis thaliana]
1010	GM_59_A2_B01_T7	g1431738	BLASTN	504	1e-18	91	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
1011	GM_59_A2_B02_MR	g1142701	BLASTN	228	5e-11	67	Glycine max satellite STR120-A.3.
1012	GM_59_A2_B03_T7	g130582	BLASTX	188	5e-17	44	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
1013	GM_59_A2_B08_T7	g507910	BLASTN	500	6e-16	76	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1014	GM_59_A2_C01_T7	g1769898	BLASTX	160	2e-13	39	Glycine max BSR-101 satellite SB92 genomic sequence. (Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1015	GM_59_A2_C05_T7	g1346388	BLASTX	183	6e-13	86	KNOTTED-LIKE HOMEBOX PROTEIN 4 gi 1045044 (X92393) KNAT4 homeobox protein [Arabidopsis thaliana] hypothetical protein - garden snapdragon (D83003) ORF(AA 1-1338) [Nicotiana tabacum] Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. Soybean nodulin 22 gene Human fragile site locus (FRA16B) minisatellite repeat G. max gene for catalase Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max satellite STR120-A.1. Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence Saccharomyces cerevisiae mitochondria tRNA-Tyr, tRNA-Asn, & tRNA-Met genes (AC004401) putative chloroplast envelope Ca2+-ATPase, 5' partial [Arabidopsis thaliana] (AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana] Glycine max gene for Bd 30K, complete cds Glycine max BSR-101 satellite SB92 genomic sequence. (Y11122) HD-Zip protein [Arabidopsis thaliana] gi 3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana] hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] (Y08010) lectin receptor kinase [Arabidopsis thaliana] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana] (AC005897) putative transposon [Arabidopsis thaliana] hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max] (Y13368) reverse transcriptase [Beta vulgaris] Homo sapiens cosmid Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens] Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
1016	GM_59_A2_D02_MR	g100484	BLASTX	196	7e-16	46	
1017	GM_59_A2_D03_T7	g1167523	BLASTX	111	5e-10	71	
1018	GM_59_A2_D06_MR	g507910	BLASTN	574	3e-19	81	
1019	GM_59_A2_D06_T7	g507910	BLASTN	536	1e-17	77	
1020	GM_59_A2_D09_T7	g18695	BLASTN	505	5e-16	75	
1021	GM_59_A2_D10_MR	g1840106	BLASTN	216	4e-10	72	
1022	GM_59_A2_D10_T7	g18559	BLASTN	1004	2e-38	77	
1023	GM_59_A2_D12_T7	g507910	BLASTN	523	5e-17	77	
1024	GM_59_A2_F02_T7	g1142699	BLASTN	1100	2e-43	80	
1025	GM_59_A2_F05_MR	g3142328	BLASTN	503	9e-16	89	
1026	GM_59_A2_F09_MR	g2879886	BLASTN	426	2e-12	68	
1027	GM_59_A2_F09_T7	g3169170	BLASTX	207	5e-16	67	
1028	GM_59_A2_G03_T7	g3377848	BLASTX	257	4e-21	56	
1029	GM_59_A2_G07_MR	g3097320	BLASTN	350	8e-09	67	
1030	GM_59_A2_H04_MR	g507910	BLASTN	402	1e-11	72	
1031	GM_59_A2_H06_T7	g2145356	BLASTX	116	1e-09	80	
1032	GM_59_A2_H09_MR	g2129618	BLASTX	183	3e-12	40	
1033	GM_59_B1_A05_MR	g1769897	BLASTX	159	6e-15	45	
1034	GM_59_B1_A05_T7	g3142328	BLASTN	1097	9e-43	77	
1035	GM_59_B1_A10_T7	g4063760	BLASTX	192	5e-13	57	
1036	GM_59_B1_B01_T7	g4038056	BLASTX	211	3e-15	47	
1037	GM_59_B1_B02_T7	g99922	BLASTX	535	9e-51	69	
1038	GM_59_B1_B10_T7	g2462134	BLASTX	137	1e-12	42	
1039	GM_59_B1_C03_T7	g2121303	BLASTN	351	8e-09	63	
1040	GM_59_B1_C07_T7	g2764526	BLASTN	424	4e-12	64	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
1041	GM_59_B1_C10_MR	g99922	BLASTX	352	2e-31	66	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA): pid:e150225 [Glycine max]
1042	GM_59_B1_C10_T7	g99721	BLASTX	362	4e-31	50	retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Tal-3 gi 16534 (X13291) polyprotein [Arabidopsis thaliana]
1043	GM_59_B1_D05_MR	g99922	BLASTX	560	2e-53	87	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA): pid:e150225 [Glycine max]
1044	GM_59_B1_D12_MR	g4063760	BLASTX	389	5e-34	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1045	GM_59_B1_D12_T7	g507910	BLASTN	528	3e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
1046	GM_59_B1_E09_MR	g2506276	BLASTX	250	9e-20	64	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (CPN- PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT)) (CPN- 60 ALPHA) gi 2129561 pir S71235 chaperonin-60 alpha chain - Arabidopsis thaliana gi 1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana]
1047	GM_59_B1_E12_T7	g3142328	BLASTN	1922	2e-80	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
1048	GM_59_B1_F10_T7	g2739003	BLASTN	684	3e-24	85	Glycine max cytochrome P450 monooxygenase CYP82C1p (CYP82C1) mRNA, complete cds
1049	GM_59_B1_G03_MR	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1050	GM_59_B1_G04_T7	g1666236	BLASTX	184	3e-13	28	(U76261) unknown [Hordeum vulgare]
1051	GM_59_B1_G10_MR	g840618	BLASTN	346	8e-09	58	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
1052	GM_59_B1_G12_T7	g905361	BLASTX	155	7e-22	51	(U22103) gag-protease polyprotein [Glycine max]
1053	GM_59_B1_H06_T7	g3021266	BLASTX	136	7e-09	69	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana] gi 3292840 gnl PID e1310083 (AL031018) serine/threonine kinase - like protein [Arabidopsis thaliana]
1054	GM_59_B1_H07_T7	g20834	BLASTN	347	9e-09	72	P.sativum PHSP1 mRNA for HSP70
1055	GM_59_B1_H08_MR	g2995405	BLASTX	121	2e-13	51	(Y12432) polyprotein [Ananas comosus]
1056	GM_59_B1_H09_MR	g507910	BLASTN	389	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1057	GM_59_B1_H09_T7	g905361	BLASTX	432	1e-39	95	(U22103) gag-protease polyprotein [Glycine max]
1058	GM_59_B1_H12_T7	g507910	BLASTN	403	1e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
1059	GM_59_B2_A05_MR	g1666236	BLASTX	168	2e-11	35	(U76261) unknown [Hordeum vulgare]
1060	GM_59_B2_A11_MR	g1666236	BLASTX	103	1e-09	33	(U76261) unknown [Hordeum vulgare]
1061	GM_59_B2_A12_MR	g2522230	BLASTX	151	2e-14	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1062	GM_59_B2_B01_T7	g4063760	BLASTX	254	1e-19	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1063	GM_59_B2_B04_T7	g18559	BLASTN	1106	4e-43	76	G-max gene for catalase
1064	GM_59_B2_B07_T7	g3738114	BLASTN	396	7e-11	62	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1065	GM_59_B2_B08_MR	g3142328	BLASTN	462	6e-14	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1066	GM_59_B2_B09_T7	g507910	BLASTN	584	9e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
1067	GM_59_B2_B10_T7	g322663	BLASTX	157	2e-25	53	S-receptor kinase-related protein - Chinese kale gi 17917 (Z18884)
1068	GM_59_B2_C01_MR	g1769898	BLASTX	316	8e-27	50	S-receptor kinase related protein [Arabidopsis thaliana]
1069	GM_59_B2_C01_T7	g4063756	BLASTN	434	1e-12	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1070	GM_59_B2_C08_T7	g2462828	BLASTX	165	2e-21	45	Arabidopsis thaliana chromosome II BAC T9J38 genomic sequence, complete sequence [Arabidopsis thaliana]
1071	GM_59_B2_C10_T7	g3599418	BLASTN	647	1e-25	71	(AF00657) hypothetical protein [Arabidopsis thaliana]
1072	GM_59_B2_C11_MR	g18559	BLASTN	595	6e-20	75	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
1073	GM_59_B2_D01_MR	g3142328	BLASTN	1199	2e-47	80	G max gene for catalase
1074	GM_59_B2_D06_T7	g2522230	BLASTX	245	5e-20	40	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1075	GM_59_B2_D07_MR	g507910	BLASTN	470	1e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
1076	GM_59_B2_D07_T7	g3777527	BLASTX	338	2e-28	49	(AF053008) gag-pol polyprotein [Glycine max]
1077	GM_59_B2_D10_MR	g3877502	BLASTX	159	4e-10	34	(Z49967) ATP-binding protein (CDC48/PAS1/SEC18 family) with strong similarity to the yeast BCS1 protein (Swiss Prot accession number P32839); cDNA EST EMBL:C07371 comes from this gene; cDNA EST EMBL:C08716 comes from this gene
1078	GM_59_B2_D11_MR	g2245136	BLASTX	381	2e-33	79	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]
1079	GM_59_B2_D11_T7	g4092471	BLASTN	473	3e-14	70	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
1080	GM_59_B2_E01_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1081	GM_59_B2_E01_T7	g576752	BLASTN	345	6e-09	61	Myrmecia pilosula H19]-035 mitochondrion cytochrome b gene, partial cds.
1082	GM_59_B2_E02_MR	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1083	GM_59_B2_E04_T7	g4063743	BLASTX	239	3e-24	63	(AC005851) hypothetical protein [Arabidopsis thaliana]
1084	GM_59_B2_E07_T7	g507910	BLASTN	412	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1085	GM_59_B2_E10_MR	g13767	BLASTN	384	3e-11	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMT1G05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
1086	GM_59_B2_E11_T7	g2501460	BLASTX	172	1e-19	71	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gml PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens] (AF053008) gag-pol polyprotein [Glycine max] (U76261) unknown [Hordeum vulgare] probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum] hypothetical protein [Arabidopsis thaliana] Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene C.parapsilosis mitochondrial DNA for right telomeric region and ATP6 gene (AC005561) putative POL3 protein [Arabidopsis thaliana] (Y13389) reverse transcriptase [Antirrhinum majus] (AC002332) putative ribonucleoprotein [Arabidopsis thaliana] (AF053008) gag-pol polyprotein [Glycine max] (Y13389) reverse transcriptase [Antirrhinum majus] hypothetical protein - garden snapdragon Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. (AC005897) putative transposon [Arabidopsis thaliana] (AC000103) F21J9.24 [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence. complete sequence [Arabidopsis thaliana] Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens] (AF053008) gag-pol polyprotein [Glycine max] Glycine max BSR-101 satellite SB92 genomic sequence. Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence. complete sequence [Arabidopsis thaliana] Glycine max partial SIRE-1 sequence ribonuclease H and envelope like genes, partial cds. and long terminal repeat, complete sequence
1087	GM_59_B2_F05_T7	g3777527	BLASTX	734	1e-70	97	
1088	GM_59_B2_F06_T7	g1666236	BLASTX	188	1e-13	28	
1089	GM_59_B2_F07_T7	g629693	BLASTX	227	8e-18	44	
1090	GM_59_B2_F10_T7	g2864621	BLASTX	146	6e-16	48	
1091	GM_59_B2_G02_MR	g1480927	BLASTN	373	6e-10	68	
1092	GM_59_B2_H02_T7	g479124	BLASTN	471	2e-14	64	
1093	GM_59_B2_H03_T7	g4063760	BLASTX	355	2e-30	58	
1094	GM_59_B2_H12_T7	g2462058	BLASTX	222	1e-17	37	
1095	GM_60_A1_A02_T7	g2459445	BLASTX	245	8e-20	64	
1096	GM_60_A1_A04_MR	g3777527	BLASTX	244	4e-24	48	
1097	GM_60_A1_A10_T7	g2462058	BLASTX	287	2e-24	64	
1098	GM_60_A1_A11_T7	g100484	BLASTX	203	2e-14	47	
1099	GM_60_A1_B04_MR	g507910	BLASTN	617	3e-21	83	
1100	GM_60_A1_B04_T7	g507910	BLASTN	611	5e-21	84	
1101	GM_60_A1_B09_MR	g4038056	BLASTX	261	2e-23	42	
1102	GM_60_A1_B10_MR	g2213632	BLASTX	148	4e-11	41	
1103	GM_60_A1_C04_MR	g507910	BLASTN	575	2e-19	82	
1104	GM_60_A1_C04_T7	g4063756	BLASTN	363	2e-09	66	
1105	GM_60_A1_C12_MR	g4150930	BLASTN	371	1e-09	64	
1106	GM_60_A1_D09_T7	g3777527	BLASTX	178	2e-11	35	
1107	GM_60_A1_E04_MR	g507910	BLASTN	581	1e-19	83	
1108	GM_60_A1_E04_T7	g4063756	BLASTN	422	5e-12	64	
1109	GM_60_A1_F01_T7	g3142328	BLASTN	571	7e-19	68	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1110	GM_60_A1_F04_MR	g2244915	BLASTX	192	4e-13	36	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
1111	GM_60_A1_F05_MR	g4038056	BLASTX	330	6e-28	48	(AC005897) putative transposon [Arabidopsis thaliana]
1112	GM_60_A1_F07_MR	g3097320	BLASTN	898	1e-33	79	Glycine max gene for Bd 30K, complete cds
1113	GM_60_A1_F08_MR	g2465527	BLASTX	342	5e-30	63	(AF000354) phosphate transporter [Medicago truncatula]
1114	GM_60_A1_G05_MR	g2522230	BLASTX	241	1e-19	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1115	GM_60_A1_G09_MR	g4063760	BLASTX	437	4e-39	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1116	GM_60_A1_G10_T7	g185559	BLASTN	667	3e-23	74	G-max gene for catalase
1117	GM_60_A1_H05_T7	g3142328	BLASTN	1245	2e-49	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1118	GM_60_A1_H08_T7	g3688328	BLASTX	293	4e-25	61	(AJ228325) reverse transcriptase [Ginkgo biloba]
1119	GM_60_A1_H10_MR	g507910	BLASTN	517	9e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1120	GM_60_A1_H10_T7	g507910	BLASTN	446	1e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1121	GM_60_A2_A03_T7	g2522227	BLASTX	143	9e-09	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
1122	GM_60_A2_A08_T7	g3059060	BLASTN	365	2e-09	66	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
1123	GM_60_A2_B02_MR	g20749	BLASTN	374	9e-11	66	Pea PSU2 gene for U2 snRNA
1124	GM_60_A2_B03_MR	g507910	BLASTN	394	3e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
1125	GM_60_A2_C04_MR	g3097320	BLASTN	424	4e-12	68	Glycine max gene for Bd 30K, complete cds
1126	GM_60_A2_C07_MR	g905361	BLASTX	211	2e-15	65	(U22103) gag-protease polypeptide [Glycine max]
1127	GM_60_A2_C08_MR	g3269288	BLASTX	182	2e-13	70	(AL030978) putative protein [Arabidopsis thaliana]
1128	GM_60_A2_C10_MR	g3859610	BLASTN	484	8e-15	64	Arabidopsis thaliana BAC T9E19
1129	GM_60_A2_D01_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1130	GM_60_A2_D04_MR	g3142328	BLASTN	1090	2e-42	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1131	GM_60_A2_D04_T7	g4038056	BLASTX	275	4e-22	46	(AC005897) putative transposon [Arabidopsis thaliana]
1132	GM_60_A2_D08_MR	g3777527	BLASTX	158	1e-15	36	(AF053008) gag-pol polypeptide [Glycine max]
1133	GM_60_A2_D09_T7	g3097320	BLASTN	879	9e-33	78	Glycine max gene for Bd 30K, complete cds
1134	GM_60_A2_D11_MR	g3097320	BLASTN	466	5e-14	66	Glycine max gene for Bd 30K, complete cds
1135	GM_60_A2_E03_T7	g3777527	BLASTX	424	1e-37	85	(AF053008) gag-pol polypeptide [Glycine max]
1136	GM_60_A2_E12_MR	g3738089	BLASTX	154	4e-10	40	(AC005617) similar to symbiotic ammonium transporter, SAT1 [Arabidopsis thaliana]
1137	GM_60_A2_F02_MR	g1769898	BLASTX	413	1e-37	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1138	GM_60_A2_F03_MR	g22490	BLASTX	176	3e-15	48	(X01380) ORF1 [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
1170	GM_60_B2_A05_MR	g13597	BLASTN	308	9e-14	63	Yeast mitochondrial tRNA genes for tRNA-Ala, tRNA-Tyr and tRNA-Ile
1171	GM_60_B2_A10_MR	g3142328	BLASTN	1136	2e-44	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (D30666) brain acyl-CoA synthase II [Rattus norvegicus]
1172	GM_60_B2_B09_MR	g1468969	BLASTX	138	1e-13	51	Glycine max gene for Bd 30K, complete cds
1173	GM_60_B2_B11_MR	g3097320	BLASTN	390	1e-10	76	Glycine max gene for common sunflower gi 1208940 (L76588)
1174	GM_60_B2_C03_MR	g2130016	BLASTX	209	2e-32	50	homeotic protein 1 - common sunflower gi 1208940 (L76588)
1175	GM_60_B2_C04_MR	g2443320	BLASTX	407	9e-50	54	homeodomain protein 1 [Helianthus annuus]
1176	GM_60_B2_C05_T7	g1431738	BLASTN	355	9e-16	92	(D85597) polyprotein [Oryza australiensis]
1177	GM_60_B2_C10_T7	g18559	BLASTN	1109	3e-43	73	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
1178	GM_60_B2_C11_MR	g507910	BLASTN	387	7e-11	74	G-max gene for catalase
1179	GM_60_B2_D03_MR	g3599418	BLASTN	617	6e-21	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1180	GM_60_B2_D05_MR	g2443320	BLASTX	233	2e-17	35	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene
1181	GM_60_B2_D06_MR	g3242700	BLASTN	364	2e-09	65	Glycine max mitochondrial protein, complete cds encoding mitochondrial protein, complete cds (D85597) polyprotein [Oryza australiensis]
1182	GM_60_B2_D07_MR	g505129	BLASTN	398	5e-11	65	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.
1183	GM_60_B2_E03_T7	g4063760	BLASTX	655	2e-62	73	complete sequence [Arabidopsis thaliana]
1184	GM_60_B2_E04_MR	g505129	BLASTN	417	2e-15	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
1185	GM_60_B2_E05_MR	g2245044	BLASTX	204	1e-21	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1186	GM_60_B2_E06_T7	g2764525	BLASTN	746	6e-27	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
1187	GM_60_B2_E07_MR	g3777527	BLASTX	621	1e-58	83	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
1188	GM_60_B2_F09_MR	g2522230	BLASTX	182	2e-13	35	Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1
							(AF053008) gag-pol polyprotein [Glycine max]
							(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
1189	GM_60_B2_E10_T7	g136636	BLASTX	222	1e-17	100	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana Ubiquitin Conjugation, Ligase Mol_id: 1; Molecule: Ubiquitin Conjugating Enzyme; Chain: Null; Synonym: Ubc1; Ec: 6.3.2.19; Engineered: Yes gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] gi 431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana] (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba] (D85597) polyprotein [Oryza australiensis] (hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max] Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. (U22103) gag-protease polyprotein [Glycine max] (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana] (AC002354) No definition line found [Arabidopsis thaliana] (AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana] (AC005561) putative POL3 protein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (AC005561) putative POL3 protein [Arabidopsis thaliana] PROTEIN KINASE PVPK-1 gi 100013 pir A30311 protein kinase C (EC 2.7.1.-) homolog - kidney bean gi 169361 (J04555) PVPK-1 protein [Phaseolus vulgaris] P.falciparum complete gene map of plastid-like DNA (IR-A) (AF053008) gag-pol polyprotein [Glycine max]
1190	GM_60_B2_E11_T7	g2522230	BLASTX	255	4e-21	44	
1191	GM_60_B2_E12_T7	g2443320	BLASTX	324	5e-27	44	
1192	GM_60_B2_F02_T7	g99922	BLASTX	348	2e-51	85	
1193	GM_60_B2_F03_MR	g995751	BLASTN	533	2e-17	59	
1194	GM_60_B2_F05_T7	g3142328	BLASTN	894	2e-33	77	
1195	GM_60_B2_F06_MR	g507910	BLASTN	597	2e-20	81	
1196	GM_60_B2_F06_T7	g507910	BLASTN	642	2e-22	85	
1197	GM_60_B2_F07_T7	g507910	BLASTN	557	1e-18	81	
1198	GM_60_B2_F08_T7	g905361	BLASTX	439	2e-40	97	
1199	GM_60_B2_G01_MR	g3319362	BLASTX	457	2e-41	51	
1200	GM_60_B2_G02_MR	g2558654	BLASTX	411	3e-36	55	
1201	GM_60_B2_G06_MR	g3319345	BLASTX	225	1e-16	35	
1202	GM_60_B2_G07_T7	g4063760	BLASTX	212	4e-15	48	
1203	GM_60_B2_G08_MR	g507910	BLASTN	430	8e-13	78	
1204	GM_60_B2_G08_T7	g4063760	BLASTX	463	6e-42	57	
1205	GM_60_B2_G10_T7	g125568	BLASTX	780	9e-77	95	
1206	GM_60_B2_H02_T7	g1171583	BLASTN	317	8e-12	64	
1207	GM_60_B2_H03_MR	g3777527	BLASTX	326	3e-34	50	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1208	GM_60_B2_H05_MR	g3142328	BLASTN	822	3e-30	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence Arabidopsis thaliana BAC F19G10, complete sequence (Y08010) lectin receptor kinase [Arabidopsis thaliana] (AC003981) F22O13.23 [Arabidopsis thaliana] G.max gene for catalase (AB007466) reverse transcriptase-like protein [Vicia faba] Glycine max BSR-101 satellite SB92 genomic sequence, Glycine max BSR-101 satellite SB92 genomic sequence, Glycine max BSR-101 satellite SB92 genomic sequence, (Y13389) reverse transcriptase [Antirrhinum majus] (AC005936) hypothetical protein [Arabidopsis thaliana] Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana] (AC005561) putative POL.3 protein [Arabidopsis thaliana] Glycine max telomere-associated sequence STAS8 (Y10860) hypothetical protein [Musa acuminata] (AC005170) putative reverse transcriptase [Arabidopsis thaliana] (AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana] (AB007466) reverse transcriptase-like protein [Vicia faba] (AB007466) reverse transcriptase-like protein [Vicia faba] Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence, (AC005561) putative POL.3 protein [Arabidopsis thaliana] G.max gene for catalase G.max gene for catalase (U72725) retrofit [Oryza longistaminata] (AF084026) NBS type putative resistance protein [Phaseolus vulgaris] (AC003673) putative reverse transcriptase [Arabidopsis thaliana] (AF000952) putative sugar transporter [Prunus armeniaca] (U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum] G.max gene for catalase (Y12432) polyprotein [Ananas comosus] (AC005561) putative POL.3 protein [Arabidopsis thaliana] (D85597) polyprotein [Oryza australiensis]
1209	GM_60_B2_H07_MR	g2098816	BLASTN	362	3e-09	59	
1210	GM_60_B2_H07_T7	g1769897	BLASTX	490	5e-46	62	
1211	GM_60_B2_H09_T7	g3063461	BLASTX	156	3e-09	32	
1212	GM_61_A1_A04_T7	g18559	BLASTN	413	1e-11	70	
1213	GM_61_A1_A05_T7	g2522228	BLASTX	263	8e-22	74	
1214	GM_61_A1_A06_MR	g507910	BLASTN	381	1e-10	73	
1215	GM_61_A1_A06_T7	g507910	BLASTN	389	6e-11	71	
1216	GM_61_A1_A08_T7	g2462058	BLASTX	196	1e-18	53	
1217	GM_61_A1_A09_MR	g4038037	BLASTX	183	4e-12	55	
1218	GM_61_A1_B02_MR	g4092471	BLASTN	431	2e-12	70	
1219	GM_61_A1_B09_MR	g4063760	BLASTX	332	6e-28	66	
1220	GM_61_A1_B12_MR	g2801679	BLASTN	594	2e-20	82	
1221	GM_61_A1_C03_MR	g1813979	BLASTX	232	9e-29	67	
1222	GM_61_A1_C03_T7	g3738337	BLASTX	296	4e-24	44	
1223	GM_61_A1_C07_T7	g3377848	BLASTX	306	2e-26	52	
1224	GM_61_A1_C10_T7	g2522228	BLASTX	359	4e-32	72	
1225	GM_61_A1_D01_MR	g2522228	BLASTX	263	9e-22	79	
1226	GM_61_A1_D02_T7	g4159706	BLASTN	423	2e-20	68	
1227	GM_61_A1_D05_MR	g507910	BLASTN	375	2e-10	72	
1228	GM_61_A1_D08_MR	g4063760	BLASTX	309	2e-25	62	
1229	GM_61_A1_D09_MR	g18559	BLASTN	831	1e-30	78	
1230	GM_61_A1_D10_MR	g18559	BLASTN	900	9e-34	75	
1231	GM_61_A1_D10_T7	g2586082	BLASTX	118	1e-09	38	
1232	GM_61_A1_D11_MR	g3493149	BLASTX	259	1e-21	63	
1233	GM_61_A1_E01_T7	g3004545	BLASTX	153	9e-09	35	
1234	GM_61_A1_E02_T7	g2688830	BLASTX	227	1e-23	96	
1235	GM_61_A1_E04_MR	g1184075	BLASTX	202	4e-14	49	
1236	GM_61_A1_E05_MR	g18559	BLASTN	749	6e-27	76	
1237	GM_61_A1_E06_T7	g2995405	BLASTX	161	7e-10	45	
1238	GM_61_A1_F06_MR	g4063760	BLASTX	188	1e-12	45	
1239	GM_61_A1_F08_T7	g2443320	BLASTX	270	3e-21	53	

Seq No	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1240	GM_61_A1_F11_T7	g3252807	BLASTX	157	1e-09	38	(AC004705) hypothetical protein [Arabidopsis thaliana]
1241	GM_61_A1_F12_MR	g1769899	BLASTX	294	3e-25	73	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1242	GM_61_A1_G01_MR	g2760170	BLASTN	469	4e-14	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]
1243	GM_61_A1_G02_MR	g3097320	BLASTN	486	7e-21	75	Glycine max gene for Bd 30K, complete cds
1244	GM_61_A1_G03_T7	g3810596	BLASTX	231	5e-22	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
1245	GM_61_A1_G07_MR	g4092471	BLASTN	473	3e-14	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
1246	GM_61_A1_G12_T7	g507910	BLASTN	344	6e-09	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1247	GM_61_A1_H01_T7	g2129618	BLASTX	185	2e-12	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
1248	GM_61_A1_H06_MR	g4063760	BLASTX	188	1e-12	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1249	GM_61_A1_H08_MR	g3097320	BLASTN	740	2e-26	75	Glycine max gene for Bd 30K, complete cds
1250	GM_61_A1_H10_T7	g3777527	BLASTX	151	5e-18	44	(AF053008) gag-pol polyprotein [Glycine max]
1251	GM_61_A1_H12_MR	g4063760	BLASTX	243	2e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1252	GM_61_A2_A10_MR	g99755	BLASTX	263	8e-30	50	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
1253	GM_61_A2_A12_T7	g2443320	BLASTX	242	3e-18	48	(D85597) polyprotein [Oryza australiensis]
1254	GM_61_A2_B02_T7	g3142328	BLASTN	1358	1e-54	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1255	GM_61_A2_B04_T7	g1167523	BLASTX	271	2e-21	38	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1256	GM_61_A2_B05_T7	g2522228	BLASTX	362	2e-32	61	(AB007466) reverse transcriptase-like protein [Vicia faba]
1257	GM_61_A2_B08_MR	g1171591	BLASTN	434	1e-12	62	P.falciparum complete gene map of plastid-like DNA (IR-B)
1258	GM_61_A2_B10_MR	g3513745	BLASTX	222	5e-16	35	P.falciparum complete gene map of plastid-like DNA (IR-B) (AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
1259	GM_61_A2_C01_T7	g255578	BLASTN	525	1e-17	85	small auxin up RNA gene cluster: orf X10A [Glycine max=soybeans, cv. Wayne, Genomic, 666 nt]
1260	GM_61_A2_C02_T7	g3820757	BLASTN	436	6e-13	65	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
1261	GM_61_A2_C06_T7	g1658457	BLASTX	243	7e-20	60	(U75248) reverse transcriptase [Gossypium barbadense]
1262	GM_61_A2_C10_MR	g905361	BLASTX	369	1e-32	85	(U22103) gag-protease polyprotein [Glycine max]
1263	GM_61_A2_C12_T7	g2924341	BLASTN	441	4e-13	61	Saccharomyces cerevisiae mitochondrial Tyr-tRNA, Asn-tRNA and Met-tRNA genes
1264	GM_61_A2_D01_T7	g1076755	BLASTX	496	5e-49	76	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
1265	GM_61_A2_D08_T7	g507910	BLASTN	349	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
1266	GM_61_A2_F03_MR	g2735841	BLASTX	284	5e-23	43	(AF010283) No definition line found [Sorghum bicolor]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
1267	GM_61_A2_F05_T7	g2522228	BLASTX	97	5e-17	52	(AB007466) reverse transcriptase-like protein [Vicia faba]
1268	GM_61_A2_F06_T7	g3142328	BLASTN	1087	3e-42	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
1269	GM_61_A2_G01_T7	g4063760	BLASTX	477	2e-43	68	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (V00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum]
1271	GM_61_A2_H07_T7	g117822	BLASTX	290	3e-39	87	CYTOCROME B6 gi 65635 pir CBNT6 plastoquinol-plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - common tobacco chloroplast gi 11858 (Z00044) cytochrome b6 [Nicotiana tabacum] gi 225226 prf 1211235BH cytochrome b6 [Nicotiana tabacum] (Z97336) hypothetical protein [Arabidopsis thaliana] (AC005561) putative POL3 protein [Arabidopsis thaliana] (U72725) retrofit [Oryza longistaminata] (AB007466) reverse transcriptase-like protein [Vicia faba] (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1272	GM_61_A2_H10_MR	g2244807	BLASTX	221	7e-18	55	hypothetical protein - garden snapdragon
1273	GM_61_A2_H11_MR	g4063760	BLASTX	248	8e-20	51	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]
1274	GM_61_A2_H11_T7	g2586082	BLASTX	196	2e-13	38	(AL031187) putative transposable element [Arabidopsis thaliana]
1275	GM_61_B1_A09_MR	g2522228	BLASTX	194	5e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1276	GM_61_B1_B03_MR	g3319362	BLASTX	200	6e-14	41	G.max gene for catalase
1277	GM_61_B1_B03_T7	g100484	BLASTX	344	1e-29	50	AUXIN-INDUCED PROTEIN PCNT115 gi 100305 pir S16390
1278	GM_61_B1_B06_T7	g3242700	BLASTN	357	4e-09	59	auxin-induced protein - common tobacco gi 19799 (X56267) auxin-induced protein [Nicotiana tabacum]
1279	GM_61_B1_B07_T7	g3402755	BLASTX	347	2e-29	43	TY3-2 orfB
1280	GM_61_B1_B09_MR	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1281	GM_61_B1_B11_MR	g18559	BLASTN	1085	3e-42	89	Glycine max BSR-101 satellite SB92 genomic sequence.
1282	GM_61_B1_C07_T7	g728744	BLASTX	128	2e-09	42	Glycine max gene for Bd 30K, complete cds
1283	GM_61_B1_D04_T7	g1326016	BLASTX	167	2e-10	40	A.thaliana ATK1 gene
1284	GM_61_B1_D05_MR	g507910	BLASTN	500	6e-16	80	(AC005560) hypothetical protein [Arabidopsis thaliana]
1285	GM_61_B1_D06_MR	g507910	BLASTN	553	2e-18	78	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
1286	GM_61_B1_D09_MR	g3097320	BLASTN	423	4e-12	79	
1287	GM_61_B1_D11_MR	g984045	BLASTN	355	5e-09	74	
1288	GM_61_B1_D12_T7	g3785980	BLASTX	323	1e-27	49	
1289	GM_61_B1_E03_MR	g3695395	BLASTX	171	4e-11	44	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1290	GM_61_B1_E03_T7	g130582	BLASTX	242	1e-33	50	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1291	GM_61_B1_E04_T7	g2980757	BLASTN	406	3e-11	66	Arabidopsis thaliana DNA chromosome 4, BAC clone F6118 (ESSAII project)
1292	GM_61_B1_E05_MR	g3599418	BLASTN	512	3e-16	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
1293	GM_61_B1_E09_T7	g2129618	BLASTX	197	1e-13	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] (AF053008) gag-pol polyprotein [Glycine max]
1294	GM_61_B1_E12_T7	g3777527	BLASTX	575	7e-62	94	Glycine max BSR-101 satellite SB92 genomic sequence.
1295	GM_61_B1_F05_MR	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
1296	GM_61_B1_F05_T7	g507910	BLASTN	578	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1297	GM_61_B1_F06_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1298	GM_61_B1_F06_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1299	GM_61_B1_F10_T7	g3777527	BLASTX	623	8e-59	93	(AF053008) gag-pol polyprotein [Glycine max]
1300	GM_61_B1_F11_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
1301	GM_61_B1_F12_T7	g4063760	BLASTX	539	4e-50	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1302	GM_61_B1_G05_T7	g2764526	BLASTN	412	1e-11	69	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
1303	GM_61_B1_G11_T7	g170029	BLASTN	371	9e-10	78	Glycine max cv. Dare nodulin 26 gene fragment.
1304	GM_61_B1_G12_MR	g507910	BLASTN	577	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1305	GM_61_B1_H03_T7	g4063760	BLASTX	349	4e-55	71	(AC005561) putative POL3 protein [Arabidopsis thaliana] (U70076) Lemir [Lycopersicon esculentum]
1306	GM_61_B1_H04_T7	g2654440	BLASTX	151	1e-18	53	(AB007466) reverse transcriptase-like protein [Vicia faba]
1307	GM_61_B1_H05_MR	g2522228	BLASTX	291	6e-25	61	(AL021768) putative protein [Arabidopsis thaliana]
1308	GM_61_B1_H05_T7	g2853084	BLASTX	130	5e-12	58	Glycine max BSR-101 satellite SB92 genomic sequence.
1309	GM_61_B1_H07_MR	g507910	BLASTN	468	1e-14	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1310	GM_61_B1_H07_T7	g4063760	BLASTX	177	2e-11	67	Glycine max BSR-101 satellite SB92 genomic sequence.
1311	GM_61_B1_H08_T7	g507910	BLASTN	563	8e-19	80	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
1312	GM_61_B1_H12_T7	g2522227	BLASTX	161	8e-11	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1313	GM_61_B2_A02_T7	g4063760	BLASTX	450	4e-44	84	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
1314	GM_61_B2_A05_MR	g505129	BLASTN	370	9e-10	63	(AF053008) envelope-like [Glycine max]
1315	GM_61_B2_A06_T7	g3142379	BLASTX	255	1e-20	60	myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) gi 499045 (Z34292) myosin [Arabidopsis thaliana]
1316	GM_61_B2_A07_T7	g2129651	BLASTX	114	4e-12	56	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1317	GM_61_B2_A08_MR	g2498732	BLASTX	386	5e-35	59	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2 gi 1362014 pir S57612 zeta-crystallin homolog - Arabidopsis thaliana gi 886430 (Z49268) zeta-crystallin homologue [Arabidopsis thaliana] G.max gene for catalase
1318	GM_61_B2_A10_MR	g18559	BLASTN	362	2e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1319	GM_61_B2_A10_T7	g507910	BLASTN	559	1e-18	81	(AF053008) gag-pol polypeptide [Glycine max]
1320	GM_61_B2_A11_MR	g3777527	BLASTX	652	7e-62	97	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1321	GM_61_B2_A11_T7	g1167523	BLASTX	240	3e-32	43	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: M1K22, complete sequence.
1322	GM_61_B2_A12_MR	g2264308	BLASTN	364	5e-11	65	(U90320) reverse transcriptase, gag, polypeptide [Volvox carteri f. nagariensis]
1323	GM_61_B2_B06_T7	g1916937	BLASTX	226	1e-16	40	(D85597) polypeptide [Oryza australiensis]
1324	GM_61_B2_B09_MR	g2443320	BLASTX	402	2e-35	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA);
1325	GM_61_B2_B10_MR	g99922	BLASTX	166	5e-29	53	pid:e150225 [Glycine max]
1326	GM_61_B2_C01_T7	g343537	BLASTN	377	5e-10	61	T-brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit 1 (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.
1327	GM_61_B2_C02_T7	g3150006	BLASTN	393	1e-10	62	C1C5B11.1 check: 4870 from: 1 to: 167234, complete sequence [Arabidopsis thaliana]
1328	GM_61_B2_C03_T7	g3377834	BLASTX	156	2e-09	29	(AF075598) No definition line found [Arabidopsis thaliana]
1329	GM_61_B2_C09_MR	g2522228	BLASTX	405	5e-37	74	(AB007466) reverse transcriptase-like protein [Vicia faba]
1330	GM_61_B2_D04_MR	g507910	BLASTN	588	6e-20	85	Glycine max BSR-101 satellite SB92 genomic sequence.
1331	GM_61_B2_D04_T7	g507910	BLASTN	557	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1332	GM_61_B2_D06_MR	g507910	BLASTN	504	4e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1333	GM_61_B2_D06_T7	g507910	BLASTN	569	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1334	GM_61_B2_D08_MR	g507910	BLASTN	451	9e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1335	GM_61_B2_D09_T7	g3777527	BLASTX	692	3e-66	89	(AF053008) gag-pol polypeptide [Glycine max]
1336	GM_61_B2_D10_MR	g99922	BLASTX	180	7e-37	54	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA);
1337	GM_61_B2_E10_MR	g421955	BLASTX	131	1e-23	56	pid:e150225 [Glycine max]
1338	GM_61_B2_E12_MR	g1480927	BLASTN	1255	5e-51	95	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
1339	GM_61_B2_E12_T7	g3377834	BLASTX	151	6e-09	30	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
1340	GM_61_B2_F01_T7	g3845307	BLASTN	424	4e-12	59	(AF075598) No definition line found [Arabidopsis thaliana]
1341	GM_61_B2_F04_MR	g4063760	BLASTX	476	2e-43	59	Plasmidium falciparum chromosome 2, section 61 of 73 of the complete sequence
1342	GM_61_B2_F08_MR	g18559	BLASTN	801	3e-29	88	(AC005561) putative POL3 protein [Arabidopsis thaliana] G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1343	GM_61_B2_F08_T7	g1369955	BLASTN	382	3e-10	64	Caenorhabditis elegans cosmid B0564, complete sequence [Caenorhabditis elegans] (AF039371) polyprotein [Arabidopsis thaliana] hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] (AC004238) putative berberine bridge enzyme [Arabidopsis thaliana] (AF049922) PGP169-12 [Petunia x hybrida] (AC004557) F17L21.7 [Arabidopsis thaliana] Helicoverpa armigera mitochondrion D-loop, partial 12S rRNA gene, and partial tRNA-Met gene. Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max gene for Bd 30K, complete cds Glycine max gene for Bd 30K, complete cds Glycine max gene for Bd 30K, complete cds Saccharomyces cerevisiae synthetic green fluorescent protein (cox3::GFPm) gene, mitochondrial gene construct, complete cds Glycine max gene for Bd 30K, complete cds (D85597) polyprotein [Oryza australiensis] (Y08010) lectin receptor kinase [Arabidopsis thaliana] (AF047697) putative high-pI laccase [Oryza sativa] AUXIN-INDUCED PROTEIN AUX28 gi 81759 pir A28993 aux28 protein - soybean gi 169921 (J03919) auxin-regulated protein (Aux28) [Glycine max] Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1 (U22103) gag-protease polyprotein [Glycine max] hypothetical protein - garden snapdragon Glycine max gene for Bd 30K, complete cds Homo sapiens chromosome 5, PAC clone 17c19 (LBNI, H148), complete sequence [Homo sapiens] (AC005970) putative reverse transcriptase [Arabidopsis thaliana] hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] Melanoplus sanguinipes entomopoxvirus, complete genome Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. (AF030881) pol polyprotein [Fugu rubripes] Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
1344	GM_61_B2_F10_MR	g2865424	BLASTX	236	4e-20	52	
1345	GM_61_B2_F11_MR	g2129618	BLASTX	210	2e-16	34	
1346	GM_61_B2_G02_T7	g3033375	BLASTX	161	1e-24	39	
1347	GM_61_B2_G03_MR	g4105782	BLASTX	138	1e-08	81	
1348	GM_61_B2_G05_MR	g3935164	BLASTX	205	3e-14	47	
1349	GM_61_B2_G05_T7	g409571	BLASTN	253	5e-11	65	
1350	GM_61_B2_G06_MR	g507910	BLASTN	391	5e-11	72	
1351	GM_61_B2_G10_T7	g3097320	BLASTN	384	2e-10	71	
1352	GM_61_B2_G12_T7	g3097320	BLASTN	430	2e-12	68	
1353	GM_61_B2_H01_MR	g1899158	BLASTN	351	5e-09	61	
1354	GM_61_B2_H03_T7	g3097320	BLASTN	1184	1e-46	75	
1355	GM_61_B2_H06_MR	g2443320	BLASTX	374	2e-32	51	
1356	GM_61_B2_H06_T7	g1769897	BLASTX	227	2e-17	38	
1357	GM_61_B2_H10_T7	g2920654	BLASTX	331	1e-28	60	
1358	GM_61_B2_H12_T7	g114734	BLASTX	189	4e-14	83	
1359	GM_63_A1_A04_T7	g2764525	BLASTN	830	8e-31	69	
1360	GM_63_A1_A08_MR	g905361	BLASTX	163	3e-10	38	
1361	GM_63_A1_A08_T7	g100484	BLASTX	373	8e-33	55	
1362	GM_63_A1_A09_MR	g3097320	BLASTN	941	1e-35	80	
1363	GM_63_A1_A12_T7	g3097836	BLASTN	376	6e-10	62	
1364	GM_63_A1_B04_MR	g4006833	BLASTX	218	2e-16	34	
1365	GM_63_A1_C02_MR	g2129618	BLASTX	250	2e-19	45	
1366	GM_63_A1_C04_MR	g4049647	BLASTN	410	2e-11	63	
1367	GM_63_A1_C05_MR	g507910	BLASTN	594	3e-20	82	
1368	GM_63_A1_C05_T7	g507910	BLASTN	619	2e-21	83	
1369	GM_63_A1_C07_MR	g3510505	BLASTX	145	3e-13	46	
1370	GM_63_A1_C09_MR	g1480927	BLASTN	370	8e-10	87	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1371	GM_63_A1_C10_MR	g2213582	BLASTX	196	2e-13	36	(AC000348) T7N9.2 [Arabidopsis thaliana]
1372	GM_63_A1_D03_T7	g1703053	BLASTX	133	9e-11	40	ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (A1 40 KD SUBUNIT) (RF-C 40 KD SUBUNIT) (RFC40) gi 2134397 pir 150704 replication factor C/activator 1 subunit - chicken gi 527669 (U12438) replication factor C/activator 1 subunit [Gallus gallus]
1373	GM_63_A1_D06_MR	g2979597	BLASTN	508	7e-16	64	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
1374	GM_63_A1_D08_MR	g3426334	BLASTN	623	3e-21	64	Pisum sativum pectin methylesterase (repml) gene, complete cds
1375	GM_63_A1_D09_MR	g507910	BLASTN	373	3e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1376	GM_63_A1_D12_MR	g629693	BLASTX	224	2e-17	42	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1377	GM_63_A1_E02_T7	g1817728	BLASTN	453	2e-13	65	Cloning vector pBeloBAC11
1378	GM_63_A1_E04_T7	g4063760	BLASTX	214	1e-23	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1379	GM_63_A1_E05_T7	g1167523	BLASTX	358	1e-30	50	(D83003) ORF(AA 1-1538) [Nicotiana tabacum]
1380	GM_63_A1_E08_T7	g4098647	BLASTX	228	1e-17	63	(U80668) homogenisate 1,2-dioxygenase [Arabidopsis thaliana]
1381	GM_63_A1_E12_T7	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1382	GM_63_A1_F02_MR	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1383	GM_63_A1_F02_T7	g507910	BLASTN	427	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1384	GM_63_A1_F06_T7	g2292907	BLASTX	317	3e-26	45	Glycine max BSR-101 satellite SB92 genomic sequence.
1385	GM_63_A1_G07_MR	g507910	BLASTN	594	3e-20	82	(Y10099) P-glycoprotein homologue [Hordeum vulgare]
1386	GM_63_A1_G07_T7	g4063760	BLASTX	285	6e-23	55	Glycine max BSR-101 satellite SB92 genomic sequence.
1387	GM_63_A1_H03_MR	g3142328	BLASTN	840	4e-31	97	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1388	GM_63_A1_H11_T7	g3097320	BLASTN	418	7e-12	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1389	GM_63_A2_A05_T7	g507910	BLASTN	388	6e-11	74	Glycine max gene for Bd 30K, complete cds
1390	GM_63_A2_A06_MR	g21430	BLASTN	382	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
1391	GM_63_A2_A08_T7	g1532167	BLASTX	145	2e-09	38	Potato DNA for copia-like transposable element
1392	GM_63_A2_A09_MR	g1769898	BLASTX	204	9e-15	35	(U63815) localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initiation codon and stop codon could not be precisely determined [Arabidopsis thaliana]
1393	GM_63_A2_B01_MR	g507910	BLASTN	576	2e-19	83	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1394	GM_63_A2_B01_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1395	GM_63_A2_B02_T7	g4063760	BLASTX	249	4e-19	47	Glycine max BSR-101 satellite SB92 genomic sequence.
1396	GM_63_A2_B06_T7	g507910	BLASTN	399	2e-11	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1397	GM_63_A2_C03_T7	g905361	BLASTX	190	3e-13	29	Glycine max BSR-101 satellite SB92 genomic sequence. (U22103) gag-protease polypeptide [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1398	GM_63_A2_C05_T7	g2738248	BLASTX	261	9e-26	94	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]
1399	GM_63_A2_C12_MR	g3080666	BLASTN	364	2e-09	63	Homo sapiens PAC clone DJ0318107 from 8q21, complete sequence [Homo sapiens]
1400	GM_63_A2_D02_T7	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
1401	GM_63_A2_D06_MR	g3402690	BLASTX	197	1e-25	46	(AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]
1402	GM_63_A2_D06_T7	g4102839	BLASTX	253	5e-20	43	(AF016713) LeOPT1 [Lycopersicon esculentum]
1403	GM_63_A2_D09_MR	g3033375	BLASTX	186	9e-24	77	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
1404	GM_63_A2_D11_T7	g3687234	BLASTX	207	1e-14	49	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
1405	GM_63_A2_D12_MR	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1406	GM_63_A2_D12_T7	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1407	GM_63_A2_E03_T7	g99922	BLASTX	347	7e-31	70	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1408	GM_63_A2_E04_MR	g2970554	BLASTN	749	8e-27	78	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
1409	GM_63_A2_E07_MR	g508826	BLASTN	360	3e-09	62	Drosophila melanogaster Oregon-R mitochondrial A+T region.
1410	GM_63_A2_E07_T7	g100484	BLASTX	374	6e-33	53	hypothetical protein - garden snapdragon
1411	GM_63_A2_E11_MR	g1363492	BLASTX	243	1e-18	68	outer envelope membrane protein OEP75 precursor - garden pea gi 576507 (L36858) outer membrane protein [Pisum sativum] gi 633607 (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]
1412	GM_63_A2_F02_MR	g2462936	BLASTX	300	6e-26	42	(Y12321) open reading frame 2 [Brassica oleracea]
1413	GM_63_A2_F05_T7	g905361	BLASTX	413	2e-37	95	(U22103) gag-protease polyprotein [Glycine max]
1414	GM_63_A2_G01_MR	g3142328	BLASTN	1179	2e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1415	GM_63_A2_G05_MR	g532706	BLASTN	432	3e-13	79	Glycine max clone GMFP6 isoprenylated protein mRNA, partial cds.
1416	GM_63_A2_G05_T7	g2443320	BLASTX	375	2e-32	49	(D85597) polyprotein [Oryza australiensis]
1417	GM_63_A2_G06_T7	g3777527	BLASTX	704	2e-67	94	(AF053008) gag-pol polyprotein [Glycine max]
1418	GM_63_A2_G07_MR	g507910	BLASTN	534	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1419	GM_63_A2_G07_T7	g507910	BLASTN	555	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1420	GM_63_A2_H01_MR	g3142328	BLASTN	1145	6e-45	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1421	GM_63_A2_H03_MR	g2970554	BLASTN	773	6e-28	73	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
1422	GM_63_A2_H04_T7	g507910	BLASTN	359	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1423	GM_63_A2_H08_T7	g2462134	BLASTX	163	2e-10	39	(Y13368) reverse transcriptase [Beta vulgaris]
1424	GM_63_A2_H11_T7	g507910	BLASTN	548	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1425	GM_63_A2_H12_T7	g2443320	BLASTX	243	2e-18	46	(D85597) polyprotein [Oryza australiensis]
1426	GM_63_B1_A05_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1427	GM_63_B1_A05_T7	g507910	BLASTN	447	1e-13	76	Glycine max BSR-101 satellite beta-glucosidase gi 3128187 (AC004392) Similar to F411.26 putative beta-glucosidase gi 3128187 from A. thaliana BAC gb AC004521. ESTs gb N97083, gb F19868 and gb F15482 come from this gene. [Arabidopsis thaliana]
1428	GM_63_B1_A06_T7	g3367517	BLASTX	233	5e-18	51	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
1429	GM_63_B1_A07_MR	g99730	BLASTX	207	6e-20	43	26S PROTEASE REGULATORY SUBUNIT S6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) gi 556560 gnl PID d1005143 (D17788) rice homologue of Tat binding protein [Oryza sativa]
1430	GM_63_B1_A08_MR	g1174613	BLASTX	201	1e-14	88	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
1431	GM_63_B1_A10_MR	g3695395	BLASTX	192	1e-15	41	(AF007271) similar to N. tabacum membrane-associated salt-inducible protein (PID:g473874) [Arabidopsis thaliana]
1432	GM_63_B1_B11_T7	g2191182	BLASTX	252	6e-20	59	(AF053008) gag-pol polyprotein [Glycine max]
1433	GM_63_B1_B12_MR	g3777527	BLASTX	775	4e-75	95	Trypanosoma brucei EAATRO 164 kinetoplast (CR4) mRNA, complete cds.
1434	GM_63_B1_C01_T7	g668325	BLASTN	355	6e-10	62	(AF053008) gag-pol polyprotein [Glycine max]
1435	GM_63_B1_C03_T7	g3777527	BLASTX	285	9e-23	43	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene
1436	GM_63_B1_C04_MR	g3599418	BLASTN	366	1e-09	72	encoding mitochondrial protein, complete cds
1437	GM_63_B1_C04_T7	g3367585	BLASTX	146	7e-09	35	(AL031135) putative polygalacturonase [Arabidopsis thaliana]
1438	GM_63_B1_C10_MR	g3777527	BLASTX	394	6e-42	87	(AF053008) gag-pol polyprotein [Glycine max]
1439	GM_63_B1_D01_MR	g2760830	BLASTX	465	2e-43	60	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
1440	GM_63_B1_D02_MR	g1707020	BLASTX	181	2e-12	34	(U78721) hypothetical protein [Arabidopsis thaliana]
1441	GM_63_B1_D02_T7	g4097585	BLASTX	221	2e-17	67	(U64925) NTGP4 [Nicotiana tabacum]
1442	GM_63_B1_D03_MR	g2522230	BLASTX	243	8e-24	47	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1443	GM_63_B1_D08_MR	g3337395	BLASTN	420	6e-12	63	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
1444	GM_63_B1_E02_T7	g1666236	BLASTX	244	6e-20	33	(U76261) unknown [Hordeum vulgare]
1445	GM_63_B1_E03_T7	g1769897	BLASTX	269	6e-22	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1446	GM_63_B1_E04_MR	g3386605	BLASTX	175	8e-12	35	(AC004665) hypothetical protein [Arabidopsis thaliana]
1447	GM_63_B1_E05_T7	g2522228	BLASTX	300	2e-46	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
1448	GM_63_B1_E10_MR	g4063760	BLASTX	205	2e-14	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1449	GM_63_B1_F03_MR	g3142328	BLASTN	1125	5e-44	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1450	GM_63_B1_F04_MR	g3142328	BLASTN	786	1e-28	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL.3 protein [Arabidopsis thaliana] (U76261) unknown [Hordeum vulgare]
1451	GM_63_B1_F06_T7	g4063760	BLASTX	230	4e-17	51	Glycine max BSR-101 satellite SB92 genomic sequence.
1452	GM_63_B1_F07_T7	g1666236	BLASTX	165	4e-11	29	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1453	GM_63_B1_F08_MR	g507910	BLASTN	696	8e-25	87	G.max gene for catalase
1454	GM_63_B1_F11_T7	g1769898	BLASTX	227	3e-17	47	Homo sapiens chromosome 16 BAC clone CTT987SK-334D11
1455	GM_63_B1_F12_T7	g18559	BLASTN	332	4e-11	71	complete sequence [Homo sapiens]
1456	GM_63_B1_G01_MR	g2335061	BLASTN	328	3e-13	71	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
1457	GM_63_B1_G03_T7	g2970554	BLASTN	1094	2e-42	90	Glycine max BSR-101 satellite SB92 genomic sequence.
1458	GM_63_B1_G05_MR	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1459	GM_63_B1_G05_T7	g507910	BLASTN	589	5e-20	82	(AL022223) putative protein [Arabidopsis thaliana]
1460	GM_63_B1_G06_MR	g3046704	BLASTX	240	4e-18	45	Glycine max gene for Bd 30K, complete cds
1461	GM_63_B1_G08_MR	g3097320	BLASTN	471	3e-14	76	Glycine max gene for Bd 30K, complete cds
1462	GM_63_B1_G10_T7	g3097320	BLASTN	536	3e-17	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1463	GM_63_B1_H01_MR	g507910	BLASTN	566	6e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1464	GM_63_B1_H01_T7	g507910	BLASTN	345	6e-09	78	Soybean nodulin 22 gene
1465	GM_63_B1_H03_MR	g18695	BLASTN	475	1e-14	82	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
1466	GM_63_B1_H03_T7	g3810596	BLASTX	345	2e-29	49	(AF053008) gag-pol polyprotein [Glycine max]
1467	GM_63_B1_H05_MR	g3777527	BLASTX	493	6e-45	78	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
1468	GM_63_B1_H08_T7	g3600044	BLASTX	221	5e-16	36	(AF042196) auxin response factor 8 [Arabidopsis thaliana]
1469	GM_63_B1_H12_T7	g4104931	BLASTX	314	2e-26	52	(U37437) PNIL34 [Ipomoea nil]
1470	GM_63_B2_A09_MR	g1052960	BLASTX	157	7e-24	87	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
1471	GM_63_B2_A10_MR	g4063760	BLASTX	229	5e-17	40	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
1472	GM_63_B2_A11_MR	g3859610	BLASTN	641	6e-22	64	Arabidopsis thaliana complete sequence [Arabidopsis thaliana]
1473	GM_63_B2_B07_MR	g2924733	BLASTN	382	3e-10	67	MUF9, complete sequence [Arabidopsis thaliana]
1474	GM_63_B2_B10_MR	g3142328	BLASTN	619	5e-21	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1475	GM_63_B2_B12_MR	g3097320	BLASTN	474	2e-14	71	Glycine max gene for Bd 30K, complete cds
1476	GM_63_B2_D03_MR	g3779030	BLASTX	201	2e-15	31	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
1477	GM_63_B2_D05_MR	g2462134	BLASTX	104	2e-11	33	(Y13368) reverse transcriptase [Beta vulgaris]
1478	GM_63_B2_D06_MR	g405321	BLASTX	117	1e-09	64	(S63758) metallothionein-I gene transcription activator [mice, L. cells, Peptide, 102 aa] [Mus sp.]
1479	GM_63_B2_D07_MR	g3645899	BLASTX	428	2e-38	57	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1480	GM_63_B2_E05_MR	g4063760	BLASTX	482	5e-44	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1481	GM_63_B2_E08_MR	g2323254	BLASTN	391	1e-10	62	Human Chromosome X, complete sequence [Homo sapiens]
1482	GM_63_B2_G03_MR	g1184075	BLASTX	281	2e-22	45	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
1483	GM_63_B2_G07_MR	g166709	BLASTN	399	4e-11	64	Arabidopsis thaliana cytosolic glyceraldehyde-3-phosphate dehydrogenase (GapC) gene, exons 1-9, complete cds. (AF053008) gag-pol polyprotein [Glycine max]
1484	GM_63_B2_G10_MR	g3777527	BLASTX	432	2e-38	82	Glycine max BSR-101 satellite SB92 genomic sequence.
1485	GM_63_B2_H07_MR	g507910	BLASTN	339	1e-08	72	(U68408) 5' end not determined experimentally [Zea mays]
1486	GM_63_B2_H08_MR	g3645899	BLASTX	401	2e-35	54	RETROVIRUS-RELATED POL POLYPYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
1487	GM_63_B2_H09_MR	g130582	BLASTX	205	2e-14	34	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1488	GM_64_A1_A11_T7	g2462058	BLASTX	140	8e-14	44	(Y13389) reverse transcriptase [Antirrhinum majus]
1489	GM_64_A1_B06_MR	g2121303	BLASTN	359	3e-09	61	Homo sapiens cosmid Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
1490	GM_64_A1_B06_T7	g3980412	BLASTX	313	2e-29	58	(AC004561) pumilio-like protein [Arabidopsis thaliana]
1491	GM_64_A1_B08_T7	g3142328	BLASTN	1925	1e-80	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1492	GM_64_A1_B09_MR	g3264565	BLASTN	353	7e-09	65	Homo sapiens chromosome 17, clone hRPC.1037.O_7, complete sequence [Homo sapiens]
1493	GM_64_A1_B10_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1494	GM_64_A1_B10_T7	g4063760	BLASTX	220	5e-16	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1495	GM_64_A1_C04_MR	g3334661	BLASTX	205	5e-15	72	(Y10490) putative cytochrome P450 [Glycine max]
1496	GM_64_A1_C05_T7	g507910	BLASTN	632	6e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
1497	GM_64_A1_C09_T7	g2832623	BLASTX	112	5e-09	72	(AL021711) protein kinase - like protein [Arabidopsis thaliana]
1498	GM_64_A1_C10_T7	g3426334	BLASTN	595	6e-20	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
1499	GM_64_A1_C12_MR	g1769899	BLASTX	262	6e-22	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1500	GM_64_A1_C12_T7	g1769898	BLASTX	420	2e-38	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1501	GM_64_A1_D02_MR	g18559	BLASTN	1053	1e-40	74	G.max gene for catalase
1502	GM_64_A1_D04_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1503	GM_64_A1_D04_T7	g507910	BLASTN	375	2e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence. (Pfam: AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
1504	GM_64_A1_D05_T7	g3377848	BLASTX	133	2e-11	31	G.max gene for catalase
1505	GM_64_A1_D06_MR	g18559	BLASTN	473	2e-14	69	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
1506	GM_64_A1_D07_T7	g130582	BLASTX	159	2e-09	41	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1507	GM_64_A1_D08_MR	g3914431	BLASTX	107	2e-11	86	PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi 2285802 gnl PID d1022501 (D78173) 26S proteasome alpha subunit [Spinacia oleracea]
1508	GM_64_A1_D08_T7	g2996647	BLASTN	507	7e-16	66	Homo sapiens chromosome 16, cosmid clone 390H12 (LANL), complete sequence [Homo sapiens]
1509	GM_64_A1_D10_MR	g3810596	BLASTX	166	9e-25	57	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
1510	GM_64_A1_E05_MR	g2764526	BLASTN	486	6e-15	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
1511	GM_64_A1_E07_MR	g4063760	BLASTX	155	5e-09	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1512	GM_64_A1_E09_T7	g3777527	BLASTX	610	2e-57	92	(AF053008) gag-pol polyprotein [Glycine max]
1513	GM_64_A1_E12_T7	g170051	BLASTN	364	6e-10	74	Glycine max RNA polymerase II fifth largest subunit mRNA, complete cds.
1514	GM_64_A1_F05_MR	g3420052	BLASTX	187	5e-13	65	(AC004680) putative ubiquinone reductase [Arabidopsis thaliana]
1515	GM_64_A1_F07_T7	g3777527	BLASTX	673	3e-64	92	(AF053008) gag-pol polyprotein [Glycine max]
1516	GM_64_A1_F09_T7	g4063760	BLASTX	171	8e-11	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1517	GM_64_A1_F11_T7	g507910	BLASTN	414	4e-12	71	Glycine max BSR-101 satellite SB92 genomic sequence.
1518	GM_64_A1_G04_T7	g1769899	BLASTX	189	3e-16	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1519	GM_64_A1_G06_MR	g3097320	BLASTN	1585	9e-65	85	Glycine max gene for Bd 30K, complete cds
1520	GM_64_A1_G10_MR	g131289	BLASTX	761	8e-75	95	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) gi 72709 pir F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast gi 225285 prf 1211235W photosystem II 44kD protein [Nicotiana tabacum]
1521	GM_64_A1_G10_T7	g131276	BLASTX	574	1e-60	92	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 72704 pir QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi 11856 (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi 225224 prf 1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]
1522	GM_64_A1_G11_T7	g421955	BLASTX	211	1e-21	50	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
1523	GM_64_A1_H10_MR	g905361	BLASTX	204	1e-14	33	(U22103) gag-protease polyprotein [Glycine max]
1524	GM_64_A2_A01_MR	g3777527	BLASTX	725	9e-70	91	(AF053008) gag-pol polyprotein [Glycine max]
1525	GM_64_A2_A07_T7	g3097320	BLASTN	350	8e-09	80	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1526	GM_64_A2_A08_T7	g507910	BLASTN	416	3e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1527	GM_64_A2_A10_MR	g3097320	BLASTN	1174	4e-46	80	Glycine max gene for Bd 30K, complete cds
1528	GM_64_A2_B01_T7	g629693	BLASTX	309	7e-27	44	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1529	GM_64_A2_B04_T7	g1142702	BLASTN	363	7e-10	70	Glycine max satellite STR120-A.4.
1530	GM_64_A2_B05_T7	g1167523	BLASTX	218	7e-34	49	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1531	GM_64_A2_B07_MR	g3319362	BLASTX	273	9e-22	39	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1532	GM_64_A2_B10_T7	g2598579	BLASTX	246	2e-19	71	(Y15295) L-ascorbate oxidase [Medicago truncatula]
1533	GM_64_A2_C01_T7	g2464905	BLASTX	230	2e-18	57	(Z99708) minor allergen [Arabidopsis thaliana]
1534	GM_64_A2_C03_MR	g1769898	BLASTX	144	4e-14	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1535	GM_64_A2_C07_MR	g3645899	BLASTX	102	9e-09	41	(U68408) 5' end not determined experimentally [Zea mays]
1536	GM_64_A2_C08_MR	g549056	BLASTX	358	4e-34	70	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) gi 631651 pir S43059 CCT (chaperonin containing TCP-1) beta chain - mouse gi 468546 (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]
1537	GM_64_A2_C09_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1538	GM_64_A2_C10_MR	g1840106	BLASTN	374	2e-10	64	Human fragile site locus (FRA16B) minisatellite repeat (Y12432) polyprotein [Ananas comosus]
1539	GM_64_A2_C11_T7	g2995405	BLASTX	340	5e-29	61	(AB007466) reverse transcriptase-like protein [Vicia faba]
1540	GM_64_A2_D01_MR	g2522228	BLASTX	220	3e-21	69	Glycine max BSR-101 satellite SB92 genomic sequence.
1541	GM_64_A2_D02_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1542	GM_64_A2_D02_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1543	GM_64_A2_D03_MR	g4151068	BLASTX	222	3e-26	84	(Y10862) ribonucleotide reductase [Nicotiana tabacum]
1544	GM_64_A2_E01_MR	g2522230	BLASTX	151	4e-10	27	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1545	GM_64_A2_E01_T7	g4063760	BLASTX	598	2e-56	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1546	GM_64_A2_E08_MR	g4063760	BLASTX	265	8e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1547	GM_64_A2_E09_MR	g3859610	BLASTN	416	9e-12	64	Arabidopsis thaliana BAC T9E19
1548	GM_64_A2_F02_MR	g505129	BLASTN	370	9e-10	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
1549	GM_64_A2_F02_T7	g1167523	BLASTX	212	7e-16	37	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1550	GM_64_A2_F06_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1551	GM_64_A2_F06_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
1552	GM_64_A2_F08_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1553	GM_64_A2_F08_T7	g507910	BLASTN	561	1e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1554	GM_64_A2_F09_T7	g3548819	BLASTX	161	3e-11	57	(AC005313) putative heterogeneous nuclear ribonucleoprotein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1555	GM_64_A2_F10_T7	g130582	BLASTX	172	8e-11	42	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum] (AC004557) F17L21.30 [Arabidopsis thaliana] G.max gene for catalase Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H1148), complete sequence [Homo sapiens] Human fragile site locus (FRA16B) minisatellite repeat Glycine max BSR-101 satellite SB92 genomic sequence. (AC005561) putative POL3 protein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (AC005561) putative POL3 protein [Arabidopsis thaliana] (Y08010) lectin receptor kinase [Arabidopsis thaliana] (AF053008) gag-pol polyprotein [Glycine max] hypothetical protein - garden snapdragon Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence G.max gene for catalase HIGH AFFINITY SULPHATE TRANSPORTER 1 gi 1085847 pir S51763 high affinity sulphate transporter - Stylosanthes hamata gi 607184 (X82255) high affinity sulphate transporter [Stylosanthes hamata] (U22103) gag-protease polyprotein [Glycine max] UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana Ubiquitin Conjugation, Ligate Mol_id: 1; Molecule: Ubiquitin Conjugating Enzyme; Chain: Null; Synonym: Ubc1; Ec: 6.3.2.19; Engineered: Yes gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] gi 431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana] Human DNA sequence from PAC 450C20 on chromosome X
1556	GM_64_A2_G02_T7	g3935187	BLASTX	501	3e-47	64	
1557	GM_64_A2_G04_T7	g18559	BLASTN	519	2e-16	68	
1558	GM_64_A2_G10_T7	g3097836	BLASTN	373	8e-10	63	
1559	GM_64_A2_H01_MR	g1840106	BLASTN	400	9e-12	63	
1560	GM_64_A2_H05_T7	g507910	BLASTN	399	2e-11	74	
1561	GM_64_A2_H10_MR	g4063760	BLASTX	179	5e-13	39	
1562	GM_64_A2_H10_T7	g507910	BLASTN	363	8e-10	72	
1563	GM_64_A2_H11_T7	g4063760	BLASTX	237	8e-18	67	
1564	GM_64_B1_A02_MR	g1769898	BLASTX	119	9e-15	40	
1565	GM_64_B1_A03_MR	g3777527	BLASTX	487	3e-44	88	
1566	GM_64_B1_A06_MR	g100484	BLASTX	267	2e-21	49	
1567	GM_64_B1_A11_MR	g3845264	BLASTN	396	7e-11	62	
1568	GM_64_B1_B05_MR	g18559	BLASTN	1242	3e-49	82	
1569	GM_64_B1_B09_MR	g1711615	BLASTX	248	2e-19	58	
1570	GM_64_B1_B10_MR	g905361	BLASTX	212	1e-15	37	
1571	GM_64_B1_B12_MR	g136636	BLASTX	216	5e-17	95	
1572	GM_64_B1_C01_MR	g2052034	BLASTN	397	7e-11	62	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1573	GM_64_B1_C03_MR	g136636	BLASTX	168	6e-12	78	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana Ubiquitin Conjugation, Ligase Mol_id: 1; Molecule: Ubiquitin Conjugating Enzyme; Chain: Null; Synonym: Ubc1; Ec: 6.3.2.19; Engineered: Yes gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] gi 431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (AC004255) TIF9.14 [Arabidopsis thaliana] Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana] (AF031471) pollen allergen [Juniperus oxycedrus] (AF053008) gag-pol polyprotein [Glycine max] putative transposase [Arabidopsis thaliana] RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum] Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana] (AB007466) reverse transcriptase-like protein [Vicia faba] probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum] P.falciiparum gene for beta subunit RNA polymerase (AL031018) putative fizzy-related protein [Arabidopsis thaliana] (D83003) ORF(AA 1-1338) [Nicotiana tabacum] (AC004450) hypothetical protein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (AB007466) reverse transcriptase-like protein [Vicia faba] (AC002510) unknown protein [Arabidopsis thaliana]
1574	GM_64_B1_C04_T7	g507910	BLASTN	341	8e-09	72	
1575	GM_64_B1_C07_MR	g3056593	BLASTX	144	7e-14	56	
1576	GM_64_B1_C08_T7	g3449327	BLASTN	477	2e-14	72	
1577	GM_64_B1_C12_T7	g3095075	BLASTX	139	7e-09	35	
1578	GM_64_B1_D01_MR	g3777527	BLASTX	391	5e-34	92	
1579	GM_64_B1_D05_MR	g3283026	BLASTX	106	2e-10	42	
1580	GM_64_B1_D06_T7	g130582	BLASTX	201	3e-27	67	
1581	GM_64_B1_D07_MR	g2564050	BLASTN	376	6e-10	62	
1582	GM_64_B1_D12_T7	g2522228	BLASTX	147	7e-09	34	
1583	GM_64_B1_E02_MR	g629693	BLASTX	229	2e-24	49	
1584	GM_64_B1_E03_MR	g587603	BLASTN	350	7e-09	61	
1585	GM_64_B1_E03_T7	g3292816	BLASTX	174	9e-12	86	
1586	GM_64_B1_E04_T7	g1167523	BLASTX	218	7e-34	49	
1587	GM_64_B1_E05_MR	g3763934	BLASTX	309	4e-26	51	
1588	GM_64_B1_E06_MR	g507910	BLASTN	366	6e-10	71	
1589	GM_64_B1_E07_MR	g2522228	BLASTX	387	4e-35	66	
1590	GM_64_B1_F03_T7	g2618698	BLASTX	128	1e-12	81	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1591	GM_64_B1_F10_T7	g2895630	BLASTN	375	3e-10	61	Phoebis sennae large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
1592	GM_64_B1_G03_T7	g3097320	BLASTN	966	1e-36	80	Glycine max gene for Bd 30K, complete cds
1593	GM_64_B1_G04_MR	g3913727	BLASTX	257	1e-20	72	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE. CYTOPLASMIC ISOFORM (G6PD) >gi 1174336 gnl PID e137420 (X84230) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
1594	GM_64_B1_H01_MR	g2129618	BLASTX	173	4e-11	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
1595	GM_64_B1_H01_T7	g2522228	BLASTX	149	4e-09	31	(AB007466) reverse transcriptase-like protein [Vicia faba]
1596	GM_64_B1_H03_MR	g4063770	BLASTX	258	3e-24	42	(AB004906) transposase [Ipomoea purpurea]
1597	GM_64_B1_H09_MR	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1598	GM_64_B1_H10_MR	g1431738	BLASTN	353	5e-09	89	Soybean (Glycine max) low MW heat shock protein gene (Gmhspl7.5-M).
1599	GM_64_B1_H11_T7	g4006831	BLASTX	164	4e-10	47	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
1600	GM_64_B2_A02_T7	g2832901	BLASTN	1639	1e-73	78	Cajanus cajan copia-like retrotransposon.Pan/ze
1601	GM_64_B2_B03_T7	g3097320	BLASTN	560	3e-18	65	Glycine max gene for Bd 30K, complete cds
1602	GM_64_B2_B04_T7	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1603	GM_64_B2_B05_T7	g4038057	BLASTX	164	3e-10	37	(AC005897) hypothetical protein [Arabidopsis thaliana]
1604	GM_64_B2_B06_T7	g585565	BLASTX	165	1e-11	75	RIBOSOME RECYCLING FACTOR HOMOLOG (NUCLEAR LOCATED PROTEIN D2) gi 629661 pir S32716 nuclear protein - carrot gi 297891 (X72384) nuclear located protein [Daucus carota]
1605	GM_64_B2_B08_T7	g131274	BLASTX	174	9e-16	68	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 12278 (X02945) P(680) apoprotein [Spinacia oleracea]
1606	GM_64_B2_C04_T7	g421955	BLASTX	192	7e-14	63	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
1607	GM_64_B2_C07_T7	g2924654	BLASTN	690	4e-24	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHK7, complete sequence [Arabidopsis thaliana]
1608	GM_64_B2_C09_T7	g3142328	BLASTN	1027	1e-39	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U39783) amino acid transport protein [Arabidopsis thaliana]
1609	GM_64_B2_D01_T7	g2576363	BLASTX	332	3e-29	48	(U39783) amino acid transport protein [Arabidopsis thaliana]
1610	GM_64_B2_D04_T7	g3645899	BLASTX	480	7e-44	52	(U39783) amino acid transport protein [Arabidopsis thaliana]
1611	GM_64_B2_D06_T7	g2522230	BLASTX	206	6e-16	32	(U39783) amino acid transport protein [Arabidopsis thaliana] (U39783) 5' end not determined experimentally [Zea mays] (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1612	GM_64_B2_D10_T7	g559273	BLASTN	288	2e-11	67	Saccharomyces cerevisiae mitochondrion ori3 gene, aap1 gene, ori2 gene, ORF4, replication of origin (ori7 and ori2), and ORF5. Glycine max BSR-101 satellite SB92 genomic sequence.
1613	GM_64_B2_D11_T7	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1614	GM_64_B2_E02_T7	g3461840	BLASTX	387	1e-33	46	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
1615	GM_64_B2_E03_T7	g185559	BLASTN	624	3e-21	68	Gmax gene for catalase
1616	GM_64_B2_F02_T7	g3779021	BLASTX	179	1e-12	45	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
1617	GM_64_B2_F03_T7	g185559	BLASTN	1046	2e-40	77	Gmax gene for catalase
1618	GM_64_B2_F04_T7	g1171591	BLASTN	366	2e-09	61	P-falciparum complete gene map of plastid-like DNA (IR-B)
1619	GM_64_B2_F09_T7	g507910	BLASTN	591	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1620	GM_64_B2_G06_T7	g3777527	BLASTX	853	2e-88	97	(AF053008) gag-pol polypeptide [Glycine max]
1621	GM_64_B2_G07_T7	g493737	BLASTN	364	2e-09	61	Honey bee mitochondrial cytochrome oxidase subunit I and II genes. complete cds, and Trp-, Leu-, Asp-, and Lys-tRNAs.
1622	GM_64_B2_H04_T7	g100484	BLASTX	401	4e-44	50	hypothetical protein - garden snapdragon
1623	GM_64_B2_H08_T7	g2781364	BLASTX	124	2e-11	35	(AC003113) F24O1.20 [Arabidopsis thaliana]
1624	GM_64_B2_H09_T7	g2522228	BLASTX	625	1e-66	71	(AB007466) reverse transcriptase-like protein [Vicia faba]
1625	GM_65_A1_A04_T7	g3184508	BLASTN	450	3e-13	67	Homo sapiens chromosome 17, clone HRP41C23, complete sequence [Homo sapiens]
1626	GM_65_A1_A09_MR	g4038056	BLASTX	291	9e-24	48	(AC005897) putative transposon [Arabidopsis thaliana]
1627	GM_65_A1_A11_T7	g3608481	BLASTX	216	4e-17	71	(AF088913) ribosomal protein L27a [Petunia x hybrida]
1628	GM_65_A1_A12_MR	g2995405	BLASTX	516	4e-48	65	(Y12432) polyprotein [Ananas comosus]
1629	GM_65_A1_B02_MR	g1666236	BLASTX	227	3e-18	30	(U76261) unknown [Hordeum vulgare]
1630	GM_65_A1_B02_T7	g3845070	BLASTN	349	9e-09	58	Plasmodium falciparum chromosome 2, section 3 of 73 of the complete sequence
1631	GM_65_A1_B03_T7	g1431738	BLASTN	598	3e-20	93	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
1632	GM_65_A1_B05_T7	g507910	BLASTN	417	3e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1633	GM_65_A1_B08_T7	g2443320	BLASTX	355	3e-30	56	(D85597) polyprotein [Oryza australiensis]
1634	GM_65_A1_B10_MR	g3021268	BLASTX	325	4e-27	50	(AL022347) putative protein [Arabidopsis thaliana]
1635	GM_65_A1_B12_T7	g4063760	BLASTX	387	8e-34	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1636	GM_65_A1_C04_MR	g3550435	BLASTN	534	4e-17	63	Hordeum vulgare Hot1 gene
1637	GM_65_A1_C04_T7	g507910	BLASTN	660	3e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
1638	GM_65_A1_D02_T7	g3695395	BLASTX	177	8e-12	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
1639	GM_65_A1_D04_MR	g4092470	BLASTN	409	2e-11	59	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
1640	GM_65_A1_D05_T7	g507910	BLASTN	530	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1641	GM_65_A1_D08_MR	g2344889	BLASTX	138	4e-14	47	(AC002388) unknown protein [Arabidopsis thaliana]
1642	GM_65_A1_D10_T7	g1769898	BLASTX	146	3e-10	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1643	GM_65_A1_D11_MR	g18559	BLASTN	598	4e-20	74	G.max gene for catalase
1644	GM_65_A1_D11_T7	g2104680	BLASTN	444	3e-13	76	V.faba mRNA for putative transcription factor (1556bp)
1645	GM_65_A1_D12_T7	g2842490	BLASTX	380	2e-34	55	(AL021749) heat-shock protein [Arabidopsis thaliana]
1646	GM_65_A1_E07_T7	g99730	BLASTX	182	9e-20	50	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975)
1647	GM_65_A1_E12_MR	g507910	BLASTN	556	2e-18	80	orf 3 [Arabidopsis thaliana]
1648	GM_65_A1_F01_T7	g2252830	BLASTX	198	8e-15	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1649	GM_65_A1_F08_MR	g507910	BLASTN	581	1e-19	81	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]
1650	GM_65_A1_F11_T7	g2462828	BLASTX	211	4e-15	41	Glycine max BSR-101 satellite SB92 genomic sequence.
1651	GM_65_A1_G01_T7	g2129613	BLASTX	177	8e-18	47	(AF000657) hypothetical protein [Arabidopsis thaliana]
1652	GM_65_A1_G03_MR	g2522227	BLASTX	213	1e-16	46	homeotic protein BEL1 - Arabidopsis thaliana gi 1122533 (U39944)
1653	GM_65_A1_G05_T7	g1142703	BLASTN	257	1e-13	73	BEL1 [Arabidopsis thaliana]
1654	GM_65_A1_G06_T7	g3212102	BLASTN	690	4e-24	68	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
1655	GM_65_A1_G08_MR	g3777527	BLASTX	171	1e-10	33	Glycine max satellite STR120-B.1.
1656	GM_65_A1_G08_T7	g535454	BLASTX	166	4e-11	43	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM.
1657	GM_65_A1_H02_MR	g2961349	BLASTX	210	5e-15	52	complete sequence [Arabidopsis thaliana]
1658	GM_65_A1_H02_T7	g2995405	BLASTX	155	3e-09	48	(AF053008) gag-pol polyprotein [Glycine max]
1659	GM_65_A1_H04_T7	g3142328	BLASTN	1840	1e-76	93	(U13940) cysteine proteinase [Alnus glutinosa]
1660	GM_65_A1_H07_MR	g3142328	BLASTN	671	2e-23	72	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
1661	GM_65_A1_H10_T7	g4115365	BLASTX	180	1e-11	41	(Y12432) polyprotein [Ananas comosus]
1662	GM_65_A2_A03_MR	g1888357	BLASTX	191	5e-13	63	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1663	GM_65_A2_B05_MR	g132866	BLASTX	205	7e-16	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1664	GM_65_A2_B11_MR	g18559	BLASTN	1374	3e-55	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1665	GM_65_A2_B12_MR	g3097320	BLASTN	467	4e-14	73	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
1666	GM_65_A2_C02_MR	g2052034	BLASTN	380	4e-10	68	(X98130) alpha-mannosidase [Arabidopsis thaliana] gi 1890154 gnl PID e307744 (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]
							CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 gi 71086 pir
							R5NT2 ribosomal protein L2 - common tobacco chloroplast gi
							435269 (Z00044) ribosomal protein L2 [Nicotiana tabacum] gi
							1223691 (Z00044) ribosomal protein L2 [Nicotiana tabacum] gi
							225238 prf 1211235BW ribosomal protein L2 [Nicotiana tabacum]
							G.max gene for catalase
							Glycine max gene for Bd 30K, complete cds
							Human DNA sequence from PAC 450C20 on chromosome X

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1667	GM_65_A2_D03_MR	g3738114	BLASTN	435	1e-12	65	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens] (AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]
1668	GM_65_A2_D06_T7	g2384671	BLASTX	128	1e-11	88	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1669	GM_65_A2_D11_MR	g3779030	BLASTX	157	9e-11	37	
1670	GM_65_A2_D12_T7	g3142328	BLASTN	842	4e-31	91	
1671	GM_65_A2_E04_T7	g3288442	BLASTN	408	2e-11	63	Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Ga... (AC002505) hypothetical protein [Arabidopsis thaliana] (AI.022603) serine/threonine protein kinase [Arabidopsis thaliana] 3402759 gnl PID e1314603 (AL031187) serine/threonine protein kinase - like protein [Arabidopsis thaliana] (AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba] (AC000375) Strong similarity to Arabidopsis oligopeptide transporter (gb X77503). [Arabidopsis thaliana] TRANSPOSON TY5-1 16.0 KD HYPOTHETICAL PROTEIN gi 83189 pir S19407 hypothetical protein YCL075w - yeast (Saccharomyces cerevisiae) gi 5284 gnl PID e264615 (X59720) YCL075w, len:146; not real ORF - included in pseudogene [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. Homo sapiens chromosome Y, clone hCIT.144_J.1, complete sequence [Homo sapiens] Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. (AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae) vacuolar sorting protein 35 (SW:P34110) [Arabidopsis thaliana] Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1672	GM_65_A2_G12_T7	g2739374	BLASTX	190	2e-13	41	
1673	GM_65_A2_H02_MR	g3080384	BLASTX	290	7e-24	38	
1674	GM_65_A2_H08_MR	g2522227	BLASTX	230	2e-18	41	
1675	GM_65_A2_H09_MR	g2160144	BLASTX	214	7e-16	44	
1676	GM_65_A2_H11_MR	g140419	BLASTX	146	1e-09	41	
1677	GM_65_B1_A03_MR	g2129618	BLASTX	195	2e-13	40	
1678	GM_65_B1_A04_MR	g507910	BLASTN	572	3e-19	80	
1679	GM_65_B1_A04_T7	g507910	BLASTN	601	1e-20	84	
1680	GM_65_B1_A08_MR	g3582347	BLASTN	353	7e-09	59	
1681	GM_65_B1_A09_MR	g507910	BLASTN	557	1e-18	80	
1682	GM_65_B1_A09_T7	g507910	BLASTN	511	2e-16	76	
1683	GM_65_B1_B03_T7	g2435519	BLASTX	206	3e-27	84	
1684	GM_65_B1_B07_T7	g4050011	BLASTN	420	6e-12	65	
1685	GM_65_B1_B11_T7	g3142328	BLASTN	608	1e-20	89	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
1686	GM_65_B1_C11_MR	g3097320	BLASTN	421	5e-12	79	Glycine max gene for Bd 30K, complete cds
1687	GM_65_B1_C12_MR	g905361	BLASTX	423	1e-38	95	(U22103) gag-protease polypeptide [Glycine max]
1688	GM_65_B1_D03_T7	g3319345	BLASTX	246	6e-19	40	(AF077407) contains similarity to maize transposon MuDR
1689	GM_65_B1_D04_MR	g3599418	BLASTN	497	2e-15	89	(GB:M76978) [Arabidopsis thaliana]
1690	GM_65_B1_D05_T7	g4063760	BLASTX	467	2e-42	68	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene
1691	GM_65_B1_D06_MR	g342963	BLASTN	390	5e-11	64	encoding mitochondrial protein, complete cds
1692	GM_65_B1_D08_T7	g507910	BLASTN	391	5e-11	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1693	GM_65_B1_D09_MR	g18559	BLASTN	642	4e-22	78	paramesium species 5.87 mt dna dimer: replication init. region.
1694	GM_65_B1_D10_MR	g1840106	BLASTN	405	5e-12	60	Glycine max BSR-101 satellite SB92 genomic sequence
1695	GM_65_B1_D11_MR	g507910	BLASTN	747	4e-27	90	Glycine max BSR-101 satellite SB92 genomic sequence
1696	GM_65_B1_D11_T7	g4063756	BLASTN	437	1e-12	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence.
1697	GM_65_B1_D12_MR	g2351067	BLASTN	384	1e-11	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; complete sequence [Arabidopsis thaliana]
1698	GM_65_B1_E03_MR	g2351067	BLASTN	398	4e-12	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; MPO12
1699	GM_65_B1_E04_MR	g1480927	BLASTN	1255	5e-51	81	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
1700	GM_65_B1_E04_T7	g99721	BLASTX	307	3e-25	37	retrovirus-related polypeptide - Arabidopsis thaliana retrotransposon
1701	GM_65_B1_E06_MR	g507910	BLASTN	401	2e-11	74	Tal-3 gi 16534 (X13291) polypeptide [Arabidopsis thaliana]
1702	GM_65_B1_E06_T7	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1703	GM_65_B1_E07_T7	g113497	BLASTX	88	2e-09	56	Glycine max BSR-101 satellite SB92 genomic sequence.
1704	GM_65_B1_E08_T7	g3426334	BLASTN	355	5e-09	61	Glycine max BSR-101 satellite SB92 genomic sequence.
1705	GM_65_B1_E09_T7	g3142328	BLASTN	2413	9e-104	96	Glycine max BSR-101 satellite SB92 genomic sequence.
1706	GM_65_B1_E10_MR	g1769898	BLASTX	270	2e-32	55	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)
1707	GM_65_B1_E11_T7	g99922	BLASTX	424	5e-39	71	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) gi 99880
1708	GM_65_B1_E12_MR	g1769897	BLASTX	269	6e-22	71	(ALPHA-D-GALACTOSIDE GALACTOXYDOLASE) gi 99880
1709	GM_65_B1_F01_T7	g3142328	BLASTN	943	9e-36	93	pir S07472 alpha-galactosidase (EC 3.2.1.22) precursor - guar gi 18292 (X14619) alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]
							Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
							Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Y08010) lectin receptor kinase [Arabidopsis thaliana]
							hypotheetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
							(Y08010) lectin receptor kinase [Arabidopsis thaliana]
							Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
1710	GM_65_B1_F03_MR	g3319351	BLASTX	261	3e-20	52	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
1711	GM_65_B1_F04_T7	g421955	BLASTX	433	5e-40	53	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387)
1712	GM_65_B1_F05_MR	g4150930	BLASTN	548	1e-17	61	ORF4 [Solanum tuberosum]
1713	GM_65_B1_F05_T7	g995751	BLASTN	354	4e-09	64	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
1714	GM_65_B1_G02_T7	g2970556	BLASTX	140	3e-18	78	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence (AF049708) aspartokinase-homoserine dehydrogenase [Glycine max]
1715	GM_65_B1_G06_T7	g18559	BLASTN	984	1e-37	76	G-max gene for catalase
1716	GM_65_B1_G07_T7	g995751	BLASTN	415	7e-12	61	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence (U22103) gag-protease polypeptide [Glycine max]
1717	GM_65_B1_G09_MR	g905361	BLASTX	894	7e-92	92	probable integrase - common tobacco (fragment) gi 530742
1718	GM_65_B1_G10_MR	g629693	BLASTX	165	2e-14	40	(X80830) integrase [Nicotiana tabacum]
1719	GM_65_B1_G11_MR	g1806119	BLASTX	182	2e-13	43	(Y10603) L-lactate dehydrogenase [Lycopodium esculentum]
1720	GM_65_B1_H01_T7	g4063760	BLASTX	332	2e-35	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1721	GM_65_B1_H03_T7	g3097320	BLASTN	383	3e-10	77	Glycine max gene for Bd 30K, complete cds
1722	GM_65_B1_H07_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1723	GM_65_B1_H07_T7	g3377834	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1724	GM_65_B1_H09_MR	g3097320	BLASTX	161	5e-10	27	(AF075598) No definition line found [Arabidopsis thaliana]
1725	GM_65_B1_H11_MR	g3097320	BLASTN	426	3e-12	62	(AF075598) No definition line found [Arabidopsis thaliana]
1726	GM_65_B1_H11_T7	g4159699	BLASTN	461	8e-14	62	Glycine max gene for Bd 30K, complete cds
1727	GM_65_B2_A02_T7	g629693	BLASTX	147	5e-20	52	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16E1, complete sequence [Arabidopsis thaliana]
1728	GM_65_B2_A03_MR	g13533	BLASTN	369	8e-14	61	probable integrase - common tobacco (fragment) gi 530742
1729	GM_65_B2_A05_MR	g9837	BLASTN	395	7e-11	60	(X80830) integrase [Nicotiana tabacum]
1730	GM_65_B2_B01_T7	g629693	BLASTX	254	6e-21	44	Yeast mitochondrial tRNA genes (several, map positions 3.5 to 8.6) encoding tRNAs for Lys, Arg, Gly, Asp, Ser, Arg, and Ala.
1731	GM_65_B2_B12_T7	g3645899	BLASTX	206	8e-28	59	P.falciptarum 3.8 gene for putative serine kinase (partial)
1732	GM_65_B2_C02_T7	g4063760	BLASTX	217	4e-27	67	gene for glycophorin binding protein (fragment) gi 530742
1733	GM_65_B2_C03_T7	g2464880	BLASTX	355	9e-32	51	probable integrase - common tobacco (fragment)
1734	GM_65_B2_D01_MR	g4160362	BLASTN	384	3e-10	60	(X80830) integrase [Nicotiana tabacum]
1735	GM_65_B2_D03_MR	g2708743	BLASTX	136	1e-13	38	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1736	GM_65_B2_D03_T7	g905361	BLASTX	226	5e-17	30	(U22103) gag-protease polyprotein [Glycine max]
1737	GM_65_B2_E02_MR	g2462134	BLASTX	170	3e-11	37	(Y13368) reverse transcriptase [Beta vulgaris]
1738	GM_65_B2_E03_T7	g3785975	BLASTX	194	1e-13	97	(AC005560) hypothetical protein [Arabidopsis thaliana]
1739	GM_65_B2_E04_MR	g4063756	BLASTN	359	3e-09	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence. complete sequence [Arabidopsis thaliana]
1740	GM_65_B2_E10_T7	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1741	GM_65_B2_F06_MR	g4006815	BLASTN	596	7e-20	72	Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence. complete sequence [Arabidopsis thaliana]
1742	GM_65_B2_F07_T7	g100484	BLASTX	344	1e-29	59	hypothetical protein - garden snapdragon
1743	GM_65_B2_F09_MR	g3426334	BLASTN	494	2e-15	61	Pisum sativum pectin methyltransferase (rcpme1) gene. complete cds
1744	GM_65_B2_F12_MR	g3777527	BLASTX	427	2e-40	65	(AF053008) gag-pol polyprotein [Glycine max]
1745	GM_65_B2_G03_MR	g3777527	BLASTX	306	5e-25	75	(AF053008) gag-pol polyprotein [Glycine max]
1746	GM_65_B2_G04_T7	g2995405	BLASTX	629	9e-61	59	(Y12432) polyprotein [Ananas comosus]
1747	GM_65_B2_G07_T7	g507910	BLASTN	388	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1748	GM_65_B2_G11_MR	g2982528	BLASTN	423	4e-12	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-01. complete sequence [Plasmodium falciparum]
1749	GM_65_B2_H02_T7	g905361	BLASTX	278	1e-22	35	(U22103) gag-protease polyprotein [Glycine max]
1750	GM_65_B2_H06_T7	g507910	BLASTN	528	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1751	GM_65_B2_H07_MR	g3128140	BLASTN	352	7e-09	61	Arabidopsis thaliana genomic DNA. chromosome 5. P1 clone: MJF4. complete sequence.
1752	GM_65_B2_H09_T7	g2828185	BLASTN	494	3e-15	74	Arabidopsis thaliana genomic DNA. chromosome 5. P1 clone: MUD21. complete sequence [Arabidopsis thaliana]
1753	GM_66_A1_A01_T7	g18695	BLASTN	350	6e-09	66	Soybean nodulin 22 gene
1754	GM_66_A1_A04_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1755	GM_66_A1_A05_MR	g99922	BLASTX	147	5e-09	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1756	GM_66_A1_A07_MR	g3319362	BLASTX	324	9e-31	54	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1757	GM_66_A1_A08_T7	g507910	BLASTN	405	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1758	GM_66_A1_A09_T7	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1759	GM_66_A1_A10_MR	g2522230	BLASTX	291	6e-25	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1760	GM_66_A1_B03_T7	g2522230	BLASTX	151	4e-10	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1761	GM_66_A1_B12_T7	g3097320	BLASTN	721	1e-25	83	Glycine max gene for Bd 30K. complete cds
1762	GM_66_A1_C03_MR	g4150930	BLASTN	373	8e-10	63	Homo sapiens BAC clone RG281G05 from 7p15-p21. complete sequence [Homo sapiens]
1763	GM_66_A1_C03_T7	g2995405	BLASTX	206	1e-14	44	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1764	GM_66_A1_C05_MR	g3777527	BLASTX	491	1e-44	78	(AF053008) gag-pol polyprotein [Glycine max]
1765	GM_66_A1_C12_MR	g3176726	BLASTX	211	3e-15	51	(AC002392) putative serine proteinase [Arabidopsis thaliana]
1766	GM_66_A1_D01_T7	g1906603	BLASTN	348	1e-08	70	Zea mays ACCase gene, intron containing colonist1 and colonist2 retrotransposons and reverse transcriptase pseudogene, complete sequence
1767	GM_66_A1_D02_T7	g18559	BLASTN	322	9e-10	75	G.max gene for catalase
1768	GM_66_A1_D03_T7	g4038592	BLASTX	208	8e-15	34	(Y10403) RNA-directed RNA polymerase [Lycopodium obscurum]
1769	GM_66_A1_D04_MR	g3097836	BLASTN	371	1e-09	64	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
1770	GM_66_A1_D04_T7	g3805845	BLASTX	219	3e-21	80	(AL031986) putative protein [Arabidopsis thaliana]
1771	GM_66_A1_D06_T7	g4063760	BLASTX	552	2e-51	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1772	GM_66_A1_D09_MR	g4063760	BLASTX	366	2e-31	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1773	GM_66_A1_D12_MR	g3068704	BLASTX	325	2e-27	70	(AF049236) unknown [Arabidopsis thaliana]
1774	GM_66_A1_E01_T7	g3287288	BLASTN	372	8e-10	63	Vicia faba L. Kleine Thueringer
1775	GM_66_A1_E03_T7	g1171499	BLASTX	232	5e-30	69	(Z68913) reverse transcriptase [Beta vulgaris]
1776	GM_66_A1_E07_MR	g905361	BLASTX	218	3e-16	36	(U22103) gag-protease polyprotein [Glycine max]
1777	GM_66_A1_E10_MR	g3777527	BLASTX	742	2e-71	94	(AF053008) gag-pol polyprotein [Glycine max]
1778	GM_66_A1_F01_T7	g3142328	BLASTN	798	6e-55	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope like genes, partial cds, and long terminal repeat, complete sequence
1779	GM_66_A1_F02_MR	g1142701	BLASTN	1364	3e-55	86	Glycine max satellite STR120-A.3.
1780	GM_66_A1_F02_T7	g3777527	BLASTX	599	3e-56	94	(AF053008) gag-pol polyprotein [Glycine max]
1781	GM_66_A1_F05_T7	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1782	GM_66_A1_F07_MR	g18559	BLASTN	1098	9e-43	77	G.max gene for catalase
1783	GM_66_A1_F10_MR	g3550435	BLASTN	530	6e-17	63	Hordeum vulgare Hotr1 gene
1784	GM_66_A1_F10_T7	g3337392	BLASTN	393	1e-10	64	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence [Homo sapiens]
1785	GM_66_A1_G01_MR	g2264318	BLASTN	415	1e-11	85	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]
1786	GM_66_A1_G02_MR	g4063760	BLASTX	194	3e-13	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1787	GM_66_A1_G03_T7	g3645899	BLASTX	154	5e-09	39	(U68408) 5' end not determined experimentally [Zea mays]
1788	GM_66_A1_G04_T7	g3513745	BLASTX	124	2e-11	36	(AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
1789	GM_66_A1_G05_MR	g3319362	BLASTX	253	1e-19	45	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1790	GM_66_A1_G10_MR	g3873182	BLASTN	351	8e-09	60	Homo sapiens chromosome 17, clone hRPK.235_1_10, complete sequence [Homo sapiens]
1791	GM_66_A1_G11_MR	g2995405	BLASTX	317	1e-26	50	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1792	GM_66_A1_G12_MR	g342963	BLASTN	515	6e-17	66	parametrium species 5.87 mt dna dimer: replication init. region (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
1793	GM_66_A1_H01_MR	g2262114	BLASTX	235	4e-19	53	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1794	GM_66_A1_H03_T7	g3142328	BLASTN	1604	7e-66	93	Glycine max BSR-101 satellite SB92 genomic sequence.
1795	GM_66_A1_H05_MR	g507910	BLASTN	585	8e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
1796	GM_66_A1_H05_T7	g3810596	BLASTX	118	6e-09	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
1797	GM_66_A2_A02_T7	g4038056	BLASTX	171	6e-11	44	(AC005897) putative transposon [Arabidopsis thaliana]
1798	GM_66_A2_A03_T7	g3057150	BLASTX	163	2e-11	80	(AF059037) chaperonin 10 [Arabidopsis thaliana]
1799	GM_66_A2_A05_T7	g3777527	BLASTX	722	2e-69	91	(AF053008) gag-pol polyprotein [Glycine max]
1800	GM_66_A2_A07_MR	g3645899	BLASTX	182	5e-12	43	(U68408) 5' end not determined experimentally [Zea mays]
1801	GM_66_A2_A12_MR	g3142379	BLASTX	325	1e-28	67	(AF053008) envelope-like [Glycine max]
1802	GM_66_A2_A12_T7	g3142328	BLASTN	825	2e-30	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (X98744) chloroplast DNA-binding protein PD3 [Pisum sativum]
1803	GM_66_A2_B02_MR	g2213540	BLASTX	297	5e-24	54	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]
1804	GM_66_A2_B02_T7	g2564048	BLASTN	566	2e-18	78	(AB004906) transposase [Ipomoea purpurea]
1805	GM_66_A2_B05_MR	g4063770	BLASTX	103	4e-09	35	S-receptor kinase-related protein - Chinese kale gi 17917 (Z18884)
1806	GM_66_A2_B08_MR	g322663	BLASTX	288	1e-24	68	S-receptor kinase related protein [Brassica oleracea]
1807	GM_66_A2_B09_MR	g3264565	BLASTN	430	2e-12	64	Homo sapiens chromosome 17, clone hRPC.1037.O.7, complete sequence [Homo sapiens]
1808	GM_66_A2_B10_MR	g1142699	BLASTN	247	2e-12	75	Glycine max satellite STR120-A.1.
1809	GM_66_A2_B10_T7	g4063770	BLASTX	180	6e-12	38	(AB004906) transposase [Ipomoea purpurea]
1810	GM_66_A2_B11_T7	g3142328	BLASTN	753	4e-27	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
1811	GM_66_A2_C02_T7	g4063760	BLASTX	317	5e-45	79	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
1812	GM_66_A2_C03_T7	g3810596	BLASTX	234	1e-17	39	Glycine max BSR-101 satellite SB92 genomic sequence.
1813	GM_66_A2_C05_MR	g507910	BLASTN	412	5e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
1814	GM_66_A2_C05_T7	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
1815	GM_66_A2_C08_MR	g3928116	BLASTN	391	1e-10	70	, complete sequence [Homo sapiens]
1816	GM_66_A2_C08_T7	g1431738	BLASTN	575	4e-19	77	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
1817	GM_66_A2_C10_MR	g905361	BLASTX	676	1e-65	98	(U22103) gag-protease polyprotein [Glycine max]
1818	GM_66_A2_C12_MR	g2880057	BLASTX	262	2e-22	51	(AC002340) putative RNA helicase A, 5' partial [Arabidopsis thaliana]
1819	GM_66_A2_D01_MR	g3820757	BLASTN	382	2e-10	60	Caenorhabditis elegans cosmid Y53C12D, complete sequence
1820	GM_66_A2_D03_MR	g3097320	BLASTN	1137	2e-44	82	[Caenorhabditis elegans] Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1821	GM_66_A2_D05_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1822	GM_66_A2_D05_T7	g507910	BLASTN	543	6e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1823	GM_66_A2_D06_MR	g304040	BLASTN	628	1e-21	81	Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene.
1824	GM_66_A2_E02_MR	g2914706	BLASTX	190	1e-22	74	(AC003974) putative homeobox protein [Arabidopsis thaliana]
1825	GM_66_A2_E04_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1826	GM_66_A2_E04_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1827	GM_66_A2_E09_MR	g905361	BLASTX	384	3e-34	89	(U22103) gag-protease polyprotein [Glycine max]
1828	GM_66_A2_E10_MR	g1870709	BLASTN	307	2e-10	62	Toxoplasma gondii chloroplast, complete genome
1829	GM_66_A2_F02_MR	g2522228	BLASTX	176	2e-16	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
1830	GM_66_A2_F03_MR	g2462058	BLASTX	196	7e-15	45	(Y13389) reverse transcriptase [Antirrhinum majus]
1831	GM_66_A2_F07_T7	g3650039	BLASTX	247	3e-19	40	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
1832	GM_66_A2_F09_MR	g18559	BLASTN	775	4e-28	75	G-max gene for catalase
1833	GM_66_A2_G04_MR	g3513747	BLASTX	181	1e-11	47	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
1834	GM_66_A2_G08_T7	g1769898	BLASTX	444	3e-41	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1835	GM_66_A2_G10_T7	g4063760	BLASTX	226	1e-16	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1836	GM_66_A2_H01_MR	g505129	BLASTN	396	6e-11	64	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
1837	GM_66_A2_H11_MR	g3777527	BLASTX	317	4e-26	43	(AF053008) gag-pol polyprotein [Glycine max]
1838	GM_66_B1_A01_MR	g2522230	BLASTX	202	2e-15	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1839	GM_66_B1_A07_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1840	GM_66_B1_A11_T7	g18559	BLASTN	778	3e-28	76	G-max gene for catalase
1841	GM_66_B1_A12_T7	g422418	BLASTX	225	1e-16	42	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
1842	GM_66_B1_C08_T7	g421955	BLASTX	182	6e-26	38	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387)
1843	GM_66_B1_C09_T7	g2462134	BLASTX	438	2e-40	50	ORF4 [Solanum tuberosum]
1844	GM_66_B1_D01_MR	g3142328	BLASTN	459	9e-14	80	(Y13368) reverse transcriptase [Beta vulgaris]
1845	GM_66_B1_D01_T7	g3599418	BLASTN	647	3e-22	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1846	GM_66_B1_D04_T7	g3142328	BLASTN	939	1e-35	84	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
1847	GM_66_B1_D08_T7	g3033400	BLASTX	203	2e-31	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1848	GM_66_B1_E03_MR	g1666236	BLASTX	188	1e-13	37	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
1849	GM_66_B1_E09_T7	g3097320	BLASTN	892	2e-33	72	(U76261) unknown [Hordeum vulgare]
							Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1850	GM_66_B1_F01_MR	g3097320	BLASTN	441	6e-13	71	Glycine max gene for Bd 30K, complete cds
1851	GM_66_B1_F02_MR	g100484	BLASTX	408	1e-36	54	hypothetical protein - garden snapdragon
1852	GM_66_B1_F03_MR	g507910	BLASTN	402	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1853	GM_66_B1_F04_T7	g4063760	BLASTX	160	1e-13	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1854	GM_66_B1_F09_MR	g18559	BLASTN	620	4e-21	71	G max gene for catalase
1855	GM_66_B1_G02_MR	g1732513	BLASTX	179	4e-13	64	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
1856	GM_66_B1_G02_T7	g2852684	BLASTX	150	8e-09	43	(AF017751) resistance protein candidate [Lactuca sativa]
1857	GM_66_B1_G04_T7	g3142328	BLASTN	772	5e-28	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1858	GM_66_B1_H05_T7	g3885341	BLASTX	185	2e-12	34	(AC005623) unknown protein [Arabidopsis thaliana]
1859	GM_66_B1_H06_T7	g1706522	BLASTX	173	2e-26	69	DIHYDROFOLATE REDUCTASE / THYMIDYLATE SYNTHASE (DHFR-TS) gi 1362048 pir S55683 dihydrofolate reductase-thymidylate synthase - soybean gi 999190 bbs 166832 (S78087) dihydrofolate reductase-thymidylate synthase, DHFR-TS=bifunctional enzyme {EC 1.5.1.3} [Glycine max, seedling, Peptide, 530 aa] [Glycine max] gi 1096144 prf 2111237A dihydrofolate reductase-thymidylate synthase [Glycine max] (Y10983) putative cytochrome P450 [Glycine max]
1860	GM_66_B1_H08_MR	g2765093	BLASTX	246	2e-19	60	pol polyprotein - mink cell focus-forming virus (fragment) >gi 50857
1861	GM_66_B1_H12_T7	g77236	BLASTX	130	6e-11	28	(X52622) integrase (409 AA) [Mus musculus]
1862	GM_66_B2_A02_T7	g99922	BLASTX	207	3e-24	76	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1863	GM_66_B2_A07_MR	g2085783	BLASTN	360	3e-09	62	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
1864	GM_66_B2_A11_T7	g4063760	BLASTX	526	1e-48	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1865	GM_66_B2_B10_MR	g3152613	BLASTX	162	4e-10	53	(AC004482) hypothetical protein [Arabidopsis thaliana]
1866	GM_66_B2_B10_T7	g3242709	BLASTX	152	1e-24	50	(AC003040) putative guanine nucleotide-binding protein [Arabidopsis thaliana]
1867	GM_66_B2_C03_MR	g2160694	BLASTX	483	3e-45	92	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
1868	GM_66_B2_C05_T7	g3790154	BLASTN	365	2e-09	62	Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs ...
1869	GM_66_B2_C09_MR	g18559	BLASTN	444	4e-13	75	G max gene for catalase
1870	GM_66_B2_D03_MR	g3738114	BLASTN	448	3e-13	65	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
1871	GM_66_B2_D05_MR	g1666236	BLASTX	224	7e-18	32	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1872	GM_66_B2_D06_MR	g2583130	BLASTX	134	1e-22	49	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
1873	GM_66_B2_D10_T7	g3142328	BLASTN	803	2e-29	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1874	GM_66_B2_D11_T7	g3810584	BLASTN	538	3e-17	67	Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence, complete sequence [Arabidopsis thaliana]
1875	GM_66_B2_E02_T7	g3777527	BLASTX	108	1e-09	31	(AF053008) gag-pol polyprotein [Glycine max]
1876	GM_66_B2_E06_MR	g507910	BLASTN	451	9e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1877	GM_66_B2_E07_MR	g2827715	BLASTX	127	9e-10	28	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
1878	GM_66_B2_E09_MR	g2924257	BLASTN	447	4e-13	69	Tobacco chloroplast genome DNA
1879	GM_66_B2_E10_MR	g3738114	BLASTN	374	7e-10	64	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
1880	GM_66_B2_E11_T7	g4063760	BLASTX	273	6e-35	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1881	GM_66_B2_F02_T7	g100484	BLASTX	346	6e-30	59	hypothetical protein - garden snapdragon
1882	GM_66_B2_F04_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1883	GM_66_B2_F05_T7	g4160362	BLASTN	390	1e-10	60	Saccharomyces cerevisiae complete mitochondrial genome
1884	GM_66_B2_F08_MR	g4063760	BLASTX	276	5e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1885	GM_66_B2_F09_MR	g3142328	BLASTN	1303	4e-52	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF053008) gag-pol polyprotein [Glycine max]
1886	GM_66_B2_G03_T7	g3777527	BLASTX	697	1e-66	90	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18
1887	GM_66_B2_G05_T7	g3080352	BLASTN	468	4e-14	64	(ESSAII project).
1888	GM_66_B2_G08_MR	g2970554	BLASTN	547	1e-17	70	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
1889	GM_66_B2_G08_T7	g3777527	BLASTX	480	2e-43	87	(AF053008) gag-pol polyprotein [Glycine max]
1890	GM_66_B2_G11_T7	g100484	BLASTX	394	4e-35	58	hypothetical protein - garden snapdragon
1891	GM_66_B2_H09_T7	g3128142	BLASTN	259	3e-09	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]
1892	GM_66_B2_H10_MR	g3426334	BLASTN	530	6e-17	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
1893	GM_66_B2_H11_MR	g100484	BLASTX	405	3e-36	54	hypothetical protein - garden snapdragon
1894	GM_66_B2_H11_T7	g4063760	BLASTX	232	3e-30	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1895	GM_67_A1_A02_T7	g1351995	BLASTX	119	4e-14	43	PROBABLE CALCIUM-TRANSPORTING ATPASE gi 2130357 pir S62557 hypothetical protein SPAC24B11.12c - fission yeast (Schizosaccharomyces pombe) gi 1061300 (Z67757) unknown [Schizosaccharomyces pombe]
1896	GM_67_A1_A04_T7	g3036804	BLASTX	153	2e-10	66	(AL022373) thaumatin-like protein [Arabidopsis thaliana]
1897	GM_67_A1_B07_T7	g510875	BLASTN	437	9e-13	77	P. vulgaris PvME1 gene
1898	GM_67_A1_B10_MR	g2245135	BLASTX	276	2e-23	68	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1899	GM_67_A1_C04_MR	g507910	BLASTN	428	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1900	GM_67_A1_C04_T7	g3777527	BLASTX	234	2e-17	90	(AF053008) gag-pol polyprotein [Glycine max]
1901	GM_67_A1_C05_MR	g2245104	BLASTX	180	1e-11	31	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
1902	GM_67_A1_C08_MR	g170602	BLASTN	570	8e-20	63	Broad bean (V.faba) BamHI repetitive element. 900 bp family.
1903	GM_67_A1_C08_T7	g4160362	BLASTN	408	2e-11	66	Saccharomyces cerevisiae complete mitochondrial genome
1904	GM_67_A1_D02_MR	g1946279	BLASTX	176	8e-13	44	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
1905	GM_67_A1_D04_T7	g2266985	BLASTX	181	3e-12	77	(Y13943) MEtRS [Arabidopsis thaliana]
1906	GM_67_A1_D06_MR	g4097522	BLASTX	170	6e-26	59	(U63534) cinnamyl alcohol dehydrogenase [Fragaria x ananassa]
1907	GM_67_A1_D07_MR	g3097320	BLASTN	879	9e-33	74	Glycine max gene for Bd 30K, complete cds
1908	GM_67_A1_D07_T7	g629693	BLASTX	278	1e-23	55	probable integrase - common tobacco (fragment) gi 530742
1909	GM_67_A1_D11_MR	g3033389	BLASTX	205	1e-14	37	(X80830) integrase [Nicotiana tabacum]
1910	GM_67_A1_E07_MR	g507910	BLASTN	591	4e-20	81	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
1911	GM_67_A1_E10_MR	g18559	BLASTN	1050	1e-40	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1912	GM_67_A1_E10_T7	g905361	BLASTX	176	1e-11	30	G.max gene for catalase
1913	GM_67_A1_F04_MR	g3047068	BLASTX	157	2e-09	28	(U22103) gag-protease polyprotein [Glycine max]
1914	GM_67_A1_F07_T7	g3097320	BLASTN	606	2e-20	77	(AF058825) similar to maize transposon MuDR (GIB:M76978)
1915	GM_67_A1_G05_MR	g3645899	BLASTX	253	1e-19	41	[Arabidopsis thaliana]
1916	GM_67_A1_G12_MR	g3142328	BLASTN	625	3e-21	75	Glycine max gene for Bd 30K, complete cds
1917	GM_67_A1_H04_MR	g3097320	BLASTN	469	3e-14	68	Glycine max gene for Bd 30K, complete cds
1918	GM_67_A1_H04_T7	g3097320	BLASTN	863	5e-32	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1919	GM_67_A1_H05_MR	g507910	BLASTN	435	5e-13	73	Glycine max BSR-101 polyprotein [Glycine max]
1920	GM_67_A1_H06_T7	g3777527	BLASTX	307	4e-25	62	(AF053008) gag-pol polyprotein [Glycine max]
1921	GM_67_A1_H07_MR	g2459437	BLASTX	210	2e-16	54	(AC002332) hypothetical protein [Arabidopsis thaliana]
1922	GM_67_A2_A02_T7	g465599	BLASTX	91	1e-08	50	(AC002332) hypothetical protein [Arabidopsis thaliana]
1923	GM_67_A2_A03_T7	g507910	BLASTN	425	1e-12	74	HYPOTHEICAL 33.7 KD PROTEIN IN NFO-FRUA
1924	GM_67_A2_A05_T7	g226407	BLASTX	256	1e-19	37	INTERGENIC REGION gi 405882 (U00007) yeik [Escherichia coli]
1925	GM_67_A2_A12_T7	g507910	BLASTN	400	2e-11	72	yeik gene [Escherichia coli]
1926	GM_67_A2_B04_T7	g4063760	BLASTX	563	1e-52	68	Glycine max BSR-101 satellite SB92 genomic sequence.
1927	GM_67_A2_B05_T7	g3142328	BLASTN	1215	4e-48	75	retrotransposon dell-46 [Lilium henryi]
							Glycine max BSR-101 satellite SB92 genomic sequence.
							(AC005561) putative POL3 protein [Arabidopsis thaliana]
							Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1928	GM_67_A2_B06_T7	g25222228	BLASTX	157	6e-10	30	(AB007466) reverse transcriptase-like protein [Vicia faba]
1929	GM_67_A2_B07_T7	g4063760	BLASTX	624	3e-59	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1930	GM_67_A2_B09_MR	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1931	GM_67_A2_B10_MR	g3097320	BLASTN	603	3e-20	81	Glycine max gene for Bd 30K. complete cds
1932	GM_67_A2_B12_MR	g4063760	BLASTX	185	3e-12	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1933	GM_67_A2_C06_MR	g1346735	BLASTX	182	2e-12	84	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
							(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM)
							gi 1076562 pir S49647 phosphoglycerate mutase (EC 5.4.2.1) -
							castor bean gi 474170 (X70652) phosphoglycerate mutase [Ricinus communis]
1934	GM_67_A2_C08_MR	g3885336	BLASTX	299	1e-24	58	(AC005623) receptor-like protein kinase [Arabidopsis thaliana]
1935	GM_67_A2_C09_MR	g3859610	BLASTN	665	5e-23	65	Arabidopsis thaliana BAC T9E19
1936	GM_67_A2_C10_T7	g3789709	BLASTN	366	2e-09	63	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
1937	GM_67_A2_D05_MR	g4063760	BLASTX	187	2e-12	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1938	GM_67_A2_D05_T7	g507910	BLASTN	724	4e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
1939	GM_67_A2_D12_MR	g3264767	BLASTX	190	3e-14	62	(AF071893) AP2 domain containing protein [Prunus armeniaca]
1940	GM_67_A2_D12_T7	g4160362	BLASTN	362	3e-09	60	Saccharomyces cerevisiae complete mitochondrial genome
1941	GM_67_A2_E02_T7	g231753	BLASTX	114	2e-15	69	60 KD CHAPERONIN 2 (PROTEIN CPN60 2) (GROEL PROTEIN 2) (HSP56) gi 80689 pir C41325 heat shock protein 56 -
							Streptomyces albus gi 153294 (M76658) open reading frame;
							GROEL1 encodes two gene products, related to a second GROEL-like gene (GROEL2) in S.albus [Streptomyces albus]
1942	GM_67_A2_E03_MR	g1732513	BLASTX	178	5e-13	66	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
1943	GM_67_A2_E03_T7	g3777527	BLASTX	233	3e-17	35	(AF053008) gag-pol polypeptide [Glycine max]
1944	GM_67_A2_E04_MR	g992916	BLASTN	350	9e-09	75	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
1945	GM_67_A2_E07_MR	g2979597	BLASTN	612	1e-20	65	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
1946	GM_67_A2_E07_T7	g3688169	BLASTN	298	9e-14	69	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)
1947	GM_67_A2_E08_MR	g505129	BLASTN	386	2e-10	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
1948	GM_67_A2_F08_T7	g4063756	BLASTN	382	3e-10	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
1949	GM_67_A2_F10_T7	g3097320	BLASTN	385	2e-10	77	Glycine max gene for Bd 30K. complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1950	GM_67_A2_F01_T7	g1666236	BLASTX	198	8e-15	29	(U76261) unknown [Hordeum vulgare]
1951	GM_67_A2_F06_T7	g170080	BLASTN	1010	7e-39	90	Soybean seed lectin gene transposable element (gm1. (AF053993) disease resistance protein [Lycopersicon esculentum])
1952	GM_67_A2_F11_T7	g3894383	BLASTX	159	1e-09	43	D.discoideum mRNA for stat protein, first finger stage
1953	GM_67_A2_G02_MR	g2230823	BLASTN	363	2e-09	64	Glycine max gene for Bd 30K, complete cds
1954	GM_67_A2_G02_T7	g3097320	BLASTN	778	6e-36	76	(AF077408) contains similarity to reverse transcriptase (Pfiam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1955	GM_67_A2_G06_T7	g3319362	BLASTX	153	5e-09	44	Pisum sativum putative IAA-related protein gene, partial cds
1956	GM_67_A2_G12_MR	g3642874	BLASTN	360	8e-10	71	Homo sapiens Xp22 bins 29-30 BAC GSHB-2271.7 (Genome Systems Human BAC Library) complete sequence [Homo sapiens]
1957	GM_67_A2_H01_T7	g3659406	BLASTN	365	2e-09	65	Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) ...
1958	GM_67_A2_H02_MR	g3550044	BLASTN	420	6e-12	68	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1959	GM_67_A2_H09_T7	g1167523	BLASTX	219	8e-16	35	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1960	GM_67_A2_H10_T7	g3142328	BLASTN	799	3e-29	75	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
1961	GM_67_A2_H12_T7	g130582	BLASTX	434	9e-39	66	(TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1962	GM_67_B1_A02_MR	g4039114	BLASTN	370	9e-10	68	Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds
1963	GM_67_B1_A08_T7	g2522228	BLASTX	229	6e-18	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
1964	GM_67_B1_B04_T7	g2995405	BLASTX	339	6e-29	62	(Y12432) polyprotein [Ananas comosus]
1965	GM_67_B1_B07_MR	g2498329	BLASTX	250	4e-19	76	PATTERN FORMATION PROTEIN EMB30 gi 2129665 pir S65571 pattern-formation protein GNOM - Arabidopsis thaliana gi 1209633 (U36433) GNOM gene product [Arabidopsis thaliana] gi 1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] gi 1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] (D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1966	GM_67_B1_B09_T7	g1167523	BLASTX	275	8e-22	41	Soybean Tgm6 transposable element 3' end
1967	GM_67_B1_C04_T7	g18768	BLASTN	361	6e-10	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1968	GM_67_B1_C08_MR	g3142328	BLASTN	1285	3e-51	90	Glycine max BSR-101 satellite SB92 genomic sequence. (Y08010) lectin receptor kinase [Arabidopsis thaliana]
1969	GM_67_B1_C08_T7	g507910	BLASTN	378	2e-10	75	
1970	GM_67_B1_D05_MR	g1769897	BLASTX	201	2e-14	56	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1971	GM_67_B1_D06_T7	g2769655	BLASTN	547	1e-17	66	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Contain...
1972	GM_67_B1_D07_T7	g3650039	BLASTX	275	3e-22	44	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
1973	GM_67_B1_D10_MR	g2842478	BLASTX	133	6e-10	58	(AL021749) receptor protein kinase like protein [Arabidopsis thaliana]
1974	GM_67_B1_D11_MR	g2104945	BLASTN	396	7e-11	78	Glycine max copia-like retrotransposon Tgmr, complete sequence. Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence.
1975	GM_67_B1_E07_T7	g4063756	BLASTN	492	3e-15	64	complete sequence [Arabidopsis thaliana]
1976	GM_67_B1_F10_MR	g294042	BLASTN	474	2e-14	64	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
1977	GM_67_B1_F01_T7	g3176776	BLASTN	346	2e-09	66	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 5' sequence
1978	GM_67_B1_F03_MR	g507910	BLASTN	562	9e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1979	GM_67_B1_F04_T7	g4063760	BLASTX	285	9e-28	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1980	GM_67_B1_F07_MR	g507910	BLASTN	364	8e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1981	GM_67_B1_F07_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1982	GM_67_B1_G01_MR	g1786115	BLASTX	152	3e-09	54	(U85250) phosphoinositide-specific phospholipase C [Vigna unguiculata]
1983	GM_67_B1_G03_T7	g2191194	BLASTX	261	8e-22	49	(AF007271) contains weak to the SAPB protein (TR:E236624) [Arabidopsis thaliana]
1984	GM_67_B1_G11_MR	g2995405	BLASTX	182	4e-12	43	(Y12432) polyprotein [Ananas comosus]
1985	GM_67_B2_A02_T7	g2129618	BLASTX	158	2e-09	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
1986	GM_67_B2_A04_MR	g18559	BLASTN	999	3e-38	77	G.max gene for catalase
1987	GM_67_B2_A12_MR	g4038056	BLASTX	314	3e-26	55	(AC005897) putative transposon [Arabidopsis thaliana]
1988	GM_67_B2_A12_T7	g2443320	BLASTX	245	1e-18	55	(D85597) polyprotein [Oryza australiensis]
1989	GM_67_B2_B06_T7	g905361	BLASTX	345	6e-30	95	(U72103) gag-protease polyprotein [Glycine max]
1990	GM_67_B2_B07_MR	g4006855	BLASTX	322	4e-27	78	(Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis thaliana]
1991	GM_67_B2_B12_MR	g3777527	BLASTX	535	2e-49	97	(AF053008) gag-pol polyprotein [Glycine max]
1992	GM_67_B2_C04_T7	g905360	BLASTN	849	1e-31	92	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
1993	GM_67_B2_C07_MR	g100484	BLASTX	276	2e-22	45	hypothetical protein - garden snapdragon
1994	GM_67_B2_D04_MR	g4038056	BLASTX	263	9e-21	53	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1995	GM_67_B2_D09_MR	g4092471	BLASTN	509	6e-16	68	Arabidopsis thaliana chromosome IV map near 21 cM. complete sequence [Arabidopsis thaliana]
1996	GM_67_B2_D11_MR	g3135969	BLASTN	404	3e-11	60	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
1997	GM_67_B2_D11_T7	g18559	BLASTN	826	2e-30	82	G.max gene for catalase
1998	GM_67_B2_E01_T7	g3193306	BLASTX	244	1e-18	54	(AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana]
1999	GM_67_B2_E06_T7	g100484	BLASTX	199	4e-14	56	hypothetical protein - garden snapdragon
2000	GM_67_B2_E11_MR	g3935200	BLASTN	522	1e-16	68	Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region. complete sequence [Homo sapiens]
2001	GM_67_B2_E12_MR	g18559	BLASTN	602	3e-20	71	G.max gene for catalase
2002	GM_67_B2_F05_MR	g2462134	BLASTX	184	1e-12	30	(Y13368) reverse transcriptase [Beta vulgaris]
2003	GM_67_B2_F06_T7	g4063760	BLASTX	187	2e-12	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2004	GM_67_B2_F11_MR	g3650035	BLASTX	207	1e-14	39	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
2005	GM_67_B2_G06_MR	g4063760	BLASTX	112	5e-09	81	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2006	GM_68_A1_A03_MR	g3695387	BLASTX	148	3e-13	68	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
2007	GM_68_A1_A08_MR	g3641838	BLASTX	246	4e-42	59	(AL023094) putative protein (fragment) [Arabidopsis thaliana]
2008	GM_68_A1_B04_MR	g507910	BLASTN	394	3e-11	78	Glycine max BSR-101 satellite SB92 genomic sequence.
2009	GM_68_A1_B05_MR	g905361	BLASTX	202	2e-14	29	(U22103) gag-protease polyprotein [Glycine max]
2010	GM_68_A1_B09_MR	g3193282	BLASTN	321	3e-14	62	Arabidopsis thaliana BAC T14P8
2011	GM_68_A1_B09_T7	g3738298	BLASTX	233	8e-18	80	(AC005309) unknown protein [Arabidopsis thaliana]
2012	GM_68_A1_B10_MR	g3738325	BLASTX	493	2e-46	58	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]
2013	GM_68_A1_B10_T7	g3766106	BLASTN	429	2e-12	70	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence. complete sequence [Arabidopsis thaliana]
2014	GM_68_A1_C03_MR	g507910	BLASTN	580	1e-19	84	Glycine max BSR-101 satellite SB92 genomic sequence.
2015	GM_68_A1_C03_T7	g507910	BLASTN	494	1e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
2016	GM_68_A1_C05_T7	g18559	BLASTN	378	4e-10	69	G.max gene for catalase
2017	GM_68_A1_C10_T7	g1144553	BLASTN	391	1e-11	62	Anopheles melas 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
2018	GM_68_A1_D04_MR	g4063760	BLASTX	473	5e-43	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2019	GM_68_A1_D07_T7	g1666236	BLASTX	210	3e-16	31	(U76261) unknown [Hordeum vulgare]
2020	GM_68_A1_D11_MR	g18683	BLASTN	717	1e-25	77	G.max N-20t gene
2021	GM_68_A1_E02_T7	g3492803	BLASTX	263	2e-20	50	(AJ002479) ENBP1 [Medicago truncatula]
2022	GM_68_A1_E03_T7	g3283026	BLASTX	198	6e-14	35	putative transposase [Arabidopsis thaliana]
2023	GM_68_A1_E04_MR	g507910	BLASTN	404	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2024	GM_68_A1_E04_T7	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2025	GM_68_A1_E05_T7	g505129	BLASTN	417	7e-12	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
2026	GM_68_A1_E07_MR	g130582	BLASTX	272	6e-28	51	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2027	GM_68_A1_E10_MR	g2522227	BLASTX	293	4e-25	40	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2028	GM_68_A1_E12_T7	g3097320	BLASTN	570	9e-19	71	Glycine max gene for Bd 30K. complete cds
2029	GM_68_A1_F03_T7	g18683	BLASTN	518	6e-25	81	G.max N-20t gene
2030	GM_68_A1_F08_T7	g170296	BLASTN	550	6e-18	65	Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma3) gene, exons 1-9.
2031	GM_68_A1_G02_T7	g629693	BLASTX	147	6e-09	33	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
2032	GM_68_A1_G06_MR	g1946279	BLASTX	155	1e-10	45	(Y12433) polyprotein; reverse transcriptase, RNase H [pincapple bacilliform virus]
2033	GM_68_A1_G12_MR	g547683	BLASTX	330	3e-28	68	HEAT SHOCK COGNATE PROTEIN 80 gi 170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] gi 445601 prf 1909348 A heat shock protein hsp80 [Lycopersicon esculentum] (AF053008) gag-pol polyprotein [Glycine max]
2034	GM_68_A1_H01_T7	g3777527	BLASTX	239	7e-18	85	Glycine max gene for Bd 30K. complete cds
2035	GM_68_A1_H03_MR	g3097320	BLASTN	1565	7e-64	82	Glycine max gene for Bd 30K. complete cds
2036	GM_68_A1_H03_T7	g3097320	BLASTN	502	1e-15	81	(AC005171) putative retrotransposon [Arabidopsis thaliana]
2037	GM_68_A1_H06_T7	g3779026	BLASTX	468	2e-42	65	Glycine max BSR-101 satellite SB92 genomic sequence.
2038	GM_68_A1_H10_MR	g507910	BLASTN	358	1e-09	72	(U96295) envelope-like [Glycine max]
2039	GM_68_A1_H10_T7	g3142330	BLASTX	595	3e-57	88	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB
2040	GM_68_A1_H11_T7	g3059060	BLASTN	452	2e-13	66	Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
2041	GM_68_A2_A03_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2042	GM_68_A2_A07_MR	g2760331	BLASTX	229	3e-17	39	(AC002130) F1N21.16 [Arabidopsis thaliana]
2043	GM_68_A2_A08_MR	g3334667	BLASTX	215	4e-16	39	(Y10493) putative cytochrome P450 [Glycine max]
2044	GM_68_A2_B01_MR	g18559	BLASTN	827	2e-30	74	G.max gene for catalase
2045	GM_68_A2_B06_MR	g3461840	BLASTX	302	1e-24	44	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
2046	GM_68_A2_C02_MR	g4063760	BLASTX	207	1e-14	41	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
2047	GM_68_A2_D06_MR	g507910	BLASTN	575	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2048	GM_68_A2_D12_MR	g507910	BLASTN	544	6e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2049	GM_68_A2_E05_MR	g507910	BLASTN	381	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2050	GM_68_A2_E11_MR	g99730	BLASTX	337	8e-30	50	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl P1D c73215 (X53975)
2051	GM_68_A2_F02_MR	g3560029	BLASTN	439	6e-13	65	orf 3 [Arabidopsis thaliana] Schistosoma intercalatum ribosomal intergenic spacer DNA (2169 bp)
2052	GM_68_A2_F03_MR	g170080	BLASTN	291	2e-14	96	Soybean seed lectin gene transposable element tgml.
2053	GM_68_A2_F09_MR	g3845197	BLASTN	536	3e-17	66	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
2054	GM_68_A2_F10_MR	g421955	BLASTX	314	2e-27	50	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387)
2055	GM_68_A2_G05_MR	g2129618	BLASTX	223	2e-16	42	ORF4 [Solanum tuberosum] hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2056	GM_68_A2_H09_MR	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2057	GM_68_B1_A02_T7	g4063760	BLASTX	402	2e-35	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2058	GM_68_B1_A03_T7	g2827516	BLASTX	518	7e-48	67	(AL021633) DNA topoisomerase like- protein [Arabidopsis thaliana]
2059	GM_68_B1_A07_T7	g2367418	BLASTX	191	2e-13	57	(AF000392) peptide transporter [Lotus japonicus]
2060	GM_68_B1_A09_T7	g18559	BLASTN	623	3e-21	69	G.max gene for catalase
2061	GM_68_B1_B05_T7	g3097320	BLASTN	463	6e-14	73	Glycine max gene for Bd 30K, complete cds
2062	GM_68_B1_B06_T7	g3777527	BLASTX	375	2e-32	93	(AF053008) gag-pol polyprotein [Glycine max]
2063	GM_68_B1_B09_T7	g507910	BLASTN	412	5e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2064	GM_68_B1_C08_T7	g507910	BLASTN	651	8e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
2065	GM_68_B1_C09_T7	g395293	BLASTN	393	9e-11	62	T.repens pseudogene for alcohol dehydrogenase
2066	GM_68_B1_E09_T7	g629693	BLASTX	200	9e-15	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
2067	GM_68_B1_E11_T7	g3319362	BLASTX	262	1e-20	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
2068	GM_68_B1_F02_T7	g18559	BLASTN	356	4e-09	65	G.max gene for catalase
2069	GM_68_B1_F05_T7	g2498731	BLASTX	168	2e-11	55	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 gi 1362013 pir S57611 zeta-crystallin homolog - Arabidopsis thaliana gi 886428 (Z49768) zeta-crystallin homologue [Arabidopsis thaliana] (U30382) expansin S1 precursor [Cucumis sativus]
2070	GM_68_B1_F06_T7	g1040875	BLASTX	524	1e-49	84	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2071	GM_68_B1_F10_T7	g114532	BLASTX	287	5e-24	65	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (V00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence Glycine max BSR-101 satellite SB92 genomic sequence (AL021633) DNA topoisomerase like- protein [Arabidopsis thaliana] (U22103) gag-protease polyprotein [Glycine max] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
2072	GM_68_B1_G01_T7	g3142328	BLASTN	484	6e-15	96	P.sativum GR gene Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. (U55803) disease resistance protein homolog [Glycine max] RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster] Glycine max gene for Bd 30K, complete cds Glycine max clathrin heavy chain mRNA, complete cds (AC005315) putative reverse transcriptase [Arabidopsis thaliana] (AC005561) putative POL3 protein [Arabidopsis thaliana] Soybean nodulin 22 gene Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana] (U68408) 5' end not determined experimentally [Zea mays] (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
2073	GM_68_B1_G03_T7	g507910	BLASTN	593	3e-20	83	
2074	GM_68_B1_H11_T7	g2827516	BLASTX	121	3e-09	43	
2075	GM_68_B2_A03_T7	g905361	BLASTX	413	1e-37	91	
2076	GM_68_B2_A10_MR	g3142328	BLASTN	1755	9e-73	95	
2077	GM_68_B2_B05_T7	g99726	BLASTX	121	2e-11	47	
2078	GM_68_B2_B10_T7	g975703	BLASTN	569	1e-18	71	
2079	GM_68_B2_C01_MR	g507910	BLASTN	381	1e-10	73	
2080	GM_68_B2_C02_MR	g507910	BLASTN	397	3e-11	74	
2081	GM_68_B2_C02_T7	g507910	BLASTN	377	2e-10	73	
2082	GM_68_B2_C06_T7	g1663537	BLASTX	339	4e-30	71	
2083	GM_68_B2_C07_MR	g130405	BLASTX	224	2e-16	39	
2084	GM_68_B2_C12_MR	g3097320	BLASTN	699	1e-24	83	
2085	GM_68_B2_D07_MR	g1335861	BLASTN	562	2e-18	85	
2086	GM_68_B2_E01_T7	g3461840	BLASTX	222	4e-16	39	
2087	GM_68_B2_E07_MR	g4063760	BLASTX	183	7e-14	53	
2088	GM_68_B2_E08_MR	g18695	BLASTN	494	2e-15	76	
2089	GM_68_B2_E10_MR	g4063756	BLASTN	456	1e-13	62	
2090	GM_68_B2_F12_T7	g3645899	BLASTX	304	5e-25	59	
2091	GM_68_B2_F06_MR	g3319362	BLASTX	251	2e-19	45	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2092	GM_68_B2_G02_T7	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2093	GM_68_B2_G05_T7	g18559	BLASTN	1166	7e-46	87	Gmax gene for catalase
2094	GM_68_B2_G08_MR	g3777527	BLASTX	200	9e-14	34	(AF053008) gag-pol polypeptide [Glycine max]
2095	GM_68_B2_G12_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2096	GM_68_B2_G12_T7	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2097	GM_68_B2_H04_MR	g3132472	BLASTX	163	4e-10	34	(AC003096) unknown protein [Arabidopsis thaliana]
2098	GM_68_B2_H05_MR	g3097320	BLASTN	463	6e-14	71	Glycine max gene for Bd 30K, complete cds
2099	GM_68_B2_H05_T7	g18695	BLASTN	568	6e-19	79	Soybean nodulin 22 gene
2100	GM_68_B2_H10_MR	g2498732	BLASTX	271	7e-23	80	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2 gi 1362014 pir S57612 zeta-crystallin homolog - Arabidopsis thaliana gi 886430 (Z49268) zeta-crystallin homolog [Arabidopsis thaliana]
2101	GM_69_A1_A02_T7	g505129	BLASTN	417	7e-12	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
2102	GM_69_A1_A05_T7	g101042	BLASTX	178	1e-11	31	hypothetical protein Tfl - fission yeast (Schizosaccharomyces pombe) gi 173477 (M38526) Tfl protein [Schizosaccharomyces pombe]
2103	GM_69_A1_A08_T7	g507910	BLASTN	478	5e-15	81	Glycine max BSR-101 satellite SB92 genomic sequence.
2104	GM_69_A1_A12_T7	g3426334	BLASTN	378	4e-10	65	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
2105	GM_69_A1_B02_T7	g2052034	BLASTN	349	1e-08	62	Human DNA sequence from PAC 450C20 on chromosome X
2106	GM_69_A1_B09_T7	g1769898	BLASTX	380	7e-34	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2107	GM_69_A1_B11_T7	g99755	BLASTX	417	3e-38	55	RNA-directed DNA polymerase (EC 2.7.49) - Arabidopsis thaliana retrotransposon Tal-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
2108	GM_69_A1_C01_T7	g1172441	BLASTX	363	1e-32	56	POSSIBLE TRANSCRIPTION FACTOR POSF21 gi 99685 pir S21883 DNA-binding protein POSF21 - Arabidopsis thaliana gi 16429 (X61031) posF21 gene product [Arabidopsis thaliana] (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
2109	GM_69_A1_D04_T7	g3522943	BLASTX	166	3e-10	68	Glycine max BSR-101 satellite SB92 genomic sequence.
2110	GM_69_A1_D06_T7	g507910	BLASTN	444	2e-13	77	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
2111	GM_69_A1_E02_T7	g1167523	BLASTX	232	4e-34	50	Glycine max BSR-101 satellite SB92 genomic sequence.
2112	GM_69_A1_F04_T7	g507910	BLASTN	382	1e-10	71	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
2113	GM_69_A1_E06_T7	g2764526	BLASTN	448	3e-13	65	(Y13368) reverse transcriptase [Beta vulgaris]
2114	GM_69_A1_E10_T7	g2462134	BLASTX	189	3e-13	34	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana]
2115	GM_69_A1_F10_T7	g3142303	BLASTX	472	8e-43	66	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]
2116	GM_69_A1_G02_T7	g2739359	BLASTN	436	1e-12	67	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
2117	GM_69_A1_G04_T7	g3142328	BLASTN	1090	2e-42	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2118	GM_69_A1_H04_T7	g629693	BLASTX	381	2e-34	55	probable integrase - common tobacco (fragment) gi 530742
2119	GM_69_A1_H10_T7	g2129618	BLASTX	229	4e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila (X80830) integrase [Nicotiana tabacum]
2120	GM_69_B1_A01_MR	g3097320	BLASTN	889	3e-33	80	gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2121	GM_69_B1_B02_MR	g507910	BLASTN	372	3e-10	71	Glycine max gene for Bd 30K, complete cds
2122	GM_69_B1_B02_T7	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2123	GM_69_B1_B08_MR	g3777527	BLASTX	187	3e-13	41	Glycine max BSR-101 satellite SB92 genomic sequence.
2124	GM_69_B1_B10_T7	g1142702	BLASTN	448	9e-14	73	(AF053008) gag-pol polyprotein [Glycine max]
2125	GM_69_B1_B11_MR	g507910	BLASTN	391	5e-11	72	Glycine max satellite STR120-A.4.
2126	GM_69_B1_C09_MR	g1872521	BLASTX	155	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2127	GM_69_B1_D01_MR	g1769898	BLASTX	472	4e-44	60	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] gi 1872523
2128	GM_69_B1_D02_MR	g3097320	BLASTN	875	1e-32	76	(U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]
2129	GM_69_B1_D06_MR	g2894591	BLASTN	400	5e-11	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2130	GM_69_B1_D07_T7	g905361	BLASTX	358	4e-36	94	Glycine max gene for Bd 30K, complete cds
2131	GM_69_B1_D11_MR	g3786011	BLASTX	129	6e-10	61	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAll project).
2132	GM_69_B1_E01_MR	g3080400	BLASTX	418	2e-38	89	(U22103) gag-protease polyprotein [Glycine max]
2133	GM_69_B1_E02_MR	g1945277	BLASTX	153	2e-09	72	(AC005499) putative elongation factor [Arabidopsis thaliana]
2134	GM_69_B1_E04_MR	g507910	BLASTN	711	2e-25	87	(AL022603) putative protein [Arabidopsis thaliana]
2135	GM_69_B1_H08_T7	g3097320	BLASTN	709	5e-25	83	(Z94180) branched chain alpha-keto acid dehydrogenase E1-alpha subunit [Lycopersicon esculentum]
2136	GM_70_A1_A07_T7	g1142701	BLASTN	251	5e-19	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2137	GM_70_A1_A08_MR	g1518540	BLASTX	686	8e-67	95	Glycine max gene for Bd 30K, complete cds
2138	GM_70_A1_A11_T7	g3367585	BLASTX	151	2e-09	35	Glycine max satellite STR120-A.3.
2139	GM_70_A1_B04_MR	g2191187	BLASTX	289	5e-28	59	(U53418) UDP-glucose dehydrogenase [Glycine max]
2140	GM_70_A1_B07_T7	g4063770	BLASTX	220	3e-16	40	(AL031135) putative polygalacturonase [Arabidopsis thaliana]
2141	GM_70_A1_B10_MR	g3645899	BLASTX	246	9e-33	57	(AF007271) contains similarity to a DNAI-like domain [Arabidopsis thaliana]
2142	GM_70_A1_B11_MR	g2522230	BLASTX	292	5e-25	39	(AB004906) transposase [Ipomoea purpurea]
2143	GM_70_A1_C03_T7	g2129618	BLASTX	220	4e-16	35	(U68408) 5' end not determined experimentally [Zea mays]
2144	GM_70_A1_C04_T7	g1167523	BLASTX	286	3e-25	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
2145	GM_70_A1_C11_MR	g2764526	BLASTN	634	1e-21	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
2146	GM_70_A1_D02_T7	g1769897	BLASTX	189	6e-16	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2147	GM_70_A1_D04_T7	g3142328	BLASTN	1880	2e-78	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2148	GM_70_A1_D07_T7	g585416	BLASTX	122	9e-14	82	LIPOXYGENASE gi 467565 (X71344) lipoxigenase [Lens culinaris]
2149	GM_70_A1_D12_MR	g507910	BLASTN	575	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2150	GM_70_A1_D12_T7	g507910	BLASTN	520	7e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2151	GM_70_A1_E05_MR	g3097320	BLASTN	1229	1e-48	82	Glycine max gene for Bd 30K, complete cds
2152	GM_70_A1_E08_T7	g507910	BLASTN	340	9e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
2153	GM_70_A1_F02_MR	g3845336	BLASTN	362	3e-09	61	Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence
2154	GM_70_A1_F03_MR	g1666236	BLASTX	197	1e-14	29	(U76261) unknown [Hordeum vulgare]
2155	GM_70_A1_F06_MR	g1663549	BLASTX	464	3e-43	78	(U55809) disease resistance protein homolog [Glycine max]
2156	GM_70_A1_F07_MR	g507910	BLASTN	568	5e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2157	GM_70_A1_F09_MR	g507910	BLASTN	480	4e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
2158	GM_70_A1_F09_T7	g4092471	BLASTN	446	4e-13	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
2159	GM_70_A1_F10_MR	g1666236	BLASTX	215	9e-17	29	(U76261) unknown [Hordeum vulgare]
2160	GM_70_A1_F10_T7	g18559	BLASTN	953	3e-36	73	G.max gene for catalase
2161	GM_70_A1_F11_MR	g3810596	BLASTX	224	1e-23	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2162	GM_70_A1_G01_MR	g2244976	BLASTX	177	4e-16	65	(Z97340) hypothetical protein [Arabidopsis thaliana]
2163	GM_70_A1_G02_T7	g2323254	BLASTN	422	5e-12	64	Human Chromosome X, complete sequence [Homo sapiens]
2164	GM_70_A1_G07_MR	g2462058	BLASTX	196	3e-17	55	(Y13389) reverse transcriptase [Antirrhinum majus]
2165	GM_70_A1_G07_T7	g3930515	BLASTX	121	2e-12	47	(AF059674) putative gag protein [Nicotiana tabacum]
2166	GM_70_A1_G11_T7	g4063760	BLASTX	456	4e-41	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2167	GM_70_A1_H01_T7	g3859610	BLASTN	552	6e-18	63	Arabidopsis thaliana BAC T9E19
2168	GM_70_A1_H09_T7	g4038056	BLASTX	199	5e-17	44	(AC005897) putative transposon [Arabidopsis thaliana]
2169	GM_70_A1_H11_MR	g3319362	BLASTX	290	1e-23	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
2170	GM_70_A2_A02_MR	g4115383	BLASTX	204	1e-14	55	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]
2171	GM_70_A2_A03_MR	g1666236	BLASTX	193	3e-14	31	(U76261) unknown [Hordeum vulgare]
2172	GM_70_A2_A03_T7	g343537	BLASTN	389	1e-10	63	T. brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.
2173	GM_70_A2_A07_T7	g507910	BLASTN	426	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2174	GM_70_A2_A08_MR	g3241916	BLASTN	375	7e-10	61	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]
2175	GM_70_A2_A09_T7	g4038056	BLASTX	292	6e-27	43	(AC005897) putative transposon [Arabidopsis thaliana]
2176	GM_70_A2_B02_MR	g4063760	BLASTX	199	7e-15	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2177	GM_70_A2_B04_T7	g4038029	BLASTN	394	9e-11	59	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]
2178	GM_70_A2_B05_MR	g1771162	BLASTX	494	6e-46	60	(X98930) SBT2 [Lycopersicon esculentum] gi 3687307 gnl PID e1299612 (AJ006379) subtilisin-like protease [Lycopersicon esculentum]
2179	GM_70_A2_B05_T7	g18559	BLASTN	737	2e-26	74	G.max gene for catalase
2180	GM_70_A2_B08_MR	g18559	BLASTN	800	3e-29	74	G.max gene for catalase
2181	GM_70_A2_B08_T7	g18559	BLASTN	417	7e-12	66	G.max gene for catalase
2182	GM_70_A2_B10_T7	g3738232	BLASTX	167	3e-11	50	(AB007791) DREB2B [Arabidopsis thaliana]
2183	GM_70_A2_B12_MR	g1171591	BLASTN	313	4e-10	61	P.falciiparum complete gene map of plastid-like DNA (IR-B)
2184	GM_70_A2_C01_T7	g687867	BLASTN	370	1e-09	60	Caenorhabditis elegans cosmid C45G9
2185	GM_70_A2_C04_T7	g2160155	BLASTN	351	8e-09	65	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
2186	GM_70_A2_C09_MR	g3810596	BLASTX	176	1e-23	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2187	GM_70_A2_C09_T7	g3510505	BLASTX	380	5e-33	44	(AF030881) pol polyprotein [Fugu rubripes]
2188	GM_70_A2_C11_T7	g4038056	BLASTX	152	1e-10	59	(AC005897) putative transposon [Arabidopsis thaliana]
2189	GM_70_A2_D01_MR	g4038056	BLASTX	308	1e-25	41	(AC005897) putative transposon [Arabidopsis thaliana]
2190	GM_70_A2_D02_T7	g2443320	BLASTX	320	1e-27	42	(D85597) polyprotein [Oryza australiensis]
2191	GM_70_A2_D04_MR	g4038056	BLASTX	417	3e-37	54	(AC005897) putative transposon [Arabidopsis thaliana]
2192	GM_70_A2_D08_MR	g3845197	BLASTN	360	3e-09	59	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
2193	GM_70_A2_D08_T7	g18559	BLASTN	488	4e-15	75	G.max gene for catalase
2194	GM_70_A2_D10_MR	g2827658	BLASTX	341	3e-30	60	(AL021637) putative protein [Arabidopsis thaliana]
2195	GM_70_A2_E02_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2196	GM_70_A2_E04_MR	g3142328	BLASTN	1415	3e-57	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
2197	GM_70_A2_E05_MR	g4115365	BLASTX	170	8e-12	53	Myrmecia pilosula H187-135 mitochondrion cytochrome b gene, partial cds.
2198	GM_70_A2_E06_MR	g576758	BLASTN	244	1e-08	64	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387)
2199	GM_70_A2_E06_T7	g421955	BLASTX	190	1e-13	42	ORF4 [Solanum tuberosum]
2200	GM_70_A2_E07_T7	g421955	BLASTX	368	9e-37	51	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2201	GM_70_A2_E08_MR	g130398	BLASTX	175	8e-17	48	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON 297) gi 85089 pir B24872 retrovirus-related polypeptide homolog - fruit fly (Drosophila melanogaster) transposon 297
2202	GM_70_A2_E10_MR	g2129677	BLASTX	512	2e-48	68	probable N-acetyltransferase hookless 1 - Arabidopsis thaliana gi 1277090 (U50399) putative N-acetyltransferase hookless 1 [Arabidopsis thaliana] gi 1277092 (U50400) putative N-acetyltransferase hookless 1 [Arabidopsis thaliana]
2203	GM_70_A2_E10_T7	g467843	BLASTN	367	1e-09	60	Prototheca wickerhamii 263-11 complete mitochondrial DNA.
2204	GM_70_A2_E12_MR	g507910	BLASTN	443	2e-13	79	Glycine max BSR-101 satellite SB92 genomic sequence.
2205	GM_70_A2_F02_T7	g2829888	BLASTX	284	1e-28	54	(AC002396) Hypothetical protein [Arabidopsis thaliana]
2206	GM_70_A2_F04_MR	g4159708	BLASTN	425	4e-12	66	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence [Arabidopsis thaliana]
2207	GM_70_A2_F04_T7	g3985934	BLASTN	432	2e-12	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJF7, complete sequence [Arabidopsis thaliana]
2208	GM_70_A2_F08_MR	g3779021	BLASTX	161	1e-09	42	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
2209	GM_70_A2_F11_MR	g2739309	BLASTX	128	5e-09	58	(Y15990) P-glycoprotein-like protein [Arabidopsis thaliana]
2210	GM_70_A2_F12_T7	g840618	BLASTN	566	5e-19	61	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
2211	GM_70_A2_G02_MR	g3426334	BLASTN	540	2e-17	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
2212	GM_70_A2_G03_MR	g3777527	BLASTX	326	3e-40	53	(AF053008) gag-pol polypeptide [Glycine max]
2213	GM_70_A2_G06_MR	g4063760	BLASTX	125	2e-09	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2214	GM_70_A2_G08_MR	g3142328	BLASTN	2044	4e-86	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U68408) 5' end not determined experimentally [Zea mays]
2215	GM_70_A2_G09_T7	g3645899	BLASTX	294	6e-24	55	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2216	GM_70_A2_G11_MR	g3810596	BLASTX	317	2e-26	47	Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, complete sequence [Homo sapiens]
2217	GM_70_A2_H02_MR	g3021697	BLASTN	362	2e-10	60	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence [Plasmodium falciparum]
2218	GM_70_A2_H04_MR	g2982576	BLASTN	437	1e-12	58	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
2219	GM_70_A2_H04_T7	g4115536	BLASTX	144	6e-09	42	G.max chloroplast DNA for tRNA (Arg)
2220	GM_70_A2_H06_MR	g11575	BLASTN	1398	7e-57	98	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2221	GM_70_A2_H06_T7	g128771	BLASTX	220	9e-18	82	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5. CHLOROPLAST gi 100110 pir S08494 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - fava bean chloroplast gi 11555 (X14804) ndhF gene product (AA 1-746) [Vicia faba] gi 12390 (X51471) NADH dehydrogenase [Vicia faba] gi 552971 (M36832) NADH dehydrogenase (ndhF) [Vicia faba] (AB019518) cyclophilin [Trichophyton mentagrophytes] C.parapsilosis mitochondrial DNA for right telomeric region and ATP6 gene Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum] IAA8 protein - Arabidopsis thaliana gi 972919 (U18410) IAA8 [Arabidopsis thaliana] hypothetical protein - garden snapdragon (AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba] (AC002409) putative protein phosphatase 2C [Arabidopsis thaliana] G.max gene for catalase (AF077409) similar to reverse transcriptases (PFam: rvt hmm. score: 60.13) [Arabidopsis thaliana] hypothetical protein - garden snapdragon (AF080118) contains similarity to reverse transcriptases (PFam: rvt.hmm. score: 11.19) [Arabidopsis thaliana] (AB004906) transposase [Ipomoea purpurea] G.max gene for catalase hypothetical protein - garden snapdragon Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence Arabidopsis thaliana DNA chromosome 4, ESSA 1 contig fragment No. 8 NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4. CHLOROPLAST Glycine max gene for Bd 30K, complete cds (Y08010) lectin receptor kinase [Arabidopsis thaliana] retrotransposon del-46 [Lilium henryi] (AC005561) putative POL3 protein [Arabidopsis thaliana] (U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
2222	GM_70_A2_H07_MR	g3869176	BLASTX	216	4e-22	80	
2223	GM_70_A2_H07_T7	g479124	BLASTN	369	8e-10	62	
2224	GM_70_A2_H09_MR	g3758836	BLASTN	412	1e-11	60	
2225	GM_70_A2_H10_MR	g1363488	BLASTX	226	5e-18	66	
2226	GM_70_A2_H12_MR	g100484	BLASTX	321	3e-27	41	
2227	GM_70_B1_A02_MR	g2522227	BLASTX	215	7e-17	53	
2228	GM_70_B1_A02_T7	g2623300	BLASTX	170	2e-11	60	
2229	GM_70_B1_A03_MR	g18559	BLASTN	1014	6e-39	74	
2230	GM_70_B1_A04_MR	g3319372	BLASTX	192	5e-13	34	
2231	GM_70_B1_A06_MR	g100484	BLASTX	290	8e-24	55	
2232	GM_70_B1_A09_MR	g3513747	BLASTX	353	5e-30	51	
2233	GM_70_B1_A10_MR	g4063770	BLASTX	161	6e-10	45	
2234	GM_70_B1_B02_MR	g18559	BLASTN	1041	3e-40	75	
2235	GM_70_B1_B04_MR	g100484	BLASTX	260	1e-20	57	
2236	GM_70_B1_B04_T7	g3142328	BLASTN	1754	1e-72	93	
2237	GM_70_B1_B06_MR	g2245073	BLASTN	359	3e-09	64	
2238	GM_70_B1_B09_MR	g2506938	BLASTX	149	9e-14	64	
2239	GM_70_B1_C01_MR	g3097320	BLASTN	1236	6e-49	78	
2240	GM_70_B1_C03_T7	g1769898	BLASTX	402	5e-43	55	
2241	GM_70_B1_C06_T7	g226407	BLASTX	448	3e-40	63	
2242	GM_70_B1_C08_T7	g4063760	BLASTX	179	2e-19	56	
2243	GM_70_B1_D01_T7	g531389	BLASTX	190	7e-24	43	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2244	GM_70_B1_D02_MR	g2811096	BLASTN	354	6e-09	63	Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence [Homo sapiens]
2245	GM_70_B1_D02_T7	g13767	BLASTN	404	4e-12	68	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
2246	GM_70_B1_D03_MR	g3676069	BLASTX	192	8e-14	71	(Y17899) ERG protein [Antirrhinum majus]
2247	GM_70_B1_D07_MR	g3924609	BLASTX	245	1e-18	48	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
2248	GM_70_B1_D07_T7	g3935164	BLASTX	218	1e-16	47	(AC004557) F17L21.7 [Arabidopsis thaliana]
2249	GM_70_B1_D09_MR	g2642431	BLASTX	374	3e-32	52	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
2250	GM_70_B1_D09_T7	g2443320	BLASTX	252	1e-30	49	(D85597) polyprotein [Oryza australiensis]
2251	GM_70_B1_E01_T7	g3777527	BLASTX	656	2e-62	94	(AF053008) gag-pol polyprotein [Glycine max]
2252	GM_70_B1_E03_MR	g3097320	BLASTN	894	2e-33	77	Glycine max gene for Bd 30K, complete cds
2253	GM_70_B1_E05_T7	g2660675	BLASTX	200	3e-14	83	T19K24.15; similar to DNA-damage-inducible protein P
2254	GM_70_B1_E10_T7	g905361	BLASTX	417	6e-38	92	(U22103) gag-protease polyprotein [Glycine max]
2255	GM_70_B1_F04_MR	g3097320	BLASTN	435	1e-12	74	Glycine max gene for Bd 30K, complete cds
2256	GM_70_B1_F06_MR	g4063760	BLASTX	168	3e-14	40	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
2257	GM_70_B1_F06_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2258	GM_70_B1_F11_T7	g2982431	BLASTX	325	3e-27	49	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
2259	GM_70_B1_G01_MR	g225268	BLASTX	242	9e-20	88	NADH dehydrogenase 2-like ORF 180 [Nicotiana tabacum]
2260	GM_70_B1_G02_MR	g2760836	BLASTX	175	1e-11	73	(AC003105) putative Ser/Thr protein kinase [Arabidopsis thaliana]
2261	GM_70_B1_G02_T7	g4150930	BLASTN	558	4e-18	66	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
2262	GM_70_B1_G04_MR	g2769655	BLASTN	357	4e-09	62	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High affinity Sodium-Glucose Cotransporter). Contain...
2263	GM_70_B1_G06_MR	g3171875	BLASTN	357	4e-09	62	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylamine Monooxygenase (N-Oxide 3, EC1.14.1... (AC005561) putative POL.3 protein [Arabidopsis thaliana]
2264	GM_70_B1_G07_MR	g4063760	BLASTX	238	4e-23	48	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
2265	GM_70_B1_G09_MR	g170606	BLASTN	718	6e-26	67	ORF 1708 [Nicotiana tabacum]
2266	GM_70_B1_H01_T7	g225242	BLASTX	251	1e-26	76	Soybean seed lectin gene transposable element tgm1.
2267	GM_70_B1_H02_T7	g170080	BLASTN	360	3e-09	78	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2268	GM_70_B1_H03_MR	g1769897	BLASTX	154	2e-09	29	

Seq No.	ClonellD	NCBI gi	Method	Score	P-value	%Ident	Description
2269	GM_70_B1_H09_MR	g2160128	BLASTN	495	2e-15	69	Genomic sequence from Human 17, complete sequence [Homo sapiens]
2270	GM_70_B2_A11_MR	g507910	BLASTN	498	7e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
2271	GM_70_B2_A12_MR	g2832901	BLASTN	1142	2e-50	76	Cajanus cajan copia-like retrotransposon.Panzee
2272	GM_70_B2_B03_MR	g2462134	BLASTX	156	1e-09	31	(Y13368) reverse transcriptase [Beta vulgaris]
2273	GM_70_B2_B04_MR	g507910	BLASTN	454	7e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2274	GM_70_B2_B04_T7	g507910	BLASTN	382	1e-10	76	Glycine max BSR-101 satellite SB92 genomic sequence.
2275	GM_70_B2_B06_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2276	GM_70_B2_B06_T7	g507910	BLASTN	398	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2277	GM_70_B2_C02_MR	g1769898	BLASTX	227	3e-17	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2278	GM_70_B2_C11_T7	g3096949	BLASTX	193	2e-13	53	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]
2279	GM_70_B2_C12_MR	g3142328	BLASTN	542	2e-17	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB007466) reverse transcriptase-like protein [Vicia faba]
2280	GM_70_B2_D03_T7	g2522228	BLASTX	236	1e-18	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2281	GM_70_B2_D06_T7	g4063760	BLASTX	303	7e-25	53	Glycine max BSR-101 satellite SB92 genomic sequence.
2282	GM_70_B2_D08_T7	g507910	BLASTN	410	6e-12	74	Glycine max cv. Dare nodulin 26 gene fragment.
2283	GM_70_B2_D11_MR	g170029	BLASTN	352	7e-09	77	(AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
2284	GM_70_B2_D11_T7	g3513745	BLASTX	161	1e-09	43	Glycine max BSR-101 satellite SB92 genomic sequence.
2285	GM_70_B2_E01_MR	g507910	BLASTN	599	2e-20	82	(AC003033) putative cellulase [Arabidopsis thaliana]
2286	GM_70_B2_E04_MR	g2702268	BLASTX	157	1e-17	69	Glycine max BSR-101 satellite SB92 genomic sequence.
2287	GM_70_B2_E06_T7	g507910	BLASTN	380	1e-10	72	(AC002291) Unknown protein [Arabidopsis thaliana]
2288	GM_70_B2_E07_T7	g2829911	BLASTX	203	3e-15	74	Glycine max gene for Bd 30K, complete cds
2289	GM_70_B2_E10_T7	g3097320	BLASTN	452	2e-13	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2290	GM_70_B2_E11_MR	g4063760	BLASTX	209	8e-15	40	Homo sapiens DNA sequence from PAC 3E5 on chromosome 20q12-13.12. Contains protein tyrosine phosphatase (RPTP-rho) EST, STS, GSS, complete sequence [Homo sapiens]
2291	GM_70_B2_F01_MR	g3297863	BLASTN	426	3e-12	62	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
2292	GM_70_B2_F02_T7	g2194136	BLASTX	210	6e-18	60	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]
2293	GM_70_B2_F03_MR	g2264313	BLASTN	419	7e-12	64	Homo sapiens 8q21.3 Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
2294	GM_70_B2_F04_MR	g4126312	BLASTN	366	2e-09	61	G-max gene for catalase
2295	GM_70_B2_F07_T7	g18559	BLASTN	819	4e-30	76	paramecium species 1.168 mt dna dimer: replication init. region.
2296	GM_70_B2_F09_MR	g342952	BLASTN	344	2e-09	62	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2297	GM_70_B2_G07_MR	g4140398	BLASTX	169	6e-12	45	(AF081794) sterol-C5(6)-desaturase [Nicotiana tabacum]
2298	GM_70_B2_G08_T7	g2564750	BLASTN	404	3e-11	60	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tryptinogen gene families
2299	GM_70_B2_G09_MR	g2522227	BLASTX	220	2e-17	56	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2300	GM_70_B2_H07_MR	g130582	BLASTX	245	1e-18	38	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2301	GM_70_B2_H09_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2302	GM_70_B2_H10_MR	g3810596	BLASTX	232	2e-17	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2303	GM_71_A1_A04_MR	g343946	BLASTN	382	4e-11	60	Yeast (S.cerevisiae) mitochondrial var1 gene, 3' flank.
2304	GM_71_A1_A05_T7	g507910	BLASTN	540	8e-18	83	Glycine max BSR-101 satellite SB92 genomic sequence.
2305	GM_71_A1_A09_MR	g3777527	BLASTX	156	2e-14	50	(AF053008) gag-pol polypeptide [Glycine max]
2306	GM_71_A1_A10_MR	g4063760	BLASTX	500	6e-46	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2307	GM_71_A1_A10_T7	g130582	BLASTX	241	2e-24	40	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2308	GM_71_A1_B04_T7	g18559	BLASTN	438	8e-13	79	G.max gene for catalase
2309	GM_71_A1_B06_MR	g3738114	BLASTN	430	2e-12	62	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
2310	GM_71_A1_B06_T7	g2880057	BLASTX	338	1e-28	50	(AC002340) putative RNA helicase A, 5' partial [Arabidopsis thaliana]
2311	GM_71_A1_B08_T7	g18559	BLASTN	857	8e-32	85	G.max gene for catalase
2312	GM_71_A1_B09_MR	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2313	GM_71_A1_B09_T7	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2314	GM_71_A1_B12_MR	g2367675	BLASTX	172	4e-14	51	(AF017040) Pol [Dictyostelium discoideum]
2315	GM_71_A1_C02_MR	g507910	BLASTN	467	2e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2316	GM_71_A1_C02_T7	g4063760	BLASTX	263	1e-20	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2317	GM_71_A1_C05_MR	g2213608	BLASTX	188	1e-12	34	(AC000103) F2I19.2 [Arabidopsis thaliana]
2318	GM_71_A1_C07_MR	g3142379	BLASTX	266	6e-22	63	(AF053008) envelope-like [Glycine max]
2319	GM_71_A1_C08_MR	g1705929	BLASTX	221	1e-17	53	ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1 (ENDOPEPTIDASE CLP 1) gi 755165 (U16135) ClpP [Synechococcus sp.]
2320	GM_71_A1_C08_T7	g3810596	BLASTX	232	2e-17	34	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2321	GM_71_A1_C09_MR	g170080	BLASTN	380	3e-10	70	Soybean seed lectin gene transposable element tgm1.
2322	GM_71_A1_D03_MR	g3645899	BLASTX	180	2e-17	52	(U68408) 5' end not determined experimentally [Zea mays]
2323	GM_71_A1_D03_T7	g3097320	BLASTN	358	4e-09	64	Glycine max gene for Bd 30K. complete cds
2324	GM_71_A1_E01_MR	g1431738	BLASTN	389	1e-10	89	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
2325	GM_71_A1_E02_T7	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
2326	GM_71_A1_E03_MR	g20861	BLASTN	366	1e-09	68	P.sativum retrotransposon
2327	GM_71_A1_E04_MR	g2160189	BLASTX	218	6e-16	37	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475.gb ATTS4362 come from this gene. [Arabidopsis thaliana]
2328	GM_71_A1_E05_T7	g3319362	BLASTX	155	3e-09	31	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm. score 19.29) [Arabidopsis thaliana]
2329	GM_71_A1_E06_MR	g09922	BLASTX	209	4e-16	52	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
2330	GM_71_A1_E06_T7	g13584	BLASTN	382	1e-10	63	Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I
2331	GM_71_A1_E07_MR	g2522228	BLASTX	383	1e-34	56	(AB007466) reverse transcriptase-like protein [Vicia faba]
2332	GM_71_A1_E11_MR	g3142328	BLASTN	654	1e-22	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds. and long terminal repeat. complete sequence
2333	GM_71_A1_F05_MR	g18559	BLASTN	1094	1e-42	75	G.max gene for catalase
2334	GM_71_A1_F09_MR	g3777527	BLASTX	198	6e-14	46	(AF053008) gag-pol polyprotein [Glycine max]
2335	GM_71_A1_G03_T7	g905361	BLASTX	190	3e-13	29	(U22103) gag-protease polyprotein [Glycine max]
2336	GM_71_A1_G04_MR	g3241926	BLASTN	363	2e-09	60	Arabidopsis thaliana genomic DNA, chromosome 5. P1 clone: MSG15, complete sequence [Arabidopsis thaliana]
2337	GM_71_A1_G09_T7	g507910	BLASTN	532	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
2338	GM_71_A1_G11_T7	g3695395	BLASTX	245	4e-19	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
2339	GM_71_A1_H01_T7	g18767	BLASTN	334	9e-09	68	Soybean Tgm6 transposable element 5' end
2340	GM_71_A1_H03_MR	g3097320	BLASTN	1158	2e-45	80	Glycine max gene for Bd 30K. complete cds
2341	GM_71_A1_H05_T7	g3763929	BLASTX	198	4e-14	61	(AC004450) hypothetical protein [Arabidopsis thaliana]
2342	GM_71_A1_H07_T7	g639722	BLASTX	504	2e-47	78	(L27484) calcium-dependent protein kinase [Zea mays]
2343	GM_71_A1_H09_T7	g3860277	BLASTX	139	8e-09	77	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana]
2344	GM_71_A1_H10_T7	g4063760	BLASTX	513	3e-47	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2345	GM_71_A1_H11_T7	g507910	BLASTN	543	6e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2346	GM_71_A2_A02_MR	g2792220	BLASTX	323	1e-30	50	(AF032688) NBS-LRR type resistance protein [Oryza sativa]
2347	GM_71_A2_A11_MR	g905361	BLASTX	432	1e-39	97	(U22103) gag-protease polyprotein [Glycine max]
2348	GM_71_A2_A12_MR	g629693	BLASTX	270	1e-22	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
2349	GM_71_A2_B04_MR	g3377834	BLASTX	170	5e-11	29	(AF075598) No definition line found [Arabidopsis thaliana]
2350	GM_71_A2_B06_MR	g4049609	BLASTN	465	6e-14	59	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
2351	GM_71_A2_C01_MR	g1142701	BLASTN	1332	7e-54	88	Glycine max satellite STR120-A.3.
2352	GM_71_A2_C02_MR	g522302	BLASTX	144	1e-21	55	(L35053) endonuclease [Magnaporthe grisea]
2353	GM_71_A2_C03_MR	g1147568	BLASTN	386	2e-10	64	H.sapiens genes for semenogelin I and semenogelin II
2354	GM_71_A2_C05_MR	g3152594	BLASTX	232	8e-18	43	(AC002986) Contains repeats similar to RECA protein gb L26100 from Acinetobacter calcoaceticus. [Arabidopsis thaliana]
2355	GM_71_A2_C07_MR	g507910	BLASTN	598	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2356	GM_71_A2_C10_MR	g3152594	BLASTX	133	5e-12	46	(AC002986) Contains repeats similar to RECA protein gb L26100 from Acinetobacter calcoaceticus. [Arabidopsis thaliana]
2357	GM_71_A2_C11_MR	g2522230	BLASTX	183	2e-13	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
2358	GM_71_A2_D01_MR	g3283026	BLASTX	193	2e-13	40	putative transposase [Arabidopsis thaliana]
2359	GM_71_A2_D04_MR	g090922	BLASTX	906	1e-99	93	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:L50225 [Glycine max]
2360	GM_71_A2_D06_MR	g4049332	BLASTN	502	1e-15	63	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)
2361	GM_71_A2_D09_MR	g3785977	BLASTX	213	2e-17	40	(AC005360) putative growth regulator protein [Arabidopsis thaliana]
2362	GM_71_A2_D12_MR	g2098713	BLASTX	355	1e-31	72	(U82977) pectinesterase [Citrus sinensis]
2363	GM_71_A2_E06_MR	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
2364	GM_71_A2_E09_MR	g2191130	BLASTX	216	4e-16	36	(AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]
2365	GM_71_A2_F04_MR	g2995405	BLASTX	171	3e-15	42	(Y12432) polyprotein [Ananas comosus]
2366	GM_71_A2_F06_MR	g1769898	BLASTX	478	8e-45	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2367	GM_71_A2_F07_MR	g1173223	BLASTX	142	4e-09	75	40S RIBOSOMAL PROTEIN S11 gi 454848 (L28831) ribosomal protein S11 [Glycine max]
2368	GM_71_A2_F12_MR	g130582	BLASTX	303	2e-46	61	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2369	GM_71_A2_G01_MR	g1769898	BLASTX	553	1e-52	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2370	GM_71_A2_G06_MR	g3097320	BLASTN	701	1e-24	71	Glycine max gene for Bd 30K, complete cds
2371	GM_71_A2_G07_MR	g1666236	BLASTX	217	5e-17	29	(U76261) unknown [Hordeum vulgare]
2372	GM_71_A2_G10_MR	g507910	BLASTN	405	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2373	GM_71_A2_G11_MR	g1666236	BLASTX	300	6e-26	33	(U76261) unknown [Hordeum vulgare]
2374	GM_71_A2_H02_MR	g3142328	BLASTN	441	6e-13	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2375	GM_71_A2_H07_MR	g100484	BLASTX	211	2e-15	38	hypothetical protein - garden snapdragon
2376	GM_71_A2_H11_MR	g100484	BLASTX	491	7e-46	48	hypothetical protein - garden snapdragon
2377	GM_71_A2_H12_MR	g1399306	BLASTN	363	1e-13	90	Glycine max phosphoinositide-specific phospholipase C P25 mRNA, complete cds.
2378	GM_71_B1_A02_MR	g2586082	BLASTX	327	3e-27	53	(U72725) retrofit [Oryza longistaminata]
2379	GM_71_B1_A03_MR	g1532163	BLASTX	233	7e-19	68	(U63815) similar to glutaredoxin encoded by GenBank Accession Number Z49699; localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initiation codon and stop codon are missing
2380	GM_71_B1_A04_T7	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2381	GM_71_B1_A07_MR	g3935164	BLASTX	192	7e-13	50	(AC004557) F17L21.7 [Arabidopsis thaliana]
2382	GM_71_B1_A09_T7	g18559	BLASTN	803	2e-29	76	G-max gene for catalase
2383	GM_71_B1_A12_MR	g3894156	BLASTN	391	1e-10	62	Arabidopsis thaliana chromosome II BAC T16F16 genomic sequence, complete sequence [Arabidopsis thaliana]
2384	GM_71_B1_B04_T7	g1039432	BLASTN	445	4e-16	70	Glycine max cellulase gene, partial cds.
2385	GM_71_B1_C02_T7	g531596	BLASTN	350	6e-09	62	M-capricolum DNA for CONTIG MC002
2386	GM_71_B1_C03_T7	g2462058	BLASTX	102	9e-13	48	(Y13389) reverse transcriptase [Antirrhinum majus]
2387	GM_71_B1_C05_T7	g4063760	BLASTX	231	3e-17	50	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
2388	GM_71_B1_C07_MR	g1769897	BLASTX	155	1e-09	29	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2389	GM_71_B1_C09_MR	g1769898	BLASTX	264	4e-21	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2390	GM_71_B1_C10_T7	g2618698	BLASTX	160	7e-10	73	(AC002510) unknown protein [Arabidopsis thaliana]
2391	GM_71_B1_C12_T7	g18559	BLASTN	490	4e-15	78	G-max gene for catalase
2392	GM_71_B1_E01_T7	g3845089	BLASTN	410	2e-11	61	Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence
2393	GM_71_B1_E02_MR	g507910	BLASTN	622	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
2394	GM_71_B1_E02_T7	g507910	BLASTN	570	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2395	GM_71_B1_E05_MR	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2396	GM_71_B1_E11_T7	g3894194	BLASTX	205	2e-15	50	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]
2397	GM_71_B1_F01_MR	g2522228	BLASTX	421	1e-38	59	(AB007466) reverse transcriptase-like protein [Vicia faba]
2398	GM_71_B1_F03_T7	g905361	BLASTX	216	5e-16	33	(U22103) gag-protease polypeptide [Glycine max]
2399	GM_71_B1_F04_T7	g2995405	BLASTX	154	4e-09	59	(Y12432) polyprotein [Ananas comosus]
2400	GM_71_B1_F05_MR	g469153	BLASTN	381	3e-10	68	P.sativum (Birt) Lox1:Ps:2 gene.
2401	GM_71_B1_F06_T7	g22635	BLASTN	579	3e-24	78	P.vulgaris mRNA for 70 kD heat shock protein
2402	GM_71_B1_G01_T7	g1785736	BLASTX	97	5e-11	54	(Y08502) orf119 [Arabidopsis thaliana]
2403	GM_71_B1_G04_MR	g629693	BLASTX	417	3e-38	57	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2404	GM_71_B1_G04_T7	g4126312	BLASTN	373	8e-10	63	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
2405	GM_71_B1_G05_MR	g505129	BLASTN	358	1e-11	73	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
2406	GM_71_B1_G07_MR	g507910	BLASTN	455	6e-14	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2407	GM_71_B1_G10_T7	g99922	BLASTX	472	4e-44	81	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
2408	GM_71_B1_G12_T7	g1142702	BLASTN	398	2e-11	86	Glycine max satellite STR120-A.4.
2409	GM_71_B1_H11_MR	g1532162	BLASTN	356	5e-09	71	Arabidopsis thaliana AT.1.24-1, AT.1.24-2, AT.1.24-3, AT.1.24-4, AT.1.24-5, AT.1.24-6, AT.1.24-9 and AT.1.24-14 genes, partial cds, AT.1.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.1....
2410	GM_71_B2_A03_MR	g3860271	BLASTX	161	7e-10	36	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
2411	GM_71_B2_A05_T7	g3810596	BLASTX	269	2e-21	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2412	GM_71_B2_A07_T7	g498931	BLASTX	177	7e-13	43	(Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
2413	GM_71_B2_B01_MR	g905361	BLASTX	193	2e-13	33	(U22103) gag-protease polyprotein [Glycine max]
2414	GM_71_B2_B01_T7	g535454	BLASTX	179	1e-12	56	(U13940) cysteine proteinase [Alnus glutinosa]
2415	GM_71_B2_B04_MR	g4063770	BLASTX	166	2e-10	37	(AB004906) transposase [Ipomoea purpurea]
2416	GM_71_B2_B09_MR	g170606	BLASTN	727	2e-26	66	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
2417	GM_71_B2_C01_T7	g2895616	BLASTN	371	4e-10	60	Colias alexandra edwardsii large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
2418	GM_71_B2_C02_T7	g130398	BLASTX	207	1e-14	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPONSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
2419	GM_71_B2_C05_T7	g18559	BLASTN	501	1e-15	68	G.max gene for catalase
2420	GM_71_B2_C07_T7	g3142328	BLASTN	568	1e-18	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2421	GM_71_B2_D02_T7	g507910	BLASTN	388	6e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
2422	GM_71_B2_D07_MR	g99922	BLASTX	317	1e-27	85	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2423	GM_71_B2_D09_MR	g2129559	BLASTX	150	6e-09	47	cellulase homolog OR16pep - Arabidopsis thaliana gi 1022807 (U37702) cellulase [Arabidopsis thaliana] gi 3493633 (AF074092) cellulase [Arabidopsis thaliana] gi 3598956 (AF074375) cellulase [Arabidopsis thaliana] [Arabidopsis thaliana] (AF015301) RhoAp108 [Arabidopsis thaliana] (AF013293) contains weak similarity to S. cerevisiae BOB1 protein (PIR:S45444) [Arabidopsis thaliana] Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens] Glycine max BSR-101 satellite SB92 genomic sequence. Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens] (AB007466) reverse transcriptase-like protein [Vicia faba] (U92460) pdr2 [Arabidopsis thaliana] (U68408) 5' end not determined experimentally [Zea mays] (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba] Glycine max cv. Dare nodulin 26 gene fragment. (U22103) gag-protease polyprotein [Glycine max] Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max satellite STR120-A.3. retrotransposon del1-46 [Lilium henryi] Glycine max gene for Bd 30K, complete cds (AB007466) reverse transcriptase-like protein [Vicia faba] (AB007466) reverse transcriptase-like protein [Vicia faba] (AC005561) putative POL3 protein [Arabidopsis thaliana] (U72725) retrofit [Oryza longistaminata] Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-65, complete sequence [Plasmodium falciparum] (AC005824) putative selenium-binding protein [Arabidopsis thaliana] (U22103) gag-protease polyprotein [Glycine max] Plasmodium falciparum chromosome 2, section 22 of 73 of the complete sequence (AF053008) gag-pol polyprotein [Glycine max] Soybean heat-shock protein (Gmhsp26-A) gene, complete cds. Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max nodule-specific glutamine synthetase gene, complete cds
2424	GM_71_B2_E01_MR	g2654868	BLASTX	154	4e-18	61	
2425	GM_71_B2_E01_T7	g2252836	BLASTX	416	2e-37	71	
2426	GM_71_B2_E02_MR	g4150930	BLASTN	384	3e-10	61	
2427	GM_71_B2_E04_T7	g507910	BLASTN	405	1e-11	82	
2428	GM_71_B2_E09_T7	g3738114	BLASTN	349	1e-08	64	
2429	GM_71_B2_E10_MR	g2522228	BLASTX	165	8e-16	48	
2430	GM_71_B2_E12_MR	g3882356	BLASTX	158	3e-10	52	
2431	GM_71_B2_F04_T7	g3645899	BLASTX	301	1e-24	56	
2432	GM_71_B2_F11_T7	g2522230	BLASTX	229	2e-18	35	
2433	GM_71_B2_G04_T7	g170029	BLASTN	394	8e-11	83	
2434	GM_71_B2_G07_T7	g905361	BLASTX	577	3e-55	91	
2435	GM_71_B2_G10_T7	g507910	BLASTN	451	9e-14	74	
2436	GM_71_B2_H05_T7	g507910	BLASTN	410	6e-12	77	
2437	GM_71_B2_H06_MR	g1142701	BLASTN	1366	2e-55	87	
2438	GM_71_B2_H06_T7	g226407	BLASTX	182	7e-12	40	
2439	GM_72_A1_A06_MR	g3097320	BLASTN	989	9e-38	80	
2440	GM_72_A1_A08_MR	g2522228	BLASTX	151	3e-09	31	
2441	GM_72_A1_A10_T7	g2522228	BLASTX	358	5e-32	78	
2442	GM_72_A1_B08_T7	g4063760	BLASTX	239	5e-18	46	
2443	GM_72_A1_B10_MR	g2586082	BLASTX	258	6e-20	45	
2444	GM_72_A1_B12_T7	g2982550	BLASTN	1120	1e-43	74	
2445	GM_72_A1_C02_MR	g3860271	BLASTX	305	3e-25	43	
2446	GM_72_A1_C04_T7	g905361	BLASTX	198	5e-14	36	
2447	GM_72_A1_C05_T7	g3845143	BLASTN	402	4e-11	60	
2448	GM_72_A1_C08_MR	g3777527	BLASTX	615	6e-58	93	
2449	GM_72_A1_D02_MR	g169980	BLASTN	2015	1e-85	94	
2450	GM_72_A1_D03_MR	g507910	BLASTN	366	6e-10	71	
2451	GM_72_A1_D05_MR	g3695294	BLASTN	417	7e-12	84	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2479	GM_72_A2_B09_MR	g3142328	BLASTN	404	3e-11	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
2480	GM_72_A2_B09_T7	g1946279	BLASTX	176	8e-13	41	hypothetical protein - garden snapdragon
2481	GM_72_A2_B11_MR	g100484	BLASTX	226	6e-17	40	Glycine max BSR-101 satellite SB92 genomic sequence.
2482	GM_72_A2_C06_MR	g507910	BLASTN	669	1e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
2483	GM_72_A2_C06_T7	g507910	BLASTN	546	5e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2484	GM_72_A2_C08_MR	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2485	GM_72_A2_C08_T7	g507910	BLASTN	355	2e-09	69	L.japonicus gln1, pge1 & krm genes
2486	GM_72_A2_C11_T7	g2073447	BLASTN	475	2e-14	68	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]
2487	GM_72_A2_D02_T7	g2244803	BLASTX	202	2e-15	42	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA);
2488	GM_72_A2_D08_MR	g99922	BLASTX	406	1e-65	77	pid:e150225 [Glycine max]
2489	GM_72_A2_D08_T7	g170080	BLASTN	610	1e-20	73	Soybean seed lectin gene transposable element tgml.
2490	GM_72_A2_D10_MR	g3264565	BLASTN	382	3e-10	62	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
2491	GM_72_A2_D10_T7	g2129618	BLASTX	194	2e-13	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2492	GM_72_A2_E04_T7	g130582	BLASTX	192	6e-13	41	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2493	GM_72_A2_F06_MR	g507910	BLASTN	384	9e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2494	GM_72_A2_F08_T7	g3928116	BLASTN	364	2e-09	60	, complete sequence [Homo sapiens]
2495	GM_72_A2_F11_MR	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence
2496	GM_72_A2_E11_T7	g507910	BLASTN	395	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2497	GM_72_A2_F04_MR	g2522230	BLASTX	267	2e-22	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
2498	GM_72_A2_F04_T7	g2194136	BLASTX	212	4e-15	44	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
2499	GM_72_A2_F08_MR	g2522227	BLASTX	185	1e-13	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2500	GM_72_A2_F10_MR	g507910	BLASTN	382	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2501	GM_72_A2_F10_T7	g507910	BLASTN	377	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2502	GM_72_A2_G01_T7	g18559	BLASTN	850	2e-31	80	G.max gene for catalase
2503	GM_72_A2_G02_MR	g3142328	BLASTN	907	4e-34	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
2504	GM_72_A2_G05_MR	g3850962	BLASTX	109	4e-09	55	(AF060421) ATP synthase beta subunit [Panopsis ferruginea]
2505	GM_72_A2_G06_T7	g18559	BLASTN	972	5e-37	76	G.max gene for catalase
2506	GM_72_A2_G07_T7	g3097320	BLASTN	694	2e-24	79	Glycine max gene for Bd 30K, complete cds
2507	GM_72_A2_G08_MR	g18559	BLASTN	504	8e-16	78	G.max gene for catalase
2508	GM_72_A2_G09_T7	g2997694	BLASTX	142	5e-09	27	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
2509	GM_72_A2_H02_MR	g398966	BLASTX	666	9e-65	93	4-COUMARATE--COA LIGASE 2 (4CL) (CLONE 4CL16) gi 541937 pir PQ0772 4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL1B) - soybean (fragment) gi 185520 (X69955) 4-coumarate--CoA ligase [Glycine max]
2510	GM_72_A2_H03_T7	g1785729	BLASTN	443	6e-13	65	A.thaliana mitochondrial genome, part B
2511	GM_72_A2_H04_T7	g3641780	BLASTN	382	3e-10	62	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
2512	GM_72_A2_H09_T7	g131254	BLASTX	546	5e-52	82	PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN) (PHOTOSYSTEM II PROTEIN D1) >gi 99477 pir S15957 photosystem II protein D1 - shore pine chloroplast >gi 320208 pir S29327 photosystem II protein D1 - Japanese black pine chloroplast >gi 12082 (X53721) D1 protein of photosystem II [Pinus contorta] >gi 12084 (X53722) D1 protein of photosystem II [Pinus contorta] >gi 12091 (X57097) D1 protein of photosystem II [Pinus contorta] >gi 12093 (X57097) D1 protein of photosystem II [Pinus contorta] >gi 344012 gnl PID d1002506 (D11467) photosystem II D1 protein [Pinus thunbergii] >gi 1262747 gnl PID d1004987 (D17510) PSII 32kDa protein [Pinus thunbergii] (AC005561) putative POL3 protein [Arabidopsis thaliana] Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
2513	GM_73_A1_A08_T7	g4063760	BLASTX	137	9e-09	32	(U22103) gag-protease polyprotein [Glycine max]
2514	GM_73_A1_B03_T7	g2764526	BLASTN	494	3e-15	65	(AF053008) gag-pol polyprotein [Glycine max]
2515	GM_73_A1_B08_T7	g905361	BLASTX	646	2e-62	95	(AC005897) putative transposon [Arabidopsis thaliana]
2516	GM_73_A1_B09_T7	g3777527	BLASTX	169	2e-10	90	(AC005897) putative POL3 protein [Arabidopsis thaliana]
2517	GM_73_A1_B11_T7	g4038056	BLASTX	252	1e-19	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2518	GM_73_A1_C07_T7	g4063760	BLASTX	297	3e-24	53	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
2519	GM_73_A1_C10_MR	g2522226	BLASTN	645	3e-22	69	(AC005897) putative transposon [Arabidopsis thaliana]
2520	GM_73_A1_D07_MR	g4038056	BLASTX	218	6e-16	40	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT
2521	GM_73_A1_D09_T7	g2506277	BLASTX	272	2e-32	88	PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) gi 806808 (U21139) chaperonin precursor [Pisum sativum]
2522	GM_73_A1_E04_MR	g3560028	BLASTN	358	3e-09	62	Schistosoma intercalatum ribosomal intergenic spacer DNA

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
2523	GM_73_A1_F10_T7	g3687234	BLASTX	109	9e-09	25	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
2524	GM_73_A1_F01_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2525	GM_73_A1_F04_MR	g3599418	BLASTN	1086	3e-42	88	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
2526	GM_73_A1_F12_T7	g3687234	BLASTX	168	2e-10	36	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
2527	GM_73_A1_G07_T7	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
2528	GM_73_A1_G11_MR	g905361	BLASTX	172	3e-11	34	(U22103) gag-protease polyprotein [Glycine max]
2529	GM_73_A1_H01_MR	g3319362	BLASTX	186	2e-12	37	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm. score 19.29) [Arabidopsis thaliana]
2530	GM_73_A1_H03_T7	g3212869	BLASTX	323	1e-27	80	(AC004005) unknown protein [Arabidopsis thaliana]
2531	GM_73_A1_H04_T7	g227238	BLASTN	1512	2e-61	95	G.max mitochondrial atpA.
2532	GM_73_A1_H06_MR	g3859610	BLASTN	413	1e-11	68	Arabidopsis thaliana BAC T9E19
2533	GM_73_A2_A02_MR	g4038056	BLASTX	379	3e-34	50	(AC005897) putative transposon [Arabidopsis thaliana]
2534	GM_73_A2_A07_MR	g3142379	BLASTX	234	2e-18	57	(AF053008) envelope-like [Glycine max]
2535	GM_73_A2_A08_T7	g2801681	BLASTN	671	5e-24	72	Glycine max telomere-associated sequence STAS10
2536	GM_73_A2_A10_MR	g4063760	BLASTX	233	1e-20	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2537	GM_73_A2_B02_MR	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2538	GM_73_A2_B02_T7	g507910	BLASTN	343	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2539	GM_73_A2_B03_MR	g3859610	BLASTN	514	3e-16	65	Arabidopsis thaliana BAC T9E19
2540	GM_73_A2_B03_T7	g905361	BLASTX	269	1e-21	39	(U22103) gag-protease polyprotein [Glycine max]
2541	GM_73_A2_B04_MR	g1769898	BLASTX	297	9e-25	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2542	GM_73_A2_B04_T7	g2462058	BLASTX	304	2e-26	47	(Y13389) reverse transcriptase [Antirrhinum majus]
2543	GM_73_A2_B09_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2544	GM_73_A2_B09_T7	g507910	BLASTN	358	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2545	GM_73_A2_C03_T7	g99721	BLASTX	401	3e-35	50	retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Ta1-3 gi 16534 (X13291) polyprotein [Arabidopsis thaliana]
2546	GM_73_A2_C06_T7	g3650026	BLASTN	369	1e-09	64	Arabidopsis thaliana chromosome II BAC T26120 genomic sequence, complete sequence [Arabidopsis thaliana]
2547	GM_73_A2_D02_T7	g1785736	BLASTX	171	1e-14	57	(Y08502) orf119 [Arabidopsis thaliana]
2548	GM_73_A2_D04_T7	g4063760	BLASTX	249	4e-19	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2549	GM_73_A2_D09_T7	g2462936	BLASTX	277	2e-23	44	(Y12321) open reading frame 2 [Brassica oleracea]
2550	GM_73_A2_E01_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2551	GM_73_A2_E01_T7	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2552	GM_73_A2_E02_MR	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2553	GM_73_A2_E02_T7	g507910	BLASTN	339	1e-08	69	Glycine max BSR-101 satellite SB92 genomic sequence.
2554	GM_73_A2_E07_MR	g18695	BLASTN	349	7e-09	67	Soybean nodulin 22 gene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2555	GM_73_A2_E08_MR	g3142328	BLASTN	708	4e-25	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2556	GM_73_A2_E10_T7	g3273387	BLASTN	455	2e-13	64	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
2557	GM_73_A2_E12_MR	g507910	BLASTN	431	7e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
2558	GM_73_A2_E12_T7	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2559	GM_73_A2_F03_T7	g1769897	BLASTX	355	2e-31	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2560	GM_73_A2_F04_T7	g4115536	BLASTX	169	7e-12	34	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
2561	GM_73_A2_F08_T7	g18559	BLASTN	433	1e-12	73	G.max gene for catalase
2562	GM_73_A2_F09_T7	g22738	BLASTN	1661	3e-68	91	G.max mitochondrial atpA.
2563	GM_73_A2_F10_MR	g4063760	BLASTX	467	2e-42	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2564	GM_73_A2_F11_T7	g2642431	BLASTX	192	2e-20	47	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
2565	GM_73_A2_F12_MR	g507910	BLASTN	539	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
2566	GM_73_A2_G03_T7	g3097320	BLASTN	795	6e-29	75	Glycine max gene for Bd 30K, complete cds
2567	GM_73_A2_G11_T7	g3097320	BLASTN	393	9e-11	68	Glycine max gene for Bd 30K, complete cds
2568	GM_73_A2_G12_MR	g130582	BLASTX	200	7e-14	35	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2569	GM_73_A2_H03_MR	g1666236	BLASTX	197	1e-14	29	(U76261) unknown [Hordeum vulgare]
2570	GM_73_A2_H04_T7	g2522230	BLASTX	272	6e-23	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
2571	GM_73_A2_H06_T7	g3004564	BLASTX	148	5e-09	49	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]
2572	GM_73_A2_H09_T7	g3845197	BLASTN	379	4e-10	58	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
2573	GM_73_A2_H10_MR	g4063760	BLASTX	203	3e-14	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2574	GM_74_A1_A02_MR	g3582333	BLASTX	150	4e-09	82	(AC005496) hypothetical protein [Arabidopsis thaliana]
2575	GM_74_A1_A05_T7	g2244950	BLASTN	332	2e-13	65	Arabidopsis thaliana DNA chromosome 4, ESSA 1 contig fragment No. 5
2576	GM_74_A1_B01_T7	g1666236	BLASTX	212	2e-16	32	(U76261) unknown [Hordeum vulgare]
2577	GM_74_A1_B03_T7	g905361	BLASTX	422	2e-38	93	(U22103) gag-protease polyprotein [Glycine max]
2578	GM_74_A1_B08_T7	g2129618	BLASTX	177	1e-11	31	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2579	GM_74_A1_B12_MR	g2995405	BLASTX	304	3e-25	60	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2580	GM_74_A1_B12_T7	g3097320	BLASTN	1116	2e-43	78	Glycine max gene for Bd 30K, complete cds
2581	GM_74_A1_C07_T7	g2769655	BLASTN	367	1e-09	60	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
2582	GM_74_A1_D04_MR	g3641780	BLASTN	375	7e-10	60	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
2583	GM_74_A1_D10_MR	g3645899	BLASTX	193	4e-15	43	(U68408) 5' end not determined experimentally [Zea mays]
2584	GM_74_A1_D11_MR	g1167523	BLASTX	464	5e-42	56	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
2585	GM_74_A1_E01_MR	g2764526	BLASTN	483	8e-15	59	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
2586	GM_74_A1_F06_MR	g185559	BLASTN	819	4e-30	72	G-max gene for catalase
2587	GM_74_A1_F09_MR	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2588	GM_74_A1_E11_MR	g3777527	BLASTX	619	2e-58	81	(AF053008) gag-pol polyprotein [Glycine max]
2589	GM_74_A1_F04_MR	g507910	BLASTN	347	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2590	GM_74_A1_F04_T7	g507910	BLASTN	385	9e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2591	GM_74_A1_F05_T7	g387902	BLASTX	179	9e-19	48	(L23524) ORF [Hordeum vulgare]
2592	GM_74_A1_F06_MR	g505129	BLASTN	347	1e-08	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
2593	GM_74_A1_F06_T7	g531389	BLASTX	170	1e-10	53	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
2594	GM_74_A1_F12_MR	g2995405	BLASTX	231	7e-21	51	(Y12432) polyprotein [Ananas comosus]
2595	GM_74_A1_G02_T7	g3378661	BLASTX	181	8e-13	35	(Y13048) putative outward rectifying potassium channel StKCO1 [Solanum tuberosum]
2596	GM_74_A1_G08_MR	g185559	BLASTN	488	4e-15	69	G-max gene for catalase
2597	GM_74_A1_G11_MR	g3513747	BLASTX	170	2e-10	44	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
2598	GM_74_A1_H02_T7	g2921210	BLASTN	425	2e-12	76	Perilla frutescens beta-ketoacyl-ACP synthase II (KAS II) mRNA, complete cds
2599	GM_74_A1_H07_T7	g4038056	BLASTX	243	1e-18	43	(AC005897) putative transposon [Arabidopsis thaliana]
2600	GM_74_A1_H09_MR	g4063760	BLASTX	235	5e-39	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2601	GM_74_A2_A03_MR	g441205	BLASTN	610	1e-20	72	Soybean lox1gm4 gene encoding lipxygenase L-4
2602	GM_74_A2_A03_T7	g3786500	BLASTN	358	4e-09	69	Caenorhabditis elegans cosmid T06A4
2603	GM_74_A2_A04_T7	g507910	BLASTN	553	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2604	GM_74_A2_A07_MR	g1142703	BLASTN	271	9e-15	73	Glycine max satellite STR120-B.1.
2605	GM_74_A2_A07_T7	g905361	BLASTX	421	2e-38	92	(U22103) gag-protease polyprotein [Glycine max]
2606	GM_74_A2_A09_T7	g3777527	BLASTX	170	1e-10	32	(AF053008) gag-pol polyprotein [Glycine max]
2607	GM_74_A2_A10_MR	g33377834	BLASTX	154	3e-09	29	(AF075598) No definition line found [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2608	GM_74_A2_A10_T7	g3142328	BLASTN	454	1e-13	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2609	GM_74_A2_B01_MR	g170080	BLASTN	359	3e-09	63	Soybean seed lectin gene transposable element tgm1.
2610	GM_74_A2_B05_MR	g3097320	BLASTN	632	1e-21	79	Glycine max gene for Bd 30K, complete cds
2611	GM_74_A2_B10_MR	g3097320	BLASTN	891	3e-33	78	Glycine max gene for Bd 30K, complete cds
2612	GM_74_A2_C09_T7	g4038056	BLASTX	155	3e-09	35	(AC005897) putative transposon [Arabidopsis thaliana]
2613	GM_74_A2_C11_T7	g2129677	BLASTX	180	1e-12	55	probable N-acetyltransferase hookless 1 - Arabidopsis thaliana gi 1277090 (U50399) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] gi 1277092 (U50400) putative N-acetyltransferase hookless1 [Arabidopsis thaliana]
2614	GM_74_A2_C12_T7	g3097320	BLASTN	1125	6e-44	83	acetyltransferase hookless1 [Arabidopsis thaliana]
2615	GM_74_A2_D01_MR	g1167523	BLASTX	176	1e-12	44	Glycine max gene for Bd 30K, complete cds
2616	GM_74_A2_D02_MR	g507910	BLASTN	579	1e-19	80	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
2617	GM_74_A2_D03_MR	g3549681	BLASTX	152	2e-09	54	Glycine max BSR-101 satellite SB92 genomic sequence.
2618	GM_74_A2_D03_T7	g1360141	BLASTX	177	4e-12	60	(AL031394) male sterility 2-like protein [Arabidopsis thaliana]
2619	GM_74_A2_D06_MR	g507910	BLASTN	399	2e-11	73	(X97980) protein kinase [Solanum berthaultii]
2620	GM_74_A2_D06_T7	g507910	BLASTN	359	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2621	GM_74_A2_D07_MR	g2522230	BLASTX	252	8e-21	38	Glycine max BSR-101 satellite SB92 genomic sequence. (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
2622	GM_74_A2_D09_MR	g18559	BLASTN	753	4e-27	77	G.max gene for catalase
2623	GM_74_A2_D10_MR	g3645899	BLASTX	319	8e-29	48	(U68408) 5' end not determined experimentally [Zea mays]
2624	GM_74_A2_D10_T7	g3142328	BLASTN	450	2e-13	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2625	GM_74_A2_E02_T7	g4063760	BLASTX	157	3e-09	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2626	GM_74_A2_E04_MR	g2995405	BLASTX	192	3e-13	52	(Y12432) polyprotein [Ananas comosus]
2627	GM_74_A2_E08_MR	g4063760	BLASTX	259	4e-20	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2628	GM_74_A2_E09_MR	g629693	BLASTX	183	7e-13	45	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
2629	GM_74_A2_E11_T7	g4063760	BLASTX	241	3e-18	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2630	GM_74_A2_F01_MR	g1666236	BLASTX	129	4e-12	39	(U76261) unknown [Hordeum vulgare]
2631	GM_74_A2_F04_MR	g4063760	BLASTX	191	7e-13	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2632	GM_74_A2_F05_MR	g100484	BLASTX	260	1e-20	57	hypothetical protein - garden snapdragon
2633	GM_74_A2_F05_T7	g3142328	BLASTN	861	5e-32	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF069298) contains similarity to a protein kinase domain (Pfam: pkinae.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido...
2634	GM_74_A2_F07_T7	g3193290	BLASTX	173	3e-11	38	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2635	GM_74_A2_G01_T7	g4063770	BLASTX	197	8e-14	42	(AB004906) transposase [Ipomoea purpurea]
2636	GM_74_A2_G04_T7	g3777527	BLASTX	691	4e-66	92	(AF053008) gag-pol polyprotein [Glycine max]
2637	GM_74_A2_G05_T7	g1785693	BLASTX	123	2e-10	47	(Y08501) orf11a [Arabidopsis thaliana]
2638	GM_74_A2_G10_MR	g2997694	BLASTX	101	2e-13	36	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
2639	GM_74_A2_G10_T7	g4063760	BLASTX	162	8e-10	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2640	GM_74_A2_H03_MR	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2641	GM_74_A2_H03_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2642	GM_74_A2_H11_T7	g2982540	BLASTN	374	7e-10	66	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-30, complete sequence [Plasmodium falciparum]
2643	GM_74_B1_A03_T7	g4115365	BLASTX	126	1e-15	38	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
2644	GM_74_B1_A09_MR	g4063760	BLASTX	485	2e-44	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2645	GM_74_B1_A10_MR	g158813	BLASTN	363	6e-10	64	Drosophila hydei Y chromosome lampbrush loop transcribed repeats.
2646	GM_74_B1_A11_T7	g3777526	BLASTN	736	3e-26	79	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
2647	GM_74_B1_B01_T7	g3777526	BLASTN	1135	2e-44	93	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
2648	GM_74_B1_B03_MR	g3928116	BLASTN	397	7e-11	60	, complete sequence [Homo sapiens]
2649	GM_74_B1_B04_MR	g3650039	BLASTX	175	1e-11	34	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
2650	GM_74_B1_B05_MR	g3777527	BLASTX	650	9e-62	96	(AF053008) gag-pol polyprotein [Glycine max]
2651	GM_74_B1_B06_MR	g1666236	BLASTX	115	1e-09	41	(U76261) unknown [Hordeum vulgare]
2652	GM_74_B1_B07_T7	g3687234	BLASTX	170	1e-10	45	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
2653	GM_74_B1_B09_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2654	GM_74_B1_C01_T7	g905361	BLASTX	437	3e-40	96	(U22103) gag-protease polyprotein [Glycine max]
2655	GM_74_B1_C02_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2656	GM_74_B1_C02_T7	g507910	BLASTN	360	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2657	GM_74_B1_C05_MR	g505129	BLASTN	362	2e-09	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
2658	GM_74_B1_C05_T7	g2129618	BLASTX	184	2e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2659	GM_74_B1_C07_MR	g4049647	BLASTN	421	6e-12	65	Melanoplus sanguinipes entomopoxvirus, complete genome
2660	GM_74_B1_C07_T7	g4160441	BLASTX	161	2e-10	37	(AF098674) lateral suppressor protein [Lycopersicon esculentum]
2661	GM_74_B1_C10_MR	g3142328	BLASTN	1167	6e-46	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2662	GM_74_B1_C12_MR	g629693	BLASTX	273	5e-23	61	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
2663	GM_74_B1_D02_T7	g2149640	BLASTX	227	8e-17	75	(U91995) Argonaute protein [Arabidopsis thaliana]
2664	GM_74_B1_D03_T7	g730526	BLASTX	235	2e-38	80	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis thaliana gi 404166 (X75162) BBC1 protein [Arabidopsis thaliana]
2665	GM_74_B1_D04_MR	g507910	BLASTN	345	6e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2666	GM_74_B1_D09_T7	g3097320	BLASTN	480	1e-14	71	Glycine max gene for Bd 30K, complete cds
2667	GM_74_B1_E04_MR	g507910	BLASTN	401	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2668	GM_74_B1_E04_T7	g507910	BLASTN	385	9e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2669	GM_74_B1_E10_MR	g905361	BLASTX	150	5e-12	27	(U22103) gag-protease polypeptide [Glycine max]
2670	GM_74_B1_F01_T7	g4038056	BLASTX	386	6e-34	53	(AC005897) putative transposon [Arabidopsis thaliana]
2671	GM_74_B1_F05_MR	g3449334	BLASTN	395	8e-11	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
2672	GM_74_B1_F07_T7	g905361	BLASTX	239	2e-18	34	(U22103) gag-protease polypeptide [Glycine max]
2673	GM_74_B1_F08_MR	g909922	BLASTX	464	3e-43	58	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
2674	GM_74_B1_F09_MR	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2675	GM_74_B1_F11_T7	g547683	BLASTX	133	4e-16	77	HEAT SHOCK COGNATE PROTEIN 80 gi 170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] gi 445601 prf 1909348A heat shock protein hsp80 [Lycopersicon esculentum]
2676	GM_74_B1_F12_T7	g3097320	BLASTN	1421	2e-57	82	Glycine max gene for Bd 30K, complete cds
2677	GM_74_B1_G01_T7	g2323254	BLASTN	405	3e-11	64	Human Chromosome X, complete sequence [Homo sapiens]
2678	GM_74_B1_G02_MR	g4160362	BLASTN	388	2e-10	61	Saccharomyces cerevisiae complete mitochondrial genome
2679	GM_74_B1_G04_MR	g3548805	BLASTX	147	3e-12	65	(AC005313) unknown protein [Arabidopsis thaliana]
2680	GM_74_B1_G08_MR	g1346736	BLASTX	162	4e-11	43	POLLEN-SPECIFIC MEMBRANE INTEGRAL PROTEIN gi 665948 (U20490) putative membrane integral protein [Nicotiana glauca]
2681	GM_74_B1_G09_MR	g4063760	BLASTX	495	2e-45	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2682	GM_74_B1_G11_T7	g3928116	BLASTN	509	6e-16	65	, complete sequence [Homo sapiens]
2683	GM_74_B1_H07_MR	g3269291	BLASTX	132	4e-14	60	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]
2684	GM_74_B1_H11_T7	g4063760	BLASTX	495	2e-45	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2685	GM_74_B1_H12_T7	g2522227	BLASTX	184	3e-17	40	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2686	GM_74_B2_A01_T7	g3650039	BLASTX	277	1e-22	41	(AC005396) putative Em/Spm transposon protein, 5' partial [Arabidopsis thaliana]
2687	GM_74_B2_A03_T7	g2982540	BLASTN	349	1e-08	66	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-30, complete sequence [Plasmodium falciparum]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
2688	GM_74_B2_A04_T7	g13096	BLASTN	362	2e-09	67	Leishmania tarentolae maxicircle DNA fragment
2689	GM_74_B2_B02_T7	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2690	GM_74_B2_B05_T7	g4063760	BLASTX	348	1e-41	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2691	GM_74_B2_B08_MR	g18559	BLASTN	583	2e-19	71	G.max gene for catalase
2692	GM_74_B2_B11_MR	g4063760	BLASTX	342	5e-29	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2693	GM_74_B2_B12_T7	g1877523	BLASTN	483	9e-15	70	Arabidopsis thaliana BAC T7123, complete sequence [Arabidopsis thaliana]
2694	GM_74_B2_C04_T7	g3097320	BLASTN	1168	7e-46	77	Glycine max gene for Bd 30K, complete cds
2695	GM_74_B2_C06_MR	g3243214	BLASTN	428	3e-12	72	Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
2696	GM_74_B2_D03_T7	g3097320	BLASTN	454	2e-13	65	Glycine max gene for Bd 30K, complete cds
2697	GM_74_B2_D05_T7	g3777527	BLASTX	306	5e-25	46	(AF053008) gag-pol polyprotein [Glycine max]
2698	GM_74_B2_D09_T7	g507910	BLASTN	405	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2699	GM_74_B2_D11_T7	g2522227	BLASTX	216	5e-17	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2700	GM_74_B2_E01_MR	g1658457	BLASTX	226	4e-18	66	(U75248) reverse transcriptase [Gossypium barbadense]
2701	GM_74_B2_E10_T7	g422418	BLASTX	210	2e-26	45	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
2702	GM_74_B2_E11_MR	g507910	BLASTN	372	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2703	GM_74_B2_F02_T7	g3097320	BLASTN	1167	8e-46	75	Glycine max gene for Bd 30K, complete cds
2704	GM_74_B2_F08_T7	g2443320	BLASTX	213	1e-26	51	(D85597) polyprotein [Oryza australiensis]
2705	GM_74_B2_G07_MR	g4056494	BLASTX	293	2e-25	69	(AC005896) putative protein translocase [Arabidopsis thaliana]
2706	GM_74_B2_G07_T7	g3785975	BLASTX	208	5e-15	76	(AC005560) hypothetical protein [Arabidopsis thaliana]
2707	GM_74_B2_G09_T7	g2443320	BLASTX	216	2e-32	52	(D85597) polyprotein [Oryza australiensis]
2708	GM_74_B2_H01_MR	g2961346	BLASTX	174	1e-11	59	(AL022140) pectinesterase like protein [Arabidopsis thaliana]
2709	GM_74_B2_H02_MR	g313189	BLASTN	367	1e-09	70	A.thaliana TMKL1 mRNA
2710	GM_74_B2_H06_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2711	GM_74_B2_H06_T7	g507910	BLASTN	378	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2712	GM_74_B2_H07_MR	g507910	BLASTN	463	3e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
2713	GM_75_A1_A08_MR	g507910	BLASTN	414	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2714	GM_75_A1_A08_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2715	GM_75_A1_B02_T7	g2244747	BLASTN	361	3e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence. Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 0
2716	GM_75_A1_B04_T7	g2464864	BLASTX	158	1e-09	52	(Z99707) selenium-binding protein homolog [Arabidopsis thaliana]
2717	GM_75_A1_B05_T7	g99755	BLASTX	378	8e-34	54	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2718	GM_75_A1_B10_MR	g8540	BLASTN	391	2e-11	61	Drosophila satellite DNA fragment 1.672-614 >gi 158379 gb M29744 DROSA02 Drosophila satellite DNA fragment 1.672-614. (AC005398) putative reverse-transcriptase [Arabidopsis thaliana] hypothetical protein - garden snapdragon (AF053008) gag-pol polyprotein [Glycine max] Helicoverpa armigera mitochondrion D-loop, partial 12S rRNA gene, and partial rRNA-Met gene.
2719	GM_75_A1_C04_T7	g3810595	BLASTX	232	3e-17	56	(Y12432) polyprotein [Ananas comosus] (U68408) 5' end not determined experimentally [Zea mays] Glycine max gene for Bd 30K, complete cds (AC005561) putative POL3 protein [Arabidopsis thaliana] G.max gene for catalase ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV) gi 67924 pir LWNT6 H+-transporting ATP synthase (EC 3.6.1.34) chain a - common tobacco chloroplast gi 11813 (Z00044) ATPase synthase IV subunit [Nicotiana tabacum] gi 225273 prf 1211235H ATPase a [Nicotiana tabacum] Glycine max BSR-101 satellite SB92 genomic sequence. Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana] (AF080119) contains similarity to proteases [Arabidopsis thaliana] (D85597) polyprotein [Oryza australiensis] (Y08010) lectin receptor kinase [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (A1228325) reverse transcriptase [Ginkgo biloba] (AC005561) putative POL3 protein [Arabidopsis thaliana] (AC005311) putative reverse transcriptase [Arabidopsis thaliana] (AF053008) gag-pol polyprotein [Glycine max] (AB007466) reverse transcriptase-like protein [Vicia faba] Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCCase-A) gene, complete cds. G.max gene for catalase (AC005171) putative gag-protease polyprotein [Arabidopsis thaliana] Soybean DNA for basic 7S globulin, complete cds (U76261) unknown [Hordeum vulgare]
2720	GM_75_A1_C12_MR	g100484	BLASTX	169	1e-19	44	
2721	GM_75_A1_D01_MR	g3777527	BLASTX	507	2e-46	80	
2722	GM_75_A1_D05_T7	g409571	BLASTN	392	1e-11	65	
2723	GM_75_A1_D09_T7	g2995405	BLASTX	200	4e-14	66	
2724	GM_75_A1_E02_T7	g3645899	BLASTX	346	2e-29	50	
2725	GM_75_A1_E03_MR	g3097320	BLASTN	558	3e-18	83	
2726	GM_75_A1_E05_MR	g4063760	BLASTX	513	3e-47	72	
2727	GM_75_A1_E11_MR	g18559	BLASTN	416	8e-12	87	
2728	GM_75_A1_G01_T7	g114661	BLASTX	182	2e-13	76	
2729	GM_75_A1_G02_MR	g507910	BLASTN	351	3e-09	72	
2730	GM_75_A1_G07_T7	g2351061	BLASTN	457	1e-13	66	
2731	GM_75_A1_G11_MR	g3241927	BLASTN	528	8e-17	66	
2732	GM_75_A1_H02_MR	g3600044	BLASTX	202	5e-14	42	
2733	GM_75_A1_H08_MR	g2443320	BLASTX	314	6e-26	46	
2734	GM_75_A1_H08_T7	g1769898	BLASTX	187	7e-13	47	
2735	GM_75_A1_H12_T7	g507910	BLASTN	500	6e-16	75	
2736	GM_76_A1_A07_MR	g3688328	BLASTX	223	3e-26	61	
2737	GM_76_A1_A10_MR	g4063760	BLASTX	279	3e-22	49	
2738	GM_76_A1_A12_T7	g3746069	BLASTX	254	1e-19	45	
2739	GM_76_A1_B04_T7	g3777527	BLASTX	233	2e-26	91	
2740	GM_76_A1_B07_T7	g2522228	BLASTX	460	7e-43	73	
2741	GM_76_A1_B09_MR	g992916	BLASTN	505	8e-16	68	
2742	GM_76_A1_B10_T7	g18559	BLASTN	1180	2e-46	76	
2743	GM_76_A1_C03_MR	g3779030	BLASTX	217	4e-17	30	
2744	GM_76_A1_C08_MR	g434060	BLASTN	509	4e-16	71	
2745	GM_76_A1_C10_MR	g1666236	BLASTX	209	4e-16	32	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2746	GM_76_A1_C10_T7	g2264320	BLASTN	724	1e-25	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
2747	GM_76_A1_D03_T7	g99922	BLASTX	519	4e-49	62	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
2748	GM_76_A1_D04_MR	g2264367	BLASTN	391	1e-10	63	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence.
2749	GM_76_A1_D05_MR	g507910	BLASTN	357	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
2750	GM_76_A1_D06_T7	g170080	BLASTN	424	3e-12	89	Soybean seed lectin gene transposable element tgml.
2751	GM_76_A1_D09_T7	g4063760	BLASTX	160	1e-09	33	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2752	GM_76_A1_D10_T7	g3776466	BLASTN	359	3e-09	61	Homo sapiens immunoglobulin-like transcript 10 protein gene, exons 7 and 8 and complete cds
2753	GM_76_A1_E03_T7	g507910	BLASTN	424	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2754	GM_76_A1_F01_T7	g2895615	BLASTN	419	3e-12	63	Colias croceus large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
2755	GM_76_A1_F02_T7	g1076570	BLASTX	172	2e-12	74	homeotic protein CHB6 - carrot
2756	GM_76_A1_F06_MR	g4063760	BLASTX	274	7e-32	81	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2757	GM_76_A1_F06_T7	g3097320	BLASTN	441	6e-13	70	Glycine max gene for Bd 30K, complete cds
2758	GM_76_A1_F08_MR	g3763921	BLASTX	297	1e-25	63	(AC004450) putative pirin protein [Arabidopsis thaliana]
2759	GM_76_A1_F08_T7	g3763915	BLASTN	395	8e-11	65	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]
2760	GM_76_A1_F12_MR	g3097320	BLASTN	711	4e-41	76	Glycine max gene for Bd 30K, complete cds
2761	GM_76_A1_G07_MR	g4050011	BLASTN	418	7e-12	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
2762	GM_76_A1_G10_MR	g507910	BLASTN	420	2e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2763	GM_76_A1_G10_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2764	GM_76_A1_G11_MR	g507910	BLASTN	620	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
2765	GM_76_A1_G11_T7	g507910	BLASTN	549	3e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
2766	GM_76_A1_H08_MR	g2507455	BLASTX	376	2e-33	75	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYL TETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) gi 322401 pir A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach gi 170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]
2767	GM_76_A1_H11_MR	g507910	BLASTN	389	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2768	GM_76_A1_H11_T7	g507910	BLASTN	423	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2769	GM_76_A1_H12_MR	g1769898	BLASTX	189	2e-27	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2770	GM_76_A2_A03_MR	g3859610	BLASTN	716	3e-25	64	Arabidopsis thaliana BAC T9E19

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2771	GM_76_A2_A04_T7	g2627181	BLASTX	216	2e-29	83	(D89619) cycloartenol synthase [Pisum sativum]
2772	GM_76_A2_A06_MR	g2583130	BLASTX	185	3e-12	35	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
2773	GM_76_A2_B06_T7	g3319362	BLASTX	204	1e-21	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
2774	GM_76_A2_B07_T7	g507910	BLASTN	581	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2775	GM_76_A2_B10_MR	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2776	GM_76_A2_C03_MR	g3319362	BLASTX	260	2e-20	40	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
2777	GM_76_A2_C05_MR	g2760839	BLASTX	306	1e-25	70	(AC003105) putative receptor kinase [Arabidopsis thaliana]
2778	GM_76_A2_C12_T7	g3641780	BLASTN	398	6e-11	64	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
2779	GM_76_A2_D01_T7	g3924609	BLASTX	251	3e-19	47	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
2780	GM_76_A2_D04_MR	g507910	BLASTN	583	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
2781	GM_76_A2_D06_MR	g3777527	BLASTX	509	1e-46	90	(AF053008) gag-pol polyprotein [Glycine max]
2782	GM_76_A2_D07_MR	g3021268	BLASTX	309	2e-25	57	(AL022347) putative protein [Arabidopsis thaliana]
2783	GM_76_A2_D09_MR	g130582	BLASTX	180	1e-11	36	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
2784	GM_76_A2_D12_MR	g3033375	BLASTX	489	6e-46	64	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2785	GM_76_A2_E02_MR	g742344	BLASTX	169	5e-23	78	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
2786	GM_76_A2_E04_MR	g343938	BLASTN	302	5e-12	70	S receptor kinase [Brassica oleracea]
2787	GM_76_A2_E04_T7	g507910	BLASTN	549	3e-18	79	Yeast (S.cerevisiae) mitochondrial Ser-tRNA and ATPase proteolipid genes.
2788	GM_76_A2_E06_MR	g3777527	BLASTX	827	1e-80	95	Glycine max BSR-101 satellite SB92 genomic sequence.
2789	GM_76_A2_F01_T7	g1504063	BLASTX	107	3e-13	77	(AF053008) gag-pol polyprotein [Glycine max]
2790	GM_76_A2_F02_MR	g3777527	BLASTX	345	4e-29	57	(Y07597) shaggy-like kinase kappa [Arabidopsis thaliana]
2791	GM_76_A2_F05_MR	g3777527	BLASTX	230	4e-18	42	(AF053008) gag-pol polyprotein [Glycine max]
2792	GM_76_A2_F06_T7	g2245136	BLASTX	283	5e-23	77	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]
2793	GM_76_A2_G02_T7	g1769898	BLASTX	179	2e-24	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2794	GM_76_A2_G06_MR	g4050011	BLASTN	408	2e-11	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
2795	GM_76_A2_H04_MR	g818849	BLASTX	244	2e-19	63	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]
2796	GM_76_A2_H06_MR	g100484	BLASTX	395	3e-35	52	hypothetical protein - garden snapdragon

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2797	GM_76_A2_H06_T7	g3176795	BLASTN	466	6e-15	64	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
2798	GM_76_A2_H08_MR	g4063760	BLASTX	299	2e-24	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2799	GM_76_A2_H08_T7	g3777527	BLASTX	554	2e-51	92	(AF053008) gag-pol polypeptide [Glycine max]
2800	GM_76_A2_H11_MR	g507910	BLASTN	409	7e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2801	GM_76_A2_H12_T7	g3097320	BLASTN	564	2e-18	75	Glycine max gene for Bd 30K, complete cds
2802	GM_76_B1_A01_T7	g507910	BLASTN	738	1e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
2803	GM_76_B1_A03_MR	g465535	BLASTX	148	2e-09	41	HYPOTHEICAL 32.7 KD PROTEIN IN NTH2-COO1 INTERGENIC REGION gi 626491 pir S44561 hypothetical protein YBR002c - yeast (Saccharomyces cerevisiae) gi 403317 (Z26494) unknown [Saccharomyces cerevisiae] gi 536188 (Z35871) ORF YBR002c [Saccharomyces cerevisiae] gi 1582565 prf 2118405F ORF YBR0107 [Saccharomyces cerevisiae]
2804	GM_76_B1_A06_MR	g507910	BLASTN	339	1e-08	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2805	GM_76_B1_A06_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2806	GM_76_B1_A07_MR	g2129618	BLASTX	154	3e-13	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] (U76261) unknown [Hordeum vulgare]
2807	GM_76_B1_A09_T7	g1666236	BLASTX	209	4e-16	33	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9
2808	GM_76_B1_A10_MR	g2696018	BLASTN	382	3e-10	67	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
2809	GM_76_B1_A10_T7	g4092471	BLASTN	420	6e-12	62	Human fragile site locus (FRA16B) minisatellite repeat (D63999) hypothetical protein [Synecocystis sp.] (AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana] (AF059674) putative gag protein [Nicotiana tabacum]
2810	GM_76_B1_B01_MR	g1840106	BLASTN	276	8e-10	62	Glycine max BSR-101 satellite SB92 genomic sequence.
2811	GM_76_B1_B01_T7	g1001478	BLASTX	208	1e-15	51	(Y07597) shaggy-like kinase kappa [Arabidopsis thaliana]
2812	GM_76_B1_B03_MR	g3810596	BLASTX	301	8e-25	53	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) gi 484529 pir JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa gi 166412 (L01660) NADH-glutamate synthase [Medicago sativa]
2813	GM_76_B1_B12_MR	g3930515	BLASTX	112	1e-10	45	G.max gene for catalase
2814	GM_76_B1_C01_T7	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2815	GM_76_B1_C03_T7	g1504063	BLASTX	173	4e-23	93	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
2816	GM_76_B1_C05_T7	g417073	BLASTX	184	8e-12	91	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
2817	GM_76_B1_C10_T7	g18559	BLASTN	793	6e-29	74	
2818	GM_76_B1_D01_T7	g507910	BLASTN	357	2e-09	70	
2819	GM_76_B1_D02_T7	g3924609	BLASTX	236	6e-19	47	
2820	GM_76_B1_D03_T7	g99922	BLASTX	532	2e-50	63	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2821	GM_76_B1_D06_T7	g3142328	BLASTN	1203	1e-47	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence [Arabidopsis thaliana]
2822	GM_76_B1_D12_T7	g1769897	BLASTX	189	3e-13	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2823	GM_76_B1_E03_MR	g507910	BLASTN	386	8e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2824	GM_76_B1_E03_T7	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2825	GM_76_B1_E04_MR	g2791289	BLASTX	186	2e-12	36	(AJ000387) protease [Drosophila melanogaster]
2826	GM_76_B1_E05_T7	g4063760	BLASTX	488	1e-44	63	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
2827	GM_76_B1_F02_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2828	GM_76_B1_F05_T7	g1769898	BLASTX	142	3e-28	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2829	GM_76_B1_F06_T7	g905360	BLASTN	1100	2e-43	93	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
2830	GM_76_B1_F09_T7	g1778843	BLASTN	424	3e-12	66	Dictyostelium discoideum LimA (limA) mRNA, partial cds
2831	GM_76_B1_G01_T7	g2921208	BLASTN	384	2e-10	63	Perilla frutescens beta-ketoacyl-ACP synthase 1 (KAS I) mRNA, complete cds
2832	GM_76_B1_G02_MR	g1769898	BLASTX	341	1e-29	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2833	GM_76_B1_G04_T7	g2443320	BLASTX	326	3e-27	42	(D85597) polyprotein [Oryza australiensis]
2834	GM_76_B1_G09_MR	g2129618	BLASTX	167	2e-10	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2835	GM_76_B1_G10_MR	g1369835	BLASTN	368	1e-09	66	Homo sapiens chromosome-19 36.3-kbp cosmid T7501, with 3 regions of similarity to olfactory receptor protein genes.
2836	GM_76_B1_G10_T7	g2642433	BLASTX	149	1e-08	33	(AC002391) putative receptor protein kinase [Arabidopsis thaliana]
2837	GM_76_B1_G12_MR	g507910	BLASTN	647	1e-22	86	Glycine max BSR-101 satellite SB92 genomic sequence.
2838	GM_76_B1_G12_T7	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
2839	GM_76_B1_H01_T7	g18559	BLASTN	1063	3e-41	81	G.max gene for catalase
2840	GM_76_B1_H08_T7	g905361	BLASTX	416	7e-38	92	(U22103) gag-protease polyprotein [Glycine max]
2841	GM_76_B1_H11_MR	g1030731	BLASTX	228	6e-17	37	(X14037) polyprotein [Drosophila melanogaster]
2842	GM_76_B2_A02_MR	g1335862	BLASTX	163	7e-23	75	(U42608) clathrin heavy chain [Glycine max]
2843	GM_76_B2_A07_MR	g4160362	BLASTN	357	4e-09	62	Saccharomyces cerevisiae complete mitochondrial genome
2844	GM_76_B2_A10_T7	g4063760	BLASTX	247	7e-19	42	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
2845	GM_76_B2_B04_MR	g3645899	BLASTX	229	4e-26	46	(U68408) 5' end not determined experimentally [Zea mays]
2846	GM_76_B2_B07_T7	g905361	BLASTX	370	9e-33	89	(U22103) gag-protease polyprotein [Glycine max]
2847	GM_76_B2_B08_T7	g3979928	BLASTN	349	1e-08	61	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
2848	GM_76_B2_B09_MR	g3097320	BLASTN	1320	9e-53	83	Glycine max gene for Bd 30K, complete cds
2849	GM_76_B2_C08_MR	g387902	BLASTX	183	2e-13	44	(L23524) ORF [Hordeum vulgare]
2850	GM_76_B2_C08_T7	g4006831	BLASTX	191	7e-13	40	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
2851	GM_76_B2_C12_MR	g2129618	BLASTX	241	2e-18	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
2852	GM_76_B2_D06_T7	g3779020	BLASTN	397	7e-11	63	Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence [Arabidopsis thaliana]
2853	GM_76_B2_D11_T7	g3097320	BLASTN	459	9e-14	78	Glycine max gene for Bd 30K, complete cds
2854	GM_76_B2_E05_T7	g3171875	BLASTN	396	7e-11	62	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylamine Monooxygenase (N-Oxide 3, EC 1.14.1.1))
2855	GM_76_B2_F06_MR	g3777526	BLASTN	369	1e-09	81	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
2856	GM_76_B2_F08_T7	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence, hypothetical protein - garden snapdragon
2857	GM_76_B2_E09_T7	g100484	BLASTX	329	4e-28	56	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
2858	GM_76_B2_F10_T7	g340798	BLASTN	337	3e-09	63	Glycine max BSR-101 satellite SB92 genomic sequence.
2859	GM_76_B2_F02_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2860	GM_76_B2_F02_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2861	GM_76_B2_F07_MR	g4063760	BLASTX	168	2e-10	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2862	GM_76_B2_F09_MR	g2262105	BLASTX	191	3e-13	78	(AC002343) unknown protein [Arabidopsis thaliana]
2863	GM_76_B2_F09_T7	g2065531	BLASTX	447	2e-41	67	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
2864	GM_76_B2_F10_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2865	GM_76_B2_F10_T7	g507910	BLASTN	407	9e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2866	GM_76_B2_G01_MR	g507910	BLASTN	371	4e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2867	GM_76_B2_G01_T7	g507910	BLASTN	371	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2868	GM_76_B2_G03_MR	g507910	BLASTN	563	8e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
2869	GM_76_B2_G04_T7	g3785980	BLASTX	181	2e-15	38	Glycine max BSR-101 satellite SB92 genomic sequence.
2870	GM_76_B2_G06_MR	g14237	BLASTN	412	1e-12	62	(AC005560) hypothetical protein [Arabidopsis thaliana]
2871	GM_76_B2_G09_MR	g3643603	BLASTX	260	2e-20	49	Yeast mitochondrial gene fragment of tRNA synthesis locus (D273-10B)
2872	GM_76_B2_H01_T7	g2894496	BLASTN	366	2e-09	60	(AC005395) unknown protein [Arabidopsis thaliana]
2873	GM_76_B2_H05_MR	g4063760	BLASTX	201	6e-14	42	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-103, complete sequence [Plasmodium falciparum]
2874	GM_76_B2_H08_MR	g3550435	BLASTN	445	4e-13	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2875	GM_76_B2_H08_T7	g507910	BLASTN	662	3e-23	85	Hordeum vulgare Hotr1 gene
2876	GM_76_B2_H11_MR	g130582	BLASTX	204	3e-14	39	Glycine max BSR-101 satellite SB92 genomic sequence.
2877	GM_77_A1_A03_T7	g507910	BLASTN	607	8e-21	81	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2878	GM_77_A1_A05_MR	g2497540	BLASTX	361	2e-32	64	PYRUVATE KINASE, CHLOROPLAST ISOZYME G (AB007466) reverse transcriptase-like protein [Vicia faba]
2879	GM_77_A1_A06_T7	g2522228	BLASTX	327	9e-29	52	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence
2880	GM_77_A1_B02_T7	g2979597	BLASTN	382	3e-10	60	[Homo sapiens]
2881	GM_77_A1_B03_T7	g99730	BLASTX	196	4e-30	53	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
2882	GM_77_A1_B04_T7	g1769898	BLASTX	289	5e-24	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2883	GM_77_A1_B07_MR	g2995405	BLASTX	330	5e-28	48	(Y12432) polyprotein [Ananas comosus]
2884	GM_77_A1_B11_T7	g2961378	BLASTX	177	6e-23	53	(AL022141) putative protein [Arabidopsis thaliana]
2885	GM_77_A1_C07_MR	g1666236	BLASTX	159	2e-10	29	(U76261) unknown [Hordeum vulgare]
2886	GM_77_A1_C09_MR	g4038056	BLASTX	351	3e-30	53	(AC005897) putative transposon [Arabidopsis thaliana]
2887	GM_77_A1_C10_T7	g18559	BLASTN	403	3e-11	71	G.max gene for catalase
2888	GM_77_A1_D01_MR	g2129618	BLASTX	127	2e-12	52	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2889	GM_77_A1_D03_MR	g3599418	BLASTN	1007	1e-38	83	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
2890	GM_77_A1_D05_MR	g421954	BLASTX	239	4e-31	48	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
2891	GM_77_A1_D05_T7	g3319351	BLASTX	277	5e-22	40	(AF077407) contains similarity to reverse transcriptases (PF:am: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
2892	GM_77_A1_D07_MR	g2829887	BLASTX	351	2e-30	50	(AC002396) Hypothetical protein [Arabidopsis thaliana]
2893	GM_77_A1_D07_T7	g2760319	BLASTX	85	2e-10	76	(AC002130) F1N21.3 [Arabidopsis thaliana]
2894	GM_77_A1_D09_MR	g4063756	BLASTN	361	3e-09	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
2895	GM_77_A1_E02_MR	g2969943	BLASTN	377	5e-10	64	Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS
2896	GM_77_A1_E06_T7	g4063760	BLASTX	231	4e-17	46	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
2897	GM_77_A1_E09_MR	g3319345	BLASTX	151	9e-09	29	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
2898	GM_77_A1_E10_T7	g4092471	BLASTN	536	4e-17	70	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
2899	GM_77_A1_F01_T7	g507910	BLASTN	404	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2900	GM_77_A1_F06_MR	g2764526	BLASTN	450	3e-13	62	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
2901	GM_77_A1_F10_MR	g1142701	BLASTN	235	1e-09	78	Glycine max satellite STR120-A.3.
2902	GM_77_A1_F11_MR	g507910	BLASTN	420	2e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2903	GM_77_A1_F12_T7	g3097320	BLASTN	438	9e-13	69	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2904	GM_77_A1_G02_MR	g170029	BLASTN	418	7e-12	82	Glycine max cv. Dare nodulin 26 gene fragment.
2905	GM_77_A1_G03_T7	g4049647	BLASTN	270	3e-09	64	Melanoplus sanguinipes entomopoxvirus, complete genome
2906	GM_77_A1_G04_T7	g3985949	BLASTN	412	1e-11	69	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone; Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; MOB24, complete sequence [Arabidopsis thaliana]
2907	GM_77_A1_G05_T7	g1666236	BLASTX	234	6e-19	32	(U76261) unknown [Hordeum vulgare]
2908	GM_77_A1_G06_MR	g3142328	BLASTN	1110	2e-43	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2909	GM_77_A1_G08_MR	g3869075	BLASTN	405	3e-11	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; MXK3, complete sequence [Arabidopsis thaliana]
2910	GM_77_A1_G09_MR	g3097320	BLASTN	422	4e-12	71	Glycine max gene for Bd 30K, complete cds
2911	GM_77_A1_G10_MR	g3063691	BLASTX	273	3e-22	56	(AL022537) putative protein [Arabidopsis thaliana]
2912	GM_77_A1_G11_MR	g3513745	BLASTX	169	2e-10	27	(AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
2913	GM_77_A1_H02_MR	g226407	BLASTX	250	4e-19	43	retrotransposon del1-46 [Lilium henryi]
2914	GM_77_A1_H04_T7	g13583	BLASTN	353	4e-09	64	Yeast mitochondrial ori(o) repeat unit of petite mutant 5 (petite strain s-10/7/2)
2915	GM_77_A1_H05_MR	g3142328	BLASTN	1232	6e-49	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2916	GM_77_A1_H06_MR	g3599418	BLASTN	377	5e-10	66	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
2917	GM_77_A1_H07_MR	g4063760	BLASTX	153	7e-09	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2918	GM_77_A1_H08_MR	g18559	BLASTN	337	8e-11	76	G max gene for catalase
2919	GM_77_A1_H09_T7	g3881505	BLASTX	231	5e-18	43	(Z47357) similar to the mouse hypothetical protein D15Kz1 (PIR accession number A30222); cDNA EST EMBL:C08599 comes from this gene; cDNA EST EMBL:C07385 comes from this gene; cDNA E...
2920	GM_77_A1_H10_MR	g507910	BLASTN	352	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2921	GM_77_A1_H10_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2922	GM_77_A1_H11_MR	g4038030	BLASTX	429	6e-39	73	(AC005936) putative protein kinase, 5' partial [Arabidopsis thaliana]
2923	GM_77_A2_A02_MR	g454847	BLASTN	435	1e-12	74	Glycine max ribosomal protein S11 gene, complete cds
2924	GM_77_A2_A03_T7	g975634	BLASTN	345	5e-09	65	Dictyostelium discoideum DDCCOF1 gene for cofilin, complete cds (exon1-2)
2925	GM_77_A2_A09_MR	g3645899	BLASTX	339	2e-33	61	(U68408) 5' end not determined experimentally [Zea mays]
2926	GM_77_A2_B04_T7	g507910	BLASTN	455	6e-14	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2927	GM_77_A2_B09_T7	g3097320	BLASTN	693	2e-24	75	Glycine max gene for Bd 30K, complete cds
2928	GM_77_A2_C01_T7	g2522227	BLASTX	216	5e-17	38	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2929	GM_77_A2_C05_MR	g2579860	BLASTN	342	3e-09	60	Homo sapiens genomic DNA, 21q region, clone: S39BG29

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2930	GM_77_A2_D01_MR	g1262440	BLASTX	230	1e-34	79	(U26457) lipoxigenase [Glycine max]
2931	GM_77_A2_D02_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2932	GM_77_A2_D05_MR	g3777527	BLASTX	269	5e-21	91	(AF053008) gag-pol polyprotein [Glycine max]
2933	GM_77_A2_D07_MR	g2809249	BLASTX	170	5e-11	33	(AC002560) F21B7.18 [Arabidopsis thaliana]
2934	GM_77_A2_D10_MR	g4038056	BLASTX	316	2e-26	42	(AC005897) putative transposon [Arabidopsis thaliana]
2935	GM_77_A2_E01_MR	g3930515	BLASTX	116	3e-10	36	(AF059674) putative gag protein [Nicotiana tabacum]
2936	GM_77_A2_E02_T7	g507910	BLASTN	524	5e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
2937	GM_77_A2_E05_MR	g3281868	BLASTX	148	2e-10	81	Glycine max BSR-101 satellite SB92 genomic sequence.
2938	GM_77_A2_E08_MR	g320565	BLASTX	151	9e-14	48	(AL031004) putative protein [Arabidopsis thaliana]
2939	GM_77_A2_F08_MR	g905361	BLASTX	160	6e-10	31	transposon TAI-1 KAS-1 - Arabidopsis thaliana (fragment)
2940	GM_77_A2_G02_MR	g507910	BLASTN	380	1e-10	73	(U22103) gag-protease polyprotein [Glycine max]
2941	GM_77_A2_G02_T7	g507910	BLASTN	506	3e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence.
2942	GM_77_A2_G03_T7	g454847	BLASTN	497	2e-15	66	Glycine max BSR-101 satellite SB92 genomic sequence.
2943	GM_77_A2_G04_T7	g2129618	BLASTX	174	3e-11	30	Glycine max ribosomal protein S11 gene, complete cds
							hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila
							gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2944	GM_77_A2_G05_MR	g18559	BLASTN	837	6e-31	74	G.max gene for catalase
2945	GM_77_A2_G05_T7	g3171875	BLASTN	353	7e-09	60	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavon-containing Monoxygenase 2 and Flavon-containing Monoxygenase 3 (Dimethylamine Monoxygenase (N-Oxide 3, EC1.14.1... (U76261) unknown [Hordeum vulgare]
2946	GM_77_A2_G06_MR	g1666236	BLASTX	197	1e-14	32	paramecium species 4.51b mt dna dimer: replication init. region, clone-1.
2947	GM_77_A2_G09_MR	g342954	BLASTN	362	4e-10	62	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
2948	GM_77_A2_G10_MR	g3738114	BLASTN	468	4e-14	62	Glycine max BSR-101 satellite SB92 genomic sequence.
2949	GM_77_A2_H01_MR	g507910	BLASTN	391	5e-11	72	Glycine max gene for Bd 30K, complete cds
2950	GM_77_A2_H03_T7	g3097320	BLASTN	1064	4e-41	79	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
2951	GM_77_A2_H05_MR	g3513747	BLASTX	183	7e-12	32	Glycine max BSR-101 satellite SB92 genomic sequence.
2952	GM_77_A2_H06_MR	g507910	BLASTN	436	4e-13	74	(AF053008) gag-pol polyprotein [Glycine max]
2953	GM_77_A2_H06_T7	g3777527	BLASTX	238	8e-18	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2954	GM_77_A2_H09_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2955	GM_77_A2_H09_T7	g507910	BLASTN	469	1e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
2956	GM_77_B1_A05_MR	g507910	BLASTN	367	6e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2957	GM_77_B1_A05_T7	g507910	BLASTN	348	4e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
2958	GM_77_B1_A11_T7	g3377855	BLASTX	181	4e-26	73	(AF076274) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zfc.CCHC.hmm, score: 14.43) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2959	GM_77_B1_B07_MR	g905361	BLASTX	235	5e-18	35	(U22103) gag-protease polypeptide [Glycine max]
2960	GM_77_B1_B10_T7	g4063760	BLASTX	374	2e-34	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2961	GM_77_B1_C03_MR	g2995405	BLASTX	186	3e-22	51	(Y12432) polypeptide [Ananas comosus]
2962	GM_77_B1_C08_MR	g1055224	BLASTX	140	6e-09	39	(U20977) cellular nucleic acid binding protein [Xenopus laevis]
2963	GM_77_B1_C10_MR	g2996647	BLASTN	356	5e-09	61	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
2964	GM_77_B1_D01_T7	g170606	BLASTN	885	8e-34	68	Broad bean (V. faba) BamHI repetitive element, 1750 bp family.
2965	GM_77_B1_D03_T7	g18559	BLASTN	1460	3e-59	87	G.max gene for catalase
2966	GM_77_B1_D11_MR	g1666236	BLASTX	163	7e-11	30	(U76261) unknown [Hordeum vulgare]
2967	GM_77_B1_F02_T7	g1666236	BLASTX	172	7e-12	31	(U76261) unknown [Hordeum vulgare]
2968	GM_77_B1_F03_MR	g1666236	BLASTX	167	2e-14	35	(U76261) unknown [Hordeum vulgare]
2969	GM_77_B1_E11_MR	g3738114	BLASTN	361	3e-09	60	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
2970	GM_77_B1_F01_MR	g2580584	BLASTX	224	1e-17	47	(AF000976) 7-O-methyltransferase [Medicago sativa]
2971	GM_77_B1_F02_T7	g1769898	BLASTX	189	2e-18	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2972	GM_77_B1_F03_T7	g3779021	BLASTX	98	6e-09	36	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
2973	GM_77_B1_F05_MR	g3777527	BLASTX	516	6e-69	95	(AF053008) gag-pol polypeptide [Glycine max]
2974	GM_77_B1_F09_MR	g461735	BLASTX	146	1e-18	96	MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR gi 478785 pir S29315 chaperonin 60 - cucurbit gi 12544 gnl PID e1188585 (X70867) chaperonin 60 [Cucurbita sp.]
2975	GM_77_B1_F09_T7	g3738337	BLASTX	101	5e-09	33	(AC005170) putative reverse transcriptase [Arabidopsis thaliana]
2976	GM_77_B1_F12_T7	g3777527	BLASTX	385	2e-33	87	(AF053008) gag-pol polypeptide [Glycine max]
2977	GM_77_B1_G04_MR	g3560029	BLASTN	434	9e-13	65	Schistosoma intercalatum ribosomal intergenic spacer DNA (2169 bp)
2978	GM_77_B1_G11_T7	g507910	BLASTN	364	8e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2979	GM_77_B1_G12_MR	g3777527	BLASTX	718	6e-69	91	(AF053008) gag-pol polypeptide [Glycine max]
2980	GM_77_B1_G12_T7	g2996647	BLASTN	379	4e-10	61	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
2981	GM_77_B1_H01_T7	g18559	BLASTN	710	4e-25	73	G.max gene for catalase
2982	GM_77_B1_H09_T7	g2522226	BLASTN	599	3e-20	67	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
2983	GM_77_B2_A03_T7	g2511590	BLASTX	268	2e-22	86	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] gi 3421111
2984	GM_77_B2_A07_MR	g2522227	BLASTX	175	2e-12	52	(AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]
2985	GM_77_B2_A10_T7	g3142328	BLASTN	598	2e-43	78	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
							Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2986	GM_77_B2_B05_T7	g3176806	BLASTN	347	1e-09	61	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
2987	GM_77_B2_B09_T7	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2988	GM_77_B2_B10_MR	g100484	BLASTX	212	2e-15	49	hypothetical protein - garden snapdragon
2989	GM_77_B2_B11_T7	g3142328	BLASTN	628	2e-21	69	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (L22847) HAHB-1 [Helianthus annuus]
2990	GM_77_B2_C03_T7	g349379	BLASTX	186	1e-13	56	(L03710) cnjB [Tetrahymena thermophila] gi 737494 prf 1922371A
2991	GM_77_B2_C04_T7	g161752	BLASTX	153	1e-08	28	cnjB gene [Tetrahymena thermophila]
2992	GM_77_B2_D01_T7	g507910	BLASTN	356	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2993	GM_77_B2_D05_T7	g507910	BLASTN	584	9e-20	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2994	GM_77_B2_D10_T7	g1769897	BLASTX	442	2e-48	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2995	GM_77_B2_E06_T7	g3097320	BLASTN	360	3e-09	64	Glycine max gene for Bd 30K, complete cds
2996	GM_77_B2_E12_MR	g507910	BLASTN	428	1e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence
2997	GM_77_B2_E12_T7	g507910	BLASTN	411	6e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2998	GM_77_B2_F01_T7	g3810596	BLASTX	271	1e-21	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2999	GM_77_B2_F02_T7	g3947433	BLASTN	354	6e-09	60	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
3000	GM_77_B2_F06_MR	g2316016	BLASTX	159	2e-09	47	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
3001	GM_77_B2_F11_T7	g2522230	BLASTX	289	1e-24	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
3002	GM_77_B2_F12_MR	g1813979	BLASTX	145	2e-09	70	(Y10860) hypothetical protein [Musa acuminata]
3003	GM_77_B2_G09_T7	g507910	BLASTN	378	2e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3004	GM_77_B2_G12_T7	g1524103	BLASTN	392	1e-10	63	Human DNA sequence from cosmid U223G7, between markers DXS6791 and DXS8038 on chromosome X
3005	GM_77_B2_H02_T7	g3080423	BLASTX	384	1e-33	53	(AL022604) putative protein [Arabidopsis thaliana]
3006	GM_77_B2_H08_T7	g2367675	BLASTX	202	3e-14	33	(AF017040) Pol [Dictyostelium discoideum]
3007	GM_77_B2_H12_T7	g2764526	BLASTN	566	1e-18	62	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
3008	GM_78_A1_A02_MR	g2367675	BLASTX	171	7e-11	35	(AF017040) Pol [Dictyostelium discoideum]
3009	GM_78_A1_A02_T7	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3010	GM_78_A1_A03_MR	g2443320	BLASTX	173	8e-12	46	(D85597) polyprotein [Oryza australiensis]
3011	GM_78_A1_A05_MR	g2997694	BLASTX	199	3e-15	42	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
3012	GM_78_A1_A08_MR	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
3013	GM_78_A1_A09_T7	g1514643	BLASTX	134	2e-10	50	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
3014	GM_78_A1_B01_MR	g100484	BLASTX	338	5e-29	62	hypothetical protein - garden snapdragon
3015	GM_78_A1_B02_T7	g226407	BLASTX	538	8e-50	62	retrotransposon del1-46 [Lilium henryi]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3016	GM_78_A1_B09_T7	g3930515	BLASTX	126	1e-10	45	(AF059674) putative gag protein [Nicotiana tabacum]
3017	GM_78_A1_C02_MR	g3142328	BLASTN	1166	7e-46	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3018	GM_78_A1_C06_MR	g170602	BLASTN	453	2e-14	64	Broad bean (V.faba) BamHI repetitive element, 900 bp family.
3019	GM_78_A1_E01_T7	g507910	BLASTN	358	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3020	GM_78_A1_E02_T7	g1666236	BLASTX	170	1e-11	29	(U76261) unknown [Hordeum vulgare]
3021	GM_78_A1_F01_MR	g1769899	BLASTX	203	1e-15	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3022	GM_78_A1_G07_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3023	GM_78_A1_H01_MR	g1431738	BLASTN	466	3e-14	90	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
3024	GM_78_A1_H12_MR	g2997694	BLASTX	166	1e-11	34	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
3025	GM_78_A2_A02_MR	g1076763	BLASTX	157	1e-11	38	AWJL218 protein - wheat gi 551212 (X81369) AWJL218 gene product [Triticum aestivum]
3026	GM_78_A2_A02_T7	g3033389	BLASTX	180	7e-12	32	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
3027	GM_78_A2_A03_MR	g507910	BLASTN	595	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3028	GM_78_A2_A06_MR	g1142703	BLASTN	261	5e-13	75	Glycine max satellite STR120-B.1.
3029	GM_78_A2_A06_T7	g2995405	BLASTX	253	1e-19	52	(Y12432) polyprotein [Ananas comosus]
3030	GM_78_A2_A08_MR	g3097320	BLASTN	690	3e-24	75	Glycine max gene for Bd 30K, complete cds
3031	GM_78_A2_A09_MR	g4063760	BLASTX	353	3e-30	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3032	GM_78_A2_A10_MR	g1666236	BLASTX	189	9e-14	30	(U76261) unknown [Hordeum vulgare]
3033	GM_78_A2_A10_T7	g905361	BLASTX	546	6e-52	86	(U22103) gag-protease polyprotein [Glycine max]
3034	GM_78_A2_B02_MR	g18559	BLASTN	981	2e-37	77	G,max gene for catalase
3035	GM_78_A2_B05_MR	g3452140	BLASTX	143	3e-09	36	(AJ004901) resistance protein [Glycine max]
3036	GM_78_A2_B05_T7	g742339	BLASTX	137	2e-20	58	S receptor kinase [Brassica oleracea]
3037	GM_78_A2_B07_T7	g3820757	BLASTN	344	1e-08	61	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
3038	GM_78_A2_B08_MR	g4115922	BLASTX	155	4e-09	40	(AF118222) contains similarity to ubiquitin carboxyl-terminal hydrolase family 2 (Pfam:PF00443, score=48.3, E=3.5e-13, N=2) and (Pfam:PF00442, Score=40.0 E=5.2e-08, N=1) [Arabidopsis thaliana]
3039	GM_78_A2_B10_MR	g3097320	BLASTN	454	2e-13	69	Glycine max gene for Bd 30K, complete cds
3040	GM_78_A2_B11_T7	g1171642	BLASTX	182	1e-14	80	PROBABLE SERINE/THREONINE-PROTEIN KINASE, NAK gi 481206 pir S38326 protein kinase - Arabidopsis thaliana gi 166809 (L07248) protein kinase [Arabidopsis thaliana]
3041	GM_78_A2_B12_MR	g340697	BLASTN	401	2e-11	79	Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA.
3042	GM_78_A2_C01_MR	g507910	BLASTN	389	6e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
3043	GM_78_A2_C03_MR	g2129618	BLASTX	183	3e-12	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3044	GM_78_A2_C08_MR	g2129618	BLASTX	157	2e-09	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3045	GM_78_A2_D02_MR	g4090200	BLASTX	173	3e-12	74	(AJ012310) WUSCHEL protein [Arabidopsis thaliana]
3046	GM_78_A2_D03_T7	g3540186	BLASTX	113	3e-13	72	(AC004122) Hypothetical protein [Arabidopsis thaliana]
3047	GM_78_A2_D06_MR	g507910	BLASTN	541	8e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3048	GM_78_A2_D11_T7	g2264320	BLASTN	356	5e-09	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
3049	GM_78_A2_E06_T7	g18559	BLASTN	349	9e-09	72	G max gene for catalase
3050	GM_78_A2_F07_MR	g3142328	BLASTN	1996	7e-84	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
3051	GM_78_A2_E07_T7	g2129618	BLASTX	182	4e-12	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3052	GM_78_A2_F10_MR	g1142702	BLASTN	265	1e-12	73	Glycine max satellite STR120-A.4.
3053	GM_78_A2_F02_T7	g507910	BLASTN	668	1e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
3054	GM_78_A2_F03_T7	g3777527	BLASTX	239	3e-20	44	(AF053008) gag-pol polyprotein [Glycine max]
3055	GM_78_A2_F09_MR	g4038056	BLASTX	339	6e-29	51	(AC005897) putative transposon [Arabidopsis thaliana]
3056	GM_78_A2_F10_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3057	GM_78_A2_F10_T7	g507910	BLASTN	458	4e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
3058	GM_78_A2_G01_MR	g4039114	BLASTN	654	1e-22	67	Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds
3059	GM_78_A2_G02_MR	g4063760	BLASTX	430	2e-38	61	Glycine max 561 putative POL3 protein [Arabidopsis thaliana]
3060	GM_78_A2_G08_MR	g3377834	BLASTX	210	3e-15	36	(AF075598) No definition line found [Arabidopsis thaliana]
3061	GM_78_A2_H05_MR	g871468	BLASTN	357	3e-09	89	H. annuus mitochondrion genes trnH and trnE
3062	GM_78_A2_H08_T7	g2129618	BLASTX	225	1e-16	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3063	GM_78_A2_H09_T7	g133750	BLASTX	196	3e-28	81	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 gi 320170 pir A26574 ribosomal protein S12 - soybean chloroplast gi 11572 (X05013) rps12 [Glycine max]
3064	GM_78_A2_H11_MR	g4063770	BLASTX	169	8e-11	44	(AB004906) transposase [Ipomoea purpurea]
3065	GM_78_A2_H12_T7	g4063760	BLASTX	172	6e-11	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3066	GM_78_B1_A07_T7	g507910	BLASTN	342	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3067	GM_78_B1_B09_T7	g2522228	BLASTX	395	2e-38	73	(AB007466) reverse transcriptase-like protein [Vicia faba]
3068	GM_78_B1_C05_MR	g3319345	BLASTX	170	8e-11	36	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
3069	GM_78_B1_C05_T7	g3645899	BLASTX	351	4e-30	54	(U68408) 5' end not determined experimentally [Zea mays]
3070	GM_78_B1_C08_T7	g2462058	BLASTX	349	4e-31	49	(Y13389) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
3071	GM_78_B1_C09_MR	g557882	BLASTX	153	4e-14	40	putative serine/threonine protein kinase; similar to product (U13923) putative serine/threonine protein kinase; similar to product encoded by <i>Lycopersicon pimpinellifolium</i> Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family [Solanum pimpinellifolium] gi 1809263 (U59317) serine/threonine protein kinase Fen [Lycopersicon pimpinellifolium] gi 1096880 prf 2112354B Fen gene [Lycopersicon esculentum] gi 1098334 prf 2115395A Fen gene [Lycopersicon esculentum] (AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
3072	GM_78_B1_D02_T7	g2827715	BLASTX	300	1e-24	77	(U66344) calreticulin [Arabidopsis thaliana] Glycine max satellite STR120-A.1. (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba] (AC005561) putative POL.3 protein [Arabidopsis thaliana] (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana] Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana] (AB007466) reverse transcriptase-like protein [Vicia faba] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U95973) BRCA1-associated RING domain protein isolog [Arabidopsis thaliana] HEAT SHOCK PROTEIN 82 gi 100685 pir S25541 heat shock protein 82 - rice (strain Taichung Native One) gi 20256 (Z11920) heat shock protein 82 (HSP82) [Oryza sativa] (AF053008) gag-pol polyprotein [Glycine max] Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. (AC005897) putative transposon [Arabidopsis thaliana] (U22103) gag-protease polyprotein [Glycine max] (AC005561) putative POL.3 protein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. G.max gene for catalase Glycine max BSR-101 satellite SB92 genomic sequence. Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
3073	GM_78_B1_D04_T7	g2052381	BLASTX	197	2e-30	81	
3074	GM_78_B1_D06_MR	g1142699	BLASTN	300	4e-15	71	
3075	GM_78_B1_D10_T7	g2522230	BLASTX	240	1e-19	37	
3076	GM_78_B1_E09_MR	g4063760	BLASTX	211	5e-15	42	
3077	GM_78_B1_E10_T7	g3355308	BLASTX	179	6e-12	40	
3078	GM_78_B1_F05_MR	g3599418	BLASTN	464	5e-14	69	
3079	GM_78_B1_F07_T7	g3319362	BLASTX	321	6e-27	42	
3080	GM_78_B1_G04_T7	g2522228	BLASTX	236	2e-26	67	
3081	GM_78_B1_G05_MR	g3142328	BLASTN	1636	2e-67	84	
3082	GM_78_B1_H01_MR	g1931654	BLASTX	123	1e-09	50	
3083	GM_78_B1_H02_MR	g417154	BLASTX	171	4e-11	80	
3084	GM_78_B1_H07_MR	g3777527	BLASTX	420	4e-37	50	
3085	GM_78_B1_H08_MR	g507910	BLASTN	402	1e-11	73	
3086	GM_78_B1_H08_T7	g507910	BLASTN	355	2e-09	73	
3087	GM_78_B1_H09_T7	g4038056	BLASTX	263	5e-23	48	
3088	GM_78_B1_H11_MR	g905361	BLASTX	240	1e-18	33	
3089	GM_78_B1_H11_T7	g4063760	BLASTX	179	1e-11	37	
3090	GM_78_B1_H12_T7	g507910	BLASTN	360	1e-09	70	
3091	GM_78_B2_A03_T7	g18559	BLASTN	1112	2e-43	79	
3092	GM_78_B2_A04_MR	g507910	BLASTN	554	2e-18	80	
3093	GM_78_B2_A09_MR	g4092471	BLASTN	528	8e-17	69	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3094	GM_78_B2_A10_MR	g3777527	BLASTX	352	7e-30	75	(AF053008) gag-pol polyprotein [Glycine max]
3095	GM_78_B2_A12_T7	g421955	BLASTX	435	3e-40	50	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
3096	GM_78_B2_B02_MR	g1326016	BLASTX	190	7e-13	40	TY3-2 orfB
3097	GM_78_B2_B09_T7	g507910	BLASTN	446	1e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
3098	GM_78_B2_C02_MR	g3097320	BLASTN	568	1e-18	80	Glycine max gene for Bd 30K, complete cds
3099	GM_78_B2_D10_MR	g132819	BLASTX	153	1e-20	72	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24) gi 71307 pir R5PM24 ribosomal protein L24 precursor, chloroplast - garden pea gi 20873 (X14020) CL24 ribosomal preprotein (AA -39 to 155) [Pisum sativum]
3100	GM_78_B2_D11_T7	g3282159	BLASTN	470	3e-14	60	Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence [Homo sapiens]
3101	GM_78_B2_E07_MR	g3142328	BLASTN	528	6e-17	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3102	GM_78_B2_F05_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3103	GM_78_B2_F05_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3104	GM_78_B2_F10_MR	g905361	BLASTX	418	4e-38	92	(U22103) gag-protease polyprotein [Glycine max]
3105	GM_78_B2_F11_MR	g3142328	BLASTN	628	2e-21	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3106	GM_78_B2_F11_T7	g1142701	BLASTN	256	1e-19	74	Glycine max satellite STR120-A.3.
3107	GM_78_B2_G03_T7	g1769898	BLASTX	334	2e-30	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3108	GM_78_B2_G04_MR	g2462058	BLASTX	251	1e-20	57	(Y13389) reverse transcriptase [Antirrhinum majus]
3109	GM_78_B2_G07_MR	g18559	BLASTN	355	5e-09	69	G.max gene for catalase
3110	GM_78_B2_G07_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3111	GM_78_B2_G10_T7	g2801677	BLASTN	947	1e-36	73	Glycine max telomere-associated sequence STAS6
3112	GM_78_B2_G11_MR	g507910	BLASTN	385	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3113	GM_78_B2_H02_T7	g3776574	BLASTX	231	8e-18	72	(AC005388) Similar to T117.13 gi 2880051 putative protein kinase from Arabidopsis thaliana BAC gb AC002340. [Arabidopsis thaliana]
3114	GM_78_B2_H03_T7	g09922	BLASTX	903	9e-90	78	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3115	GM_78_B2_H04_MR	g507910	BLASTN	377	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3116	GM_78_B2_H06_T7	g2315153	BLASTX	229	7e-31	72	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
3117	GM_78_B2_H08_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3118	GM_78_B2_H08_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
3119	GM_78_B2_H09_T7	g3171875	BLASTN	397	7e-11	65	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavon-containing Monooxygenase 2 and Flavon-containing Monooxygenase 3 (Dimethylamine Monooxygenase (N-Oxide 3, EC1.14.1... S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
3120	GM_79_A2_A02_MR	g12212	BLASTN	1277	4e-52	93	POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229) gi 984314 (U26948) unknown [Glycine max] (AF038649) similar to resistance gene; region between conserved kinase-2 and P-Loop domains [Pinus radiata]
3121	GM_79_A2_A02_T7	g1346258	BLASTX	301	5e-26	80	(AC005561) putative POL3 protein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence.
3122	GM_79_A2_A04_MR	g2708524	BLASTX	211	2e-16	37	(AC005561) putative POL3 protein [Arabidopsis thaliana] (AF017751) resistance protein candidate [Lactuca sativa]
3123	GM_79_A2_A04_T7	g4063760	BLASTX	501	5e-46	65	Glycine max BSR-101 satellite SB92 genomic sequence.
3124	GM_79_A2_A07_MR	g507910	BLASTN	562	9e-19	81	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3125	GM_79_A2_A08_MR	g4063760	BLASTX	238	6e-18	53	(AF017751) resistance protein candidate [Lactuca sativa]
3126	GM_79_A2_B02_MR	g2852684	BLASTX	244	7e-19	48	Glycine max BSR-101 satellite SB92 genomic sequence.
3127	GM_79_A2_B04_T7	g507910	BLASTN	572	3e-19	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3128	GM_79_A2_B05_T7	g3142328	BLASTN	1627	6e-67	93	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Cont...
3129	GM_79_A2_B06_MR	g2769655	BLASTN	554	5e-18	63	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
3130	GM_79_A2_B08_MR	g4092470	BLASTN	561	3e-18	62	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Z97336) retrovirus-related polypeptide homolog [Arabidopsis thaliana]
3131	GM_79_A2_B10_T7	g3142328	BLASTN	528	6e-17	84	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3132	GM_79_A2_C03_MR	g2244802	BLASTX	410	4e-36	53	Human DNA sequence from cosmid U223G7, between markers DXS6791 and DXS8038 on chromosome X
3133	GM_79_A2_C06_T7	g4063760	BLASTX	250	3e-19	66	(AB004906) transposase [Ipomoea purpurea]
3134	GM_79_A2_C09_T7	g1524103	BLASTN	328	3e-09	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3135	GM_79_A2_C10_T7	g4063770	BLASTX	362	2e-31	49	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3136	GM_79_A2_C12_MR	g4063760	BLASTX	241	3e-18	46	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
3137	GM_79_A2_D03_MR	g2522227	BLASTX	146	4e-09	39	gi 542022 pir S39558 HSP90 homolog - Madagascar periwinkle gi 348696 (L14594) heat shock protein 90 [Catharanthus roseus]
3138	GM_79_A2_D05_T7	g462013	BLASTX	100	7e-09	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3139	GM_79_A2_D10_T7	g507910	BLASTN	582	1e-19	81	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3140	GM_79_A2_E03_T7	g4063760	BLASTX	400	3e-35	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3141	GM_79_A2_E07_MR	g2864621	BLASTX	121	1e-10	42	hypothetical protein [Arabidopsis thaliana]
3142	GM_79_A2_E08_T7	g2407790	BLASTX	192	2e-13	39	(AF019910) grr1 [Glycine max]
3143	GM_79_A2_E10_MR	g2828773	BLASTN	352	7e-09	63	Homo sapiens chromosome 17, clone hRPC.18_F_17, complete sequence [Homo sapiens]
3144	GM_79_A2_F09_MR	g2129618	BLASTX	192	4e-13	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3145	GM_79_A2_F09_T7	g3319362	BLASTX	268	3e-22	52	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
3146	GM_79_A2_F10_T7	g1769898	BLASTX	135	7e-12	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3147	GM_79_A2_F11_MR	g507910	BLASTN	529	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
3148	GM_79_A2_G07_MR	g2289010	BLASTX	171	3e-12	82	(AC002335) FKBP type peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]
3149	GM_79_A2_G11_MR	g3779026	BLASTX	352	5e-30	51	(AC005171) putative retrotransposon [Arabidopsis thaliana]
3150	GM_79_A2_H01_MR	g18559	BLASTN	296	5e-09	76	G-max gene for catalase
3151	GM_79_A2_H03_MR	g905361	BLASTX	749	2e-73	92	(U22103) gag-protease polypeptide [Glycine max]
3152	GM_79_B2_A03_T7	g2642431	BLASTX	157	4e-19	56	(AC002391) putative retrotransposon polypeptide [Arabidopsis thaliana]
3153	GM_79_B2_A04_T7	g3777527	BLASTX	219	3e-35	54	(AF053008) gag-pol polypeptide [Glycine max]
3154	GM_79_B2_A06_T7	g3219627	BLASTN	347	2e-09	64	Sesarma windsor 16S rRNA gene, isolate PC1
3155	GM_79_B2_A08_MR	g342964	BLASTN	419	7e-13	63	parametrium species 5.311 mt dna dimer: replication init. region.
3156	GM_79_B2_A11_T7	g3142328	BLASTN	1868	6e-78	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3157	GM_79_B2_B03_T7	g2618603	BLASTN	716	3e-25	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]
3158	GM_79_B2_B10_T7	g3281850	BLASTX	276	1e-22	94	(AL031004) monogalactosyl diacylglycerol synthase - like protein [Arabidopsis thaliana]
3159	GM_79_B2_B11_T7	g18559	BLASTN	417	7e-12	65	G-max gene for catalase
3160	GM_79_B2_C02_MR	g4063760	BLASTX	224	2e-16	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3161	GM_79_B2_C09_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3162	GM_79_B2_C09_T7	g507910	BLASTN	454	7e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3163	GM_79_B2_C11_T7	g3152618	BLASTX	236	2e-18	77	(AC004482) putative pectinesterase [Arabidopsis thaliana] gi 3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]
3164	GM_79_B2_D01_T7	g18559	BLASTN	518	2e-16	68	G-max gene for catalase
3165	GM_79_B2_D02_MR	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3166	GM_79_B2_D02_T7	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3167	GM_79_B2_D03_MR	g3142328	BLASTN	1178	2e-46	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3168	GM_79_B2_E02_MR	g99730	BLASTX	287	5e-24	48	hypothetical protein 3 - Arabidopsis thaliana retrotransposon TAl-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
3169	GM_79_B2_E03_T7	g3645899	BLASTX	239	9e-21	45	(U68408) 5' end not determined experimentally [Zea mays]
3170	GM_79_B2_E06_T7	g4063760	BLASTX	295	5e-24	55	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3171	GM_79_B2_E09_T7	g4063760	BLASTX	163	6e-10	38	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3172	GM_79_B2_E11_MR	g3176806	BLASTN	361	4e-10	62	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
3173	GM_79_B2_E11_T7	g2104945	BLASTN	394	8e-13	70	Glycine max copia-like retrotransposon Tgmr, complete sequence
3174	GM_79_B2_F06_MR	g3097320	BLASTN	1167	8e-46	83	Glycine max gene for Bd 30K, complete cds
3175	GM_79_B2_F11_T7	g22490	BLASTX	187	6e-14	49	(X01380) ORF1 [Zea mays]
3176	GM_79_B2_G04_MR	g4063756	BLASTN	399	6e-11	68	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3177	GM_79_B2_G04_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3178	GM_79_B2_G05_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
3179	GM_79_B2_G06_MR	g2435510	BLASTN	451	2e-13	71	Arabidopsis thaliana BAC TM017A05
3180	GM_79_B2_G06_T7	g2244839	BLASTX	215	9e-16	37	(Z97337) hypothetical protein [Arabidopsis thaliana]
3181	GM_79_B2_G08_MR	g226407	BLASTX	158	3e-09	28	retrotransposon del1-46 [Lilium henryi]
3182	GM_79_B2_G12_MR	g2511590	BLASTX	286	2e-24	88	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] gi 3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]
3183	GM_79_B2_H01_MR	g18559	BLASTN	487	5e-15	75	G-max gene for catalase
3184	GM_79_B2_H03_T7	g507910	BLASTN	437	4e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
3185	GM_79_B2_H04_MR	g4063760	BLASTX	233	5e-19	53	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3186	GM_79_B2_H08_MR	g2522230	BLASTX	287	2e-24	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
3187	GM_79_B2_H08_T7	g1666236	BLASTX	213	1e-16	28	(U76261) unknown [Hordeum vulgare]
3188	GM_79_B2_H11_MR	g3097320	BLASTN	485	6e-15	71	Glycine max gene for Bd 30K, complete cds
3189	GM_80_A1_A02_T7	g4063760	BLASTX	194	3e-13	43	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3190	GM_80_A1_A04_T7	g507910	BLASTN	370	4e-10	77	Glycine max BSR-101 satellite SB92 genomic sequence.
3191	GM_80_A1_A10_T7	g3746069	BLASTX	127	4e-12	32	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
3192	GM_80_A1_A11_MR	g729092	BLASTX	491	4e-46	78	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) gi 477484 pir A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana gi 304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]
3193	GM_80_A1_B04_T7	g3860246	BLASTX	170	9e-12	52	(AC005824) putative reverse transcriptase protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3194	GM_80_A1_B05_T7	g2995405	BLASTX	223	2e-16	45	(Y12432) polyprotein [Ananas comosus]
3195	GM_80_A1_B06_MR	g3513747	BLASTX	190	1e-12	46	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
3196	GM_80_A1_B07_MR	g18559	BLASTN	767	9e-28	78	G.max gene for catalase
3197	GM_80_A1_B07_T7	g507910	BLASTN	418	3e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
3198	GM_80_A1_B10_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3199	GM_80_A1_B10_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3200	GM_80_A1_B11_MR	g729092	BLASTX	523	2e-49	79	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) gi 477484 pir A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana gi 304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]
3201	GM_80_A1_C12_T7	g507910	BLASTN	466	2e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
3202	GM_80_A1_D01_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3203	GM_80_A1_D02_MR	g99922	BLASTX	387	4e-35	73	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3204	GM_80_A1_D03_T7	g3142328	BLASTN	1044	2e-40	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3205	GM_80_A1_D04_MR	g3097320	BLASTN	471	3e-14	70	Glycine max gene for Bd 30K, complete cds
3206	GM_80_A1_D04_T7	g100484	BLASTX	169	7e-11	56	hypothetical protein - garden snapdragon
3207	GM_80_A1_D05_T7	g3859610	BLASTN	450	3e-13	68	Arabidopsis thaliana BAC T9E]9
3208	GM_80_A1_D07_T7	g18559	BLASTN	363	2e-09	72	G.max gene for catalase
3209	GM_80_A1_D09_T7	g4156188	BLASTN	358	4e-09	59	Homo sapiens clone DJ0784G16, complete sequence [Homo sapiens]
3210	GM_80_A1_E02_MR	g2098816	BLASTN	351	8e-09	72	Arabidopsis thaliana BAC F19G10, complete sequence
3211	GM_80_A1_E10_MR	g3777527	BLASTX	243	3e-38	76	(AF053008) gag-pol polyprotein [Glycine max]
3212	GM_80_A1_F01_MR	g2194136	BLASTX	111	5e-11	30	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
3213	GM_80_A1_F03_MR	g2995405	BLASTX	292	7e-24	46	(Y12432) polyprotein [Ananas comosus]
3214	GM_80_A1_F06_MR	g113515	BLASTX	88	4e-09	53	FLORAL HOMEOTIC PROTEIN AGL5 gi 81613 pir E39534 floral homeotic protein AGL5 - Arabidopsis thaliana gi 166596 (M55553) transcription factor [Arabidopsis thaliana]
3215	GM_80_A1_G02_MR	g507910	BLASTN	401	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3216	GM_80_A1_G06_MR	g4063760	BLASTX	175	3e-11	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3217	GM_80_A1_G07_T7	g3810596	BLASTX	192	4e-13	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3218	GM_80_A1_H01_MR	g507910	BLASTN	375	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3219	GM_80_A1_H01_T7	g3777527	BLASTX	726	8e-70	95	(AF053008) gag-pol polyprotein [Glycine max]

3220	GM_80_A1_H02_MR	g4115363	BLASTX	210	4e-15	41	(AC005957) putative disease resistance protein [Arabidopsis thaliana]
3221	GM_80_A1_H02_T7	g4115373	BLASTX	193	3e-13	46	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]
3222	GM_80_A1_H03_MR	g3097320	BLASTN	1031	1e-39	79	Glycine max gene for Bd 30K, complete cds
3223	GM_80_A1_H03_T7	g3142328	BLASTN	1208	8e-48	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Y08010) lectin receptor kinase [Arabidopsis thaliana]
3224	GM_80_A1_H05_MR	g1769898	BLASTX	164	1e-16	34	Glycine max BSR-101 satellite SB92 genomic sequence.
3225	GM_80_A1_H06_MR	g507910	BLASTN	541	8e-18	81	Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1
3226	GM_80_A1_H08_MR	g3790154	BLASTN	360	3e-09	62	Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs ...
3227	GM_80_A2_A07_T7	g3097320	BLASTN	404	3e-11	71	Glycine max gene for Bd 30K, complete cds
3228	GM_80_A2_A10_MR	g4063760	BLASTX	284	7e-23	55	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3229	GM_80_A2_B01_MR	g2529677	BLASTX	100	1e-08	52	(AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]
3230	GM_80_A2_B02_T7	g2586081	BLASTX	186	8e-13	45	(U72725) receptor kinase-like protein [Oryza longistaminata]
3231	GM_80_A2_B03_MR	g4006831	BLASTX	308	2e-25	34	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
3232	GM_80_A2_C04_MR	g2997694	BLASTX	279	1e-23	39	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
3233	GM_80_A2_C07_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3234	GM_80_A2_C07_T7	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3235	GM_80_A2_D06_MR	g3142328	BLASTN	2141	1e-90	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3236	GM_80_A2_E01_T7	g3142328	BLASTN	1024	2e-39	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3237	GM_80_A2_E02_MR	g4164556	BLASTN	381	3e-10	60	Rhizopnephalus sanguineus mitochondrial DNA, complete genome
3238	GM_80_A2_E03_MR	g3914199	BLASTX	168	5e-12	76	OLEOSIN 1 >gi 460803 (X78118) oleosin [Prunus dulcis]
3239	GM_80_A2_E08_MR	g4063760	BLASTX	211	5e-15	55	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3240	GM_80_A2_E10_MR	g14227	BLASTN	405	4e-12	65	Yeast cytochrome c oxidase transcription initiation region subunit 1 (COX1) from mitochondrial DNA
3241	GM_80_A2_E10_T7	g1431738	BLASTN	681	5e-24	83	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
3242	GM_80_A2_F02_MR	g2129618	BLASTX	220	4e-16	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806555 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3243	GM_80_A2_F05_MR	g2832245	BLASTX	162	3e-11	28	(AF031569) hypothetical protein [Zea mays]
3244	GM_80_A2_F06_MR	g4063760	BLASTX	256	7e-20	56	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3245	GM_80_A2_F07_MR	g3097320	BLASTN	1069	2e-41	76	Glycine max gene for Bd 30K, complete cds
3246	GM_80_A2_F09_MR	g320565	BLASTX	205	8e-16	46	transposon TA1-KAS-1 - Arabidopsis thaliana (fragment)
3247	GM_80_A2_F11_MR	g3928086	BLASTX	281	6e-24	52	(AC005770) unknown protein [Arabidopsis thaliana]

3248	GM_80_A2_G01_T7	g13773	BLASTN	474	2e-15	67	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
3249	GM_80_A2_G03_T7	g2522228	BLASTX	344	6e-37	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
3250	GM_80_A2_G04_T7	g3033375	BLASTX	530	3e-50	74	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
3251	GM_80_A2_G08_MR	g507910	BLASTN	481	4e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
3252	GM_80_A2_G08_T7	g507910	BLASTN	431	7e-13	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3253	GM_80_A2_H01_MR	g3645899	BLASTX	282	1e-22	43	(U68408) 5' end not determined experimentally [Zea mays]
3254	GM_80_A2_H03_T7	g507910	BLASTN	343	7e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3255	GM_80_A2_H04_MR	g505129	BLASTN	348	9e-09	63	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
3256	GM_80_A2_H08_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3257	GM_80_A2_H08_T7	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
3258	GM_80_A2_H10_T7	g2764526	BLASTN	358	4e-09	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
3259	GM_80_A2_H11_MR	g100484	BLASTX	406	2e-36	54	hypothetical protein - garden snapdragon
3260	GM_80_B1_A02_T7	g4038056	BLASTX	89	9e-12	65	(AC005897) putative transposon [Arabidopsis thaliana]
3261	GM_80_B1_A04_MR	g1709814	BLASTX	171	5e-11	56	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1 >gi 2147916 pir S73205 photosystem I p700 chlorophyll A apoprotein A1 - Porphyra purpurea chloroplast >gi 1276750 (U38804) Photosystem I p700 chlorophyll A apoprotein A1 [Porphyra purpurea]
3262	GM_80_B1_A10_MR	g2246449	BLASTN	497	2e-15	66	Lycopodium esculentum copia-like retrotransposon ToRTL1.3-hydroxy-3-methylglutaryl CoA reductase 2 (HMG2) gene, complete cds.
3263	GM_80_B1_B07_T7	g905361	BLASTX	120	5e-11	47	(U22103) gag-protease polypeptide [Glycine max]
3264	GM_80_B1_C10_MR	g2995405	BLASTX	229	4e-17	49	(Y12432) polyprotein [Ananas comosus]
3265	GM_80_B1_D01_MR	g3449330	BLASTN	595	8e-20	65	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]
3266	GM_80_B1_D02_T7	g18559	BLASTN	788	1e-28	74	G.max gene for catalase
3267	GM_80_B1_D03_T7	g3319351	BLASTX	292	1e-23	48	(AF077407) contains similarity to reverse transcriptases (PF:am:rvt.hmm, score: 116.22) [Arabidopsis thaliana]
3268	GM_80_B1_D05_MR	g131276	BLASTX	550	2e-52	90	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 72704 pir QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi 11856 (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi 225224 prf 1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

3269	GM_80_B1_D05_T7	g114532	BLASTX	433	5e-40	92	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (V00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum]
3270	GM_80_B1_D07_T7	g3097320	BLASTN	876	1e-32	77	Glycine max gene for Bd 30K, complete cds
3271	GM_80_B1_D11_T7	g13596	BLASTN	353	8e-10	62	Yeast mit DNA for promoter upstream of tRNA-Leu gene 3 *Source: probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
3272	GM_80_B1_D12_T7	g629693	BLASTX	158	4e-10	34	(Y10860) hypothetical protein [Musa acuminata]
3273	GM_80_B1_E02_T7	g1813979	BLASTX	254	4e-21	67	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3274	GM_80_B1_E03_MR	g3142328	BLASTN	1139	1e-44	92	Glycine max BSR-101 satellite SB92 genomic sequence
3275	GM_80_B1_E05_T7	g507910	BLASTN	372	3e-10	72	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID c73215 (X53975) orf 3 [Arabidopsis thaliana]
3276	GM_80_B1_E08_MR	g99730	BLASTX	221	3e-20	55	G.max gene for catalase
3277	GM_80_B1_F08_T7	g18559	BLASTN	946	7e-36	76	Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence
3278	GM_80_B1_F11_MR	g3845097	BLASTN	376	6e-10	64	(U68408) 5' end not determined experimentally [Zea mays]
3279	GM_80_B1_E12_T7	g3645899	BLASTX	207	1e-14	46	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
3280	GM_80_B1_F04_T7	g4115365	BLASTX	318	2e-26	45	Glycine max BSR-101 satellite SB92 genomic sequence
3281	GM_80_B1_G02_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence
3282	GM_80_B1_G04_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence
3283	GM_80_B1_G04_T7	g507910	BLASTN	350	3e-09	69	Glycine max gene for Bd 30K, complete cds
3284	GM_80_B1_G05_MR	g3097320	BLASTN	1195	4e-47	78	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]
3285	GM_80_B1_G05_T7	g2651310	BLASTX	282	3e-23	38	Soybean Tgm6 transposable element 3' end
3286	GM_80_B1_G06_T7	g18768	BLASTN	515	6e-17	68	Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence
3287	GM_80_B1_G12_T7	g3171159	BLASTN	509	6e-16	62	[Homo sapiens]
3288	GM_80_B1_H01_T7	g1171583	BLASTN	529	7e-17	63	P.falciparum complete gene map of plastid-like DNA (IR-A)
3289	GM_80_B1_H04_MR	g4115365	BLASTX	177	2e-11	38	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
3290	GM_80_B1_H04_T7	g507910	BLASTN	372	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence
3291	GM_80_B1_H05_T7	g18559	BLASTN	875	1e-32	75	G.max gene for catalase
3292	GM_80_B1_H07_MR	g3142328	BLASTN	1025	2e-39	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3293	GM_80_B1_H09_T7	g18559	BLASTN	1358	1e-54	81	G.max gene for catalase
3294	GM_80_B1_H10_MR	g2443320	BLASTX	162	7e-15	36	(D85597) polyprotein [Oryza australiensis]

3295	GM_80_B2_A01_T7	g2464864	BLASTX	239	2e-18	37	(Z99707) selenium-binding protein homolog [Arabidopsis thaliana]
3296	GM_80_B2_A02_MR	g4063760	BLASTX	164	5e-10	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3297	GM_80_B2_A02_T7	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3298	GM_80_B2_A03_T7	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3299	GM_80_B2_A04_MR	g3777526	BLASTN	463	6e-14	82	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
3300	GM_80_B2_A05_MR	g2827514	BLASTX	356	3e-31	74	(AL021633) predicted protein [Arabidopsis thaliana]
3301	GM_80_B2_A08_MR	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3302	GM_80_B2_A11_T7	g4038056	BLASTX	303	5e-25	48	(AC005897) putative transposon [Arabidopsis thaliana]
3303	GM_80_B2_A12_T7	g462137	BLASTX	180	1e-24	75	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
3304	GM_80_B2_B03_MR	g2618698	BLASTX	118	2e-11	77	(AC002510) unknown protein [Arabidopsis thaliana]
3305	GM_80_B2_B06_T7	g4063760	BLASTX	453	8e-49	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3306	GM_80_B2_B07_MR	g2522228	BLASTX	377	4e-46	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
3307	GM_80_B2_B09_T7	g3777527	BLASTX	649	1e-61	90	(AF053008) gag-pol polyprotein [Glycine max]
3308	GM_80_B2_B11_T7	g4106061	BLASTX	164	3e-11	45	(AF053318) CCR4-associated factor 1 [Homo sapiens]
3309	GM_80_B2_B12_MR	g507910	BLASTN	405	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
3310	GM_80_B2_C01_T7	g3241935	BLASTN	459	1e-13	64	Arabidopsis thaliana chromosome IV from 19 cM, complete sequence [Arabidopsis thaliana]
3311	GM_80_B2_C04_MR	g3738114	BLASTN	496	2e-15	57	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
3312	GM_80_B2_C05_MR	g507910	BLASTN	645	1e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
3313	GM_80_B2_C09_T7	g3097320	BLASTN	1142	1e-44	83	Glycine max gene for Bd 30K, complete cds
3314	GM_80_B2_C10_T7	g3779030	BLASTX	258	2e-21	39	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
3315	GM_80_B2_D01_T7	g421955	BLASTX	180	1e-12	40	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387)
3316	GM_80_B2_D04_T7	g226407	BLASTX	307	4e-25	43	ORF4 [Solanum tuberosum]
3317	GM_80_B2_D05_MR	g1142702	BLASTN	423	1e-12	73	retrotransposon del1-46 [Lilium henryi]
3318	GM_80_B2_D10_MR	g507910	BLASTN	374	3e-10	73	Glycine max satellite STR120-A.4.
3319	GM_80_B2_E01_MR	g1750376	BLASTX	170	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3320	GM_80_B2_E02_MR	g18559	BLASTN	488	4e-15	68	Glycine max BSR-101 satellite SB92 genomic sequence.
3321	GM_80_B2_E08_MR	g1666236	BLASTX	220	2e-17	32	(U76261) unknown [Hordeum vulgare]
3322	GM_80_B2_E12_MR	g3548803	BLASTX	327	5e-28	82	(AC005313) putative DNA-binding protein [Arabidopsis thaliana]
3323	GM_80_B2_F02_T7	g3845197	BLASTN	525	1e-16	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence

3324	GM_80_B2_F07_T7	g3142328	BLASTN	754	4e-27	76	Glycine max partial SIRE-1 sequence ribonuclease II and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3325	GM_80_B2_G02_MR	g3599418	BLASTN	543	1e-17	92	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
3326	GM_80_B2_G02_T7	g25222230	BLASTX	180	3e-13	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
3327	GM_80_B2_G09_T7	g18559	BLASTN	1366	6e-55	76	G.max gene for catalase
3328	GM_80_B2_H03_T7	g4038056	BLASTX	247	5e-19	44	(AC005897) putative transposon [Arabidopsis thaliana]
3329	GM_80_B2_H04_T7	g130582	BLASTX	154	9e-18	48	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE), REVERSE TRANSCRIPTASE; ENDONUCLEASE
3330	GM_80_B2_H05_MR	g4063760	BLASTX	288	3e-23	51	(TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
3331	GM_80_B2_H05_T7	g507910	BLASTN	411	6e-12	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3332	GM_80_B2_H07_T7	g3033389	BLASTX	188	1e-12	36	Glycine max BSR-101 satellite SB92 genomic sequence.
3333	GM_80_B2_H08_MR	g3273115	BLASTN	401	4e-11	63	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
3334	GM_81_A1_A03_MR	g3550435	BLASTN	565	2e-18	61	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-15, complete sequence [Plasmodium falciparum]
3335	GM_81_A1_A03_T7	g2642431	BLASTX	253	2e-19	49	Hordeum vulgare Hotr1 gene
3336	GM_81_A1_A04_MR	g3337361	BLASTX	213	1e-15	45	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
3337	GM_81_A1_B01_MR	g2104945	BLASTN	362	2e-09	72	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
3338	GM_81_A1_B05_MR	g1146165	BLASTX	155	7e-10	72	Glycine max copia-like retrotransposon Tgm1, complete sequence (L47479) urophorphyrin III methylase [Arabidopsis thaliana]
3339	GM_81_A1_B07_T7	g3810596	BLASTX	288	2e-23	49	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3340	GM_81_A1_B11_MR	g2443320	BLASTX	189	1e-12	35	(D85597) polyprotein [Oryza australiensis]
3341	GM_81_A1_B12_T7	g1769898	BLASTX	216	5e-16	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3342	GM_81_A1_C01_MR	g4063760	BLASTX	368	8e-32	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3343	GM_81_A1_C01_T7	g507910	BLASTN	440	3e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
3344	GM_81_A1_C04_MR	g507910	BLASTN	600	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3345	GM_81_A1_C04_T7	g4063756	BLASTN	404	3e-11	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3346	GM_81_A1_C06_MR	g2995405	BLASTX	383	1e-33	51	(Y12432) polyprotein [Ananas comosus]
3347	GM_81_A1_C07_MR	g18559	BLASTN	951	4e-36	77	G.max gene for catalase
3348	GM_81_A1_C09_MR	g3777527	BLASTX	568	6e-53	94	(AF053008) gag-pol polyprotein [Glycine max]
3349	GM_81_A1_D04_MR	g3810596	BLASTX	246	6e-19	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3350	GM_81_A1_D05_MR	g2213608	BLASTX	173	5e-11	40	(AC000103) F21J9.2 [Arabidopsis thaliana]
3351	GM_81_A1_D09_MR	g1236334	BLASTX	144	2e-09	77	(U34283) T3/T7-like RNA polymerase [Oryza sativa]
3352	GM_81_A1_D10_MR	g18559	BLASTN	789	9e-29	74	G.max gene for catalase

3353	GM_81_A1_E02_MR	g840618	BLASTN	347	7e-09	64	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
3354	GM_81_A1_E07_T7	g4063760	BLASTX	461	1e-41	66	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3355	GM_81_A1_E11_T7	g905361	BLASTX	252	7e-20	88	(U22103) gag-protease polyprotein [Glycine max]
3356	GM_81_A1_F03_T7	g100484	BLASTX	353	1e-30	61	hypothetical protein - garden snapdragon
3357	GM_81_A1_F04_T7	g507910	BLASTN	348	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3358	GM_81_A1_F05_T7	g133917	BLASTX	245	4e-20	84	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir
							R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814
							(Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf
							1211235] ribosomal protein S2 [Nicotiana tabacum]
3359	GM_81_A1_F07_T7	g905361	BLASTX	522	1e-54	89	(U22103) gag-protease polyprotein [Glycine max]
3360	GM_81_A1_F08_T7	g505129	BLASTN	375	5e-10	62	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene
							homologous region
3361	GM_81_A1_F09_T7	g3142328	BLASTN	397	6e-11	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-
							like genes, partial cds, and long terminal repeat, complete sequence
3362	GM_81_A1_F12_T7	g1769898	BLASTX	237	3e-18	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3363	GM_81_A1_G03_MR	g3319372	BLASTX	175	3e-11	33	(AF077409) similar to reverse transcriptases (PF-am: rvt.hmm, score:
							60.13) [Arabidopsis thaliana]
3364	GM_81_A1_G05_T7	g3287696	BLASTX	488	3e-45	72	(AC003979) Strong similarity to phosphoribosylanthranilate
							transferase gb D86180 from Pisum sativum. This ORF may be part
							of a larger gene that lies in the overlapping region. [Arabidopsis
							thaliana]
3365	GM_81_A1_G07_MR	g3142328	BLASTN	1804	5e-75	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-
							like genes, partial cds, and long terminal repeat, complete sequence
3366	GM_81_A1_G10_T7	g18559	BLASTN	522	1e-16	73	G-max gene for catalase
3367	GM_81_A1_H02_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3368	GM_81_A1_H03_MR	g421948	BLASTX	220	1e-16	35	UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase -
							garden petunia
3369	GM_81_A1_H04_MR	g4063760	BLASTX	589	2e-55	71	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3370	GM_81_A1_H05_T7	g507910	BLASTN	365	7e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3371	GM_81_A1_H08_MR	g13558	BLASTN	553	3e-18	67	Yeast mitochondrial DNA with the gene for tRNA-Glu >gi 13599
							emb X04566 MISCTRNE Yeast mitochondrial gene for transfer
							RNA-Glu >gi 343972 gb K03309 YSTMTTGE Saccharomyces
							cerevisiae mitochondrial tRNA-Glu gene.
3372	GM_81_A1_H12_T7	g3695062	BLASTN	426	2e-12	74	Lotus japonicus rac GTPase activating protein 3 mRNA, partial cds
3373	GM_81_A2_A03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3374	GM_81_A2_A03_T7	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3375	GM_81_A2_A06_T7	g170080	BLASTN	523	1e-16	93	Soybean seed lectin gene transposable element (gm1.
3376	GM_81_A2_A08_MR	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3377	GM_81_A2_A08_T7	g507910	BLASTN	393	4e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.

3378	GM_81_A2_A09_T7	g3353375	BLASTX	206	6e-15	74	(AC003028) putative amidase [Arabidopsis thaliana]
3379	GM_81_A2_A11_MR	g531389	BLASTX	217	1e-15	43	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
3380	GM_81_A2_A12_MR	g2995405	BLASTX	394	7e-35	66	(Y12432) polyprotein [Ananas comosus]
3381	GM_81_A2_B01_T7	g18559	BLASTN	944	9e-36	73	G-max gene for catalase
3382	GM_81_A2_B02_MR	g2522228	BLASTX	390	2e-35	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
3383	GM_81_A2_B02_T7	g3097320	BLASTN	466	5e-14	71	Glycine max gene for Bd 30K, complete cds
3384	GM_81_A2_B05_T7	g1666236	BLASTX	206	1e-15	31	(U76261) unknown [Hordeum vulgare]
3385	GM_81_A2_B08_MR	g3645899	BLASTX	270	2e-21	43	(U68408) 5' end not determined experimentally [Zea mays]
3386	GM_81_A2_B09_T7	g3142328	BLASTN	1183	1e-46	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3387	GM_81_A2_B11_T7	g2462936	BLASTX	308	9e-27	48	(Y12321) open reading frame 2 [Brassica oleracea]
3388	GM_81_A2_B12_MR	g4063760	BLASTX	572	1e-53	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3389	GM_81_A2_C04_T7	g2827713	BLASTX	149	5e-09	82	(AL021684) pyridoxal-phosphate-dependent aminotransferase - like protein [Arabidopsis thaliana]
3390	GM_81_A2_C05_MR	g507910	BLASTN	548	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3391	GM_81_A2_C05_T7	g507910	BLASTN	583	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence
3392	GM_81_A2_C06_T7	g905361	BLASTX	176	1e-11	29	(U22103) gag-protease polyprotein [Glycine max]
3393	GM_81_A2_C07_T7	g507910	BLASTN	693	1e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
3394	GM_81_A2_C10_T7	g4063760	BLASTX	265	7e-21	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3395	GM_81_A2_D01_MR	g18767	BLASTN	365	4e-18	78	Soybean Tgm6 transposable element 5' end
3396	GM_81_A2_D03_MR	g507910	BLASTN	666	2e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
3397	GM_81_A2_D04_MR	g18559	BLASTN	1021	3e-39	76	G-max gene for catalase
3398	GM_81_A2_D10_T7	g4063760	BLASTX	566	6e-53	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3399	GM_81_A2_F03_MR	g3169065	BLASTX	191	4e-14	40	(AL023704) translocation elongation factor [Schizosaccharomyces pombe]
3400	GM_81_A2_E03_T7	g13100	BLASTN	406	2e-11	62	M. javanica mitochondrion ATPase 6, and putative tRNA-f-Met and tRNA-His genes
3401	GM_81_A2_E05_T7	g3695395	BLASTX	251	9e-20	39	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
3402	GM_81_A2_F06_T7	g3645899	BLASTX	203	2e-16	41	(U68408) 5' end not determined experimentally [Zea mays]
3403	GM_81_A2_F10_T7	g2660669	BLASTX	617	7e-58	90	(AC002342) human Mi-2 autoantigen-like protein [Arabidopsis thaliana]
3404	GM_81_A2_F12_MR	g4063760	BLASTX	203	3e-14	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3405	GM_81_A2_G03_MR	g2956679	BLASTN	351	8e-09	62	Human DNA sequence from clone 343C1 on chromosome 22, complete sequence [Homo sapiens]
3406	GM_81_A2_G04_MR	g2443320	BLASTX	313	6e-26	45	(D85597) polyprotein [Oryza australiensis]
3407	GM_81_A2_G06_MR	g3142379	BLASTX	213	2e-28	80	(AF053008) envelope-like [Glycine max]
3408	GM_81_A2_G09_MR	g3426334	BLASTN	364	2e-09	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds

3409	GM_81_A2_H01_T7	g507910	BLASTN	560	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3410	GM_81_A2_H03_MR	g2443320	BLASTX	277	5e-22	41	(D85597) polyprotein [Oryza australiensis]
3411	GM_81_A2_H03_T7	g4063756	BLASTN	469	4e-14	62	Arabidopsis thaliana chromosome II BAC T9F-8 genomic sequence, complete sequence [Arabidopsis thaliana]
3412	GM_81_A2_H04_MR	g505129	BLASTN	360	3e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
3413	GM_81_A2_H05_MR	g3097320	BLASTN	434	1e-12	73	Glycine max gene for Bd 30K, complete cds
3414	GM_81_A2_H09_MR	g4063760	BLASTX	303	7e-25	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3415	GM_81_A2_H09_T7	g170608	BLASTN	352	2e-09	66	Broad bean (V faba) BamHI repetitive element, clone 1.
3416	GM_81_A2_H10_MR	g3738114	BLASTN	360	3e-09	60	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
3417	GM_81_B1_A08_MR	g2522227	BLASTX	221	2e-17	56	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3418	GM_81_B1_A08_T7	g3777527	BLASTX	283	8e-42	87	(AF053008) gag-pol polyprotein [Glycine max]
3419	GM_81_B1_A10_T7	g2121303	BLASTN	573	7e-19	64	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
3420	GM_81_B1_B05_MR	g14293	BLASTN	370	1e-10	65	Yeast R0.54 mutant mitochondrial DNA lacking ori1 sequence recombination junction with tRNA-Pro and 15S rRNA genes
3421	GM_81_B1_B06_MR	g3786414	BLASTN	381	4e-10	59	Caenorhabditis elegans cosmid H28G03
3422	GM_81_B1_B07_MR	g13533	BLASTN	416	7e-12	62	Yeast mitochondrial tRNA genes (several, map positions 3.5 to 8.6) encoding tRNAs for Lys, Arg, Gly, Asp, Ser, Arg, and Ala.
3423	GM_81_B1_B07_T7	g3953479	BLASTX	198	1e-13	46	(AC002328) F22O2.24 [Arabidopsis thaliana]
3424	GM_81_B1_B12_T7	g3810596	BLASTX	229	4e-17	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3425	GM_81_B1_C01_MR	g2262177	BLASTX	339	1e-29	71	(AC002329) hypothetical protein similar to T18A10.3 [Arabidopsis thaliana]
3426	GM_81_B1_C02_MR	g4063760	BLASTX	278	3e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3427	GM_81_B1_C03_MR	g3810596	BLASTX	190	5e-13	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3428	GM_81_B1_C08_MR	g2121303	BLASTN	387	2e-10	61	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
3429	GM_81_B1_C09_T7	g226407	BLASTX	186	4e-13	54	retrotransposon del1-46 [Lilium henryi]
3430	GM_81_B1_D02_MR	g2832611	BLASTN	426	3e-12	68	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)
3431	GM_81_B1_D02_T7	g629626	BLASTX	212	1e-16	81	Rab protein - alfalfa gi 488700 (X79278) Rab gene product [Medicago sativa]
3432	GM_81_B1_D06_T7	g3176798	BLASTN	365	3e-10	64	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
3433	GM_81_B1_D08_MR	g3777527	BLASTX	701	4e-67	97	(AF053008) gag-pol polyprotein [Glycine max]
3434	GM_81_B1_E02_T7	g2443320	BLASTX	216	1e-22	41	(D85597) polyprotein [Oryza australiensis]

3435	GM_81_B1_E06_MR	g4150930	BLASTN	437	1e-12	63	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
3436	GM_81_B1_E07_T7	g1514043	BLASTX	241	4e-18	57	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
3437	GM_81_B1_E09_T7	g2618600	BLASTN	324	7e-09	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]
3438	GM_81_B1_F05_MR	g2961349	BLASTX	279	2e-22	52	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
3439	GM_81_B1_G02_MR	g3097320	BLASTN	353	6e-09	72	Glycine max gene for Bd 30K, complete cds
3440	GM_81_B1_G04_T7	g2969943	BLASTN	444	5e-13	62	Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS
3441	GM_81_B1_G06_MR	g3687828	BLASTN	391	1e-10	62	Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence [Homo sapiens]
3442	GM_81_B1_G07_MR	g2129709	BLASTX	275	8e-22	40	reverse transcriptase - Arabidopsis thaliana retrotransposon Tal1-1 gi 976278 (147193) reverse transcriptase [Arabidopsis thaliana]
3443	GM_81_B1_G08_T7	g2995405	BLASTX	249	3e-19	44	(Y12432) polyprotein [Ananas comosus]
3444	GM_81_B1_H01_MR	g18768	BLASTN	421	1e-12	64	Soybean Tgm6 transposable element 3' end
3445	GM_81_B1_H11_MR	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3446	GM_81_B2_A03_MR	g2129709	BLASTX	259	4e-20	38	reverse transcriptase - Arabidopsis thaliana retrotransposon Tal1-1 gi 976278 (147193) reverse transcriptase [Arabidopsis thaliana]
3447	GM_81_B2_A03_T7	g3930515	BLASTX	115	8e-11	45	(AF059674) putative gag protein [Nicotiana tabacum]
3448	GM_81_B2_A08_MR	g1351834	BLASTX	298	1e-25	62	PROBABLE ATP-DEPENDENT TRANSPORTER YCF16 gi 1016162 (U30821) ABC transporter subunit [Cyanophora paradoxa]
3449	GM_81_B2_A10_MR	g507910	BLASTN	668	1e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
3450	GM_81_B2_B11_MR	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3451	GM_81_B2_D06_MR	g2649054	BLASTX	296	2e-27	60	(AE000998) long-chain-fatty-acid--CoA ligase (fadD-6) [Archaeoglobus fulgidus]
3452	GM_81_B2_D09_MR	g2462745	BLASTX	242	8e-19	50	(AC002292) Hypothetical protein [Arabidopsis thaliana]
3453	GM_81_B2_E03_MR	g2979574	BLASTN	468	4e-14	66	Homo sapiens Chromosome 16 BAC clone C11987SK-A-279B10, complete sequence [Homo sapiens]
3454	GM_81_B2_F02_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3455	GM_81_B2_F04_MR	g2522227	BLASTX	222	1e-17	56	(AB007406) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3456	GM_81_B2_F06_MR	g2586082	BLASTX	140	9e-17	47	(U72725) retrofit [Oryza longistaminata]
3457	GM_81_B2_F08_MR	g3777527	BLASTX	493	5e-46	79	(AF053008) gag-pol polyprotein [Glycine max]
3458	GM_81_B2_G03_MR	g2809249	BLASTX	209	3e-15	33	(AC002560) F21B7.18 [Arabidopsis thaliana]
3459	GM_81_B2_H06_MR	g1480927	BLASTN	353	5e-09	84	Glycine max cdc2 protein kinase (cdc2(1)) nonprocessed pseudogene
3460	GM_82_A1_A04_MR	g2995405	BLASTX	304	3e-25	48	(Y12432) polyprotein [Ananas comosus]
3461	GM_82_A1_A05_T7	g4063756	BLASTN	472	3e-14	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]

3462	GM_82_A1_A06_MR	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3463	GM_82_A1_A10_MR	g1045530	BLASTN	356	3e-09	62	Magnaporthe grisea host-species specificity (Pw11) gene, complete cds.
3464	GM_82_A1_A11_T7	g2245073	BLASTN	444	5e-13	65	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
3465	GM_82_A1_A12_T7	g2462935	BLASTX	152	8e-09	30	(Y12321) open reading frame 1 [Brassica oleracea]
3466	GM_82_A1_B04_MR	g3264565	BLASTN	425	4e-12	65	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
3467	GM_82_A1_B08_T7	g3097320	BLASTN	675	2e-23	72	Glycine max gene for Bd 30K, complete cds
3468	GM_82_A1_C03_T7	g4063760	BLASTX	186	1e-22	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3469	GM_82_A1_C05_T7	g3142328	BLASTN	1037	5e-40	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3470	GM_82_A1_C06_T7	g2995405	BLASTX	366	8e-32	54	(Y12432) polyprotein [Ananas comosus]
3471	GM_82_A1_D04_MR	g507910	BLASTN	513	1e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
3472	GM_82_A1_D12_MR	g1769898	BLASTX	142	1e-10	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3473	GM_82_A1_E01_MR	g3645899	BLASTX	195	2e-13	50	(U68408) 5' end not determined experimentally [Zea mays]
3474	GM_82_A1_E03_T7	g2764526	BLASTN	408	2e-11	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
3475	GM_82_A1_E05_MR	g1084334	BLASTX	217	2e-16	81	calcium-dependent protein kinase (EC 2.7.1.-) 1 - Arabidopsis thaliana gi 604880 gnl PID d1005364 (D21805) calcium-dependent protein kinase [Arabidopsis thaliana]
3476	GM_82_A1_E05_T7	g3548803	BLASTX	267	2e-21	71	(AC005313) putative DNA-binding protein [Arabidopsis thaliana]
3477	GM_82_A1_E06_MR	g3645899	BLASTX	291	1e-23	56	(U68408) 5' end not determined experimentally [Zea mays]
3478	GM_82_A1_E06_T7	g1666236	BLASTX	147	4e-09	28	(U76261) unknown [Hordeum vulgare]
3479	GM_82_A1_E07_MR	g1143016	BLASTN	349	6e-09	62	Spiroplasma citri Spiroplasma virus SpV1-derived ORF3 gene, partial cds.
3480	GM_82_A1_E10_T7	g4063760	BLASTX	220	5e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3481	GM_82_A1_F02_T7	g3059060	BLASTN	402	4e-11	62	Homo sapiens DNA sequence from PAC 931.7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
3482	GM_82_A1_F03_T7	g3142328	BLASTN	1151	3e-45	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3483	GM_82_A1_F04_MR	g3097320	BLASTN	367	1e-09	71	Glycine max gene for Bd 30K, complete cds
3484	GM_82_A1_F05_T7	g2522228	BLASTX	403	4e-41	64	(AB007466) reverse transcriptase-like protein [Vicia faba]
3485	GM_82_A1_F06_MR	g4063760	BLASTX	444	6e-40	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3486	GM_82_A1_F06_T7	g1769897	BLASTX	99	2e-10	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3487	GM_82_A1_F08_T7	g3645899	BLASTX	203	3e-14	42	(U68408) 5' end not determined experimentally [Zea mays]
3488	GM_82_A1_F11_MR	g507910	BLASTN	505	3e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.

3489	GM_82_A1_F12_T7	g100484	BLASTX	208	5e-15	44	hypothetical protein - garden snapdragon
3490	GM_82_A1_G05_T7	g2129618	BLASTX	202	3e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence.
3491	GM_82_A1_G06_MR	g507910	BLASTN	388	6e-11	72	Arabidopsis thaliana BAC T9E19
3492	GM_82_A1_G10_MR	g3859610	BLASTN	518	2e-16	65	Glycine max extensin (SbHRGP3) gene, complete cds
3493	GM_82_A1_H02_MR	g1165321	BLASTN	771	6e-28	82	Glycine max gene for Bd 30K, complete cds
3494	GM_82_A1_H03_MR	g3097320	BLASTN	665	4e-23	69	(Y12432) polypeptide [Ananas comosus]
3495	GM_82_A1_H04_T7	g2995405	BLASTX	220	4e-19	46	(AB007466) reverse transcriptase-like protein [Vicia faba]
3496	GM_82_A1_H08_MR	g2522228	BLASTX	209	3e-19	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
3497	GM_82_A1_H09_MR	g1167523	BLASTX	329	1e-27	54	Caenorhabditis elegans cosmid Y18D10A, complete sequence
3498	GM_82_A2_A02_MR	g3979928	BLASTN	429	2e-12	62	[Caenorhabditis elegans]
3499	GM_82_A2_A03_T7	g576752	BLASTN	346	6e-09	62	Myrmecia pilosula H191-035 mitochondrion cytochrome b gene, partial cds.
3500	GM_82_A2_A06_T7	g3777527	BLASTX	705	1e-67	95	(AF053008) gag-pol polyprotein [Glycine max]
3501	GM_82_A2_A08_MR	g507910	BLASTN	398	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3502	GM_82_A2_A12_MR	g507910	BLASTN	523	5e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
3503	GM_82_A2_B02_T7	g507910	BLASTN	344	6e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
3504	GM_82_A2_B05_MR	g1480526	BLASTN	342	3e-09	62	Rhagoletis meigeni cytochrome oxidase subunit II (COII) gene, mitochondrial gene encoding mitochondrial protein, partial cds
3505	GM_82_A2_B09_MR	g18559	BLASTN	359	3e-09	71	G-max gene for catalase
3506	GM_82_A2_B10_MR	g2598589	BLASTX	225	1e-22	41	(Y15367) MtN19 [Medicago truncatula]
3507	GM_82_A2_B11_MR	g905361	BLASTX	676	1e-65	93	(U22103) gag-protease polyprotein [Glycine max]
3508	GM_82_A2_C02_T7	g507910	BLASTN	589	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3509	GM_82_A2_C06_T7	g507910	BLASTN	621	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3510	GM_82_A2_C08_MR	g180902	BLASTN	370	1e-10	60	Human variable number tandem repeat (VNTR) region, allele 14R2 3' to collagen type II (COL2A1) gene.
3511	GM_82_A2_C09_MR	g3142328	BLASTN	915	2e-34	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
3512	GM_82_A2_C10_T7	g4038057	BLASTX	163	4e-10	44	(AC005897) hypothetical protein [Arabidopsis thaliana]
3513	GM_82_A2_D03_MR	g1168471	BLASTX	145	2e-09	86	PROTEIN KINASE APK1B gi 2160295 gnl PID d1001485 (D10152) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]
3514	GM_82_A2_D05_MR	g2769655	BLASTN	378	5e-10	63	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
3515	GM_82_A2_D07_T7	g2459440	BLASTX	126	4e-09	40	(AC002332) putative receptor kinase [Arabidopsis thaliana]
3516	GM_82_A2_D08_MR	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.

3517	GM_82_A2_D10_MR	g2392895	BLASTX	307	3e-25	50	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]
3518	GM_82_A2_D11_T7	g2129618	BLASTX	188	9e-13	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3519	GM_82_A2_D12_MR	g4056421	BLASTX	410	1e-37	78	(AC005322) Similar to gb Z30094 basic transcription factor 2, 44 kD subunit from Homo sapiens. EST gb W43325 comes from this gene. [Arabidopsis thaliana]
3520	GM_82_A2_E02_MR	g4063760	BLASTX	489	1e-44	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3521	GM_82_A2_E02_T7	g1769897	BLASTX	173	2e-11	30	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3522	GM_82_A2_E04_MR	g130582	BLASTX	101	1e-08	36	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
3523	GM_82_A2_E04_T7	g2865424	BLASTX	393	3e-34	52	(TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
3524	GM_82_A2_E05_T7	g3892061	BLASTX	147	1e-08	25	(AF039371) polyprotein [Arabidopsis thaliana]
3525	GM_82_A2_E11_MR	g99730	BLASTX	270	4e-22	50	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
3526	GM_82_A2_F05_MR	g1669680	BLASTN	459	1e-13	63	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Kashmir) (fragment) gi 1345512 gnt PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
3527	GM_82_A2_F05_T7	g13596	BLASTN	335	6e-09	58	Human DNA sequence from PAC 293E14 contains ESTs, STS
3528	GM_82_A2_F07_MR	g507910	BLASTN	525	4e-17	79	Yeast mit DNA for promoter upstream of tRNA-Leu gene 3 *Source: Glycine max BSR-101 satellite SB92 genomic sequence.
3529	GM_82_A2_F11_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3530	GM_82_A2_F11_T7	g3777527	BLASTX	208	2e-16	47	(AF053008) gag-pol polyprotein [Glycine max]
3531	GM_82_A2_G03_T7	g3201682	BLASTX	157	9e-14	67	(AF060942) extra-large G-protein [Arabidopsis thaliana]
3532	GM_82_A2_G12_MR	g3287270	BLASTX	134	3e-11	44	(Y09533) involved in starch metabolism [Solanum tuberosum]
3533	GM_82_A2_G12_T7	g170029	BLASTN	405	3e-11	81	Glycine max cv. Dare nodulin 26 gene fragment.
3534	GM_82_A2_H01_MR	g1326016	BLASTX	298	2e-24	45	TY3-2 orfB
3535	GM_82_A2_H04_MR	g987979	BLASTX	166	1e-11	67	(X91248) high mobility group-like protein [Zinnia elegans]
3536	GM_82_A2_H05_MR	g2462134	BLASTX	183	1e-12	36	(Y13368) reverse transcriptase [Beta vulgaris]
3537	GM_82_A2_H06_MR	g3928116	BLASTN	430	2e-12	63	. complete sequence [Homo sapiens]
3538	GM_82_A2_H11_MR	g2522226	BLASTN	537	2e-17	63	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
3539	GM_82_B1_A09_T7	g4063760	BLASTX	321	8e-27	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3540	GM_82_B1_A10_MR	g2335061	BLASTN	457	1e-13	70	Homo sapiens chromosome 16 BAC clone CTT987SK-334D11 complete sequence [Homo sapiens]
3541	GM_82_B1_A12_MR	g2443320	BLASTX	461	1e-41	44	(D85597) polyprotein [Oryza australiensis]
3542	GM_82_B1_B01_MR	g2522230	BLASTX	171	3e-12	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
3543	GM_82_B1_B03_T7	g4038056	BLASTX	304	4e-25	53	(AC005897) putative transposon [Arabidopsis thaliana]
3544	GM_82_B1_B07_MR	g3097320	BLASTN	1034	8e-40	79	Glycine max gene for Bd 30K, complete cds

3545	GM_82_B1_C02_MR	g2995405	BLASTX	288	1e-38	46	(Y12432) polyprotein [Ananas comosus]
3546	GM_82_B1_C02_T7	g4063760	BLASTX	517	1e-47	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3547	GM_82_B1_C07_T7	g18559	BLASTN	496	2e-15	86	G.max gene for catalase
3548	GM_82_B1_C10_T7	g3142328	BLASTN	708	4e-25	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3549	GM_82_B1_D01_MR	g2995405	BLASTX	423	5e-38	66	(Y12432) polyprotein [Ananas comosus]
3550	GM_82_B1_D05_MR	g2760839	BLASTX	225	6e-17	45	(AC003105) putative receptor kinase [Arabidopsis thaliana]
3551	GM_82_B1_D05_T7	g2969888	BLASTN	476	1e-14	68	Daucus carota mRNA for sucrose-H ⁺ symporter, SUT1b, retrotransposon del1-46 [Lilium henryi]
3552	GM_82_B1_D10_MR	g226407	BLASTX	295	2e-26	48	Glycine max BSR-101 satellite SB92 genomic sequence.
3553	GM_82_B1_D12_MR	g507910	BLASTN	411	6e-12	74	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]
3554	GM_82_B1_F03_T7	g2618601	BLASTN	403	4e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3555	GM_82_B1_F06_T7	g507910	BLASTN	563	8e-19	80	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3556	GM_82_B1_F07_T7	g99922	BLASTX	332	3e-29	72	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]
3557	GM_82_B1_F08_MR	g4115379	BLASTX	195	1e-29	47	(U22103) gag-protease polyprotein [Glycine max]
3558	GM_82_B1_F12_MR	g905361	BLASTX	174	2e-11	29	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3559	GM_82_B1_F02_T7	g4063756	BLASTN	349	1e-08	64	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3560	GM_82_B1_F04_MR	g2522227	BLASTX	222	1e-17	56	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3561	GM_82_B1_F04_T7	g3142328	BLASTN	819	4e-30	77	(AF053008) gag-pol polyprotein [Glycine max]
3562	GM_82_B1_F07_T7	g3777527	BLASTX	642	8e-61	95	(AL022603) putative protein [Arabidopsis thaliana]
3563	GM_82_B1_F09_MR	g3080401	BLASTX	261	9e-22	65	Glycine max BSR-101 satellite SB92 genomic sequence.
3564	GM_82_B1_F10_MR	g507910	BLASTN	572	3e-19	81	(U22103) gag-protease polyprotein [Glycine max]
3565	GM_82_B1_F11_MR	g905361	BLASTX	789	4e-87	89	(AF017751) resistance protein candidate [Lactuca sativa]
3566	GM_82_B1_G01_MR	g2852684	BLASTX	324	2e-27	40	(Z92770) fadE2 [Mycobacterium tuberculosis]
3567	GM_82_B1_G03_T7	g1877279	BLASTX	176	3e-14	50	G.max gene for catalase
3568	GM_82_B1_G04_MR	g18559	BLASTN	409	2e-11	65	(U78721) hypothetical protein [Arabidopsis thaliana]
3569	GM_82_B1_G04_T7	g1707020	BLASTX	321	2e-27	67	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3570	GM_82_B1_G05_T7	g2129618	BLASTX	191	5e-13	42	(AF053008) gag-pol polyprotein [Glycine max]
3571	GM_82_B1_G06_MR	g3777527	BLASTX	396	1e-34	41	Glycine max BSR-101 satellite SB92 genomic sequence.
3572	GM_82_B1_G09_MR	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3573	GM_82_B1_G09_T7	g507910	BLASTN	384	9e-11	75	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3574	GM_82_B1_G10_T7	g99922	BLASTX	516	9e-49	81	

3575	GM_82_B1_G12_MR	g3142328	BLASTN	1423	1e-57	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3576	GM_82_B1_H02_MR	g3142328	BLASTN	1416	3e-57	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Y12465) serine/threonine kinase [Sorghum bicolor]
3577	GM_82_B1_H03_MR	g26322254	BLASTX	131	5e-15	70	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3578	GM_82_B1_H03_T7	g25222227	BLASTX	169	1e-11	45	(Y12321) open reading frame 2 [Brassica oleracea]
3579	GM_82_B1_H05_MR	g2462936	BLASTX	298	1e-25	35	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
3580	GM_82_B1_H05_T7	g33319362	BLASTX	188	9e-13	44	Glycine max BSR-101 satellite SB92 genomic sequence.
3581	GM_82_B2_A01_T7	g507910	BLASTN	533	2e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3582	GM_82_B2_A04_MR	g507910	BLASTN	561	1e-18	81	Glycine max partial SIRE-1 sequence ribonuclease II and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3583	GM_82_B2_A05_T7	g3142328	BLASTN	907	4e-34	89	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
3584	GM_82_B2_A06_MR	g421955	BLASTX	170	2e-11	44	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3585	GM_82_B2_A10_MR	g4063756	BLASTN	483	9e-15	63	Glycine max BSR-101 satellite SB92 genomic sequence.
3586	GM_82_B2_A10_T7	g507910	BLASTN	693	1e-24	86	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
3587	GM_82_B2_B01_MR	g2129709	BLASTX	173	6e-11	42	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
3588	GM_82_B2_B02_T7	g1431738	BLASTN	353	5e-09	77	(Y10098) 7-ethoxycoumarin O-deethylase [Helianthus tuberosus]
3589	GM_82_B2_B03_MR	g2689221	BLASTX	255	2e-20	39	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE II
3590	GM_82_B2_B04_MR	g729460	BLASTX	86	1e-11	72	(BETA-KETOACYL-ACP SYNTHASE II) (KAS II) >gi 2121046 pir I41060 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II - Escherichia coli >gi 572680 (Z34979) beta ketoacyl-acyl carrier protein synthase [Escherichia coli] >gi 664870 (U20767) beta-ketoacyl-acyl carrier protein synthase II [Escherichia coli] >gi 1787337 (AE000210) 3-oxoacyl-[acyl-carrier-protein] synthase II [Escherichia coli]
3591	GM_82_B2_B07_MR	g130398	BLASTX	220	5e-16	40	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related polypeptide homolog - fruit fly (Drosophila melanogaster) transposon 297

3592	GM_82_B2_C01_MR	g13581	BLASTN	482	1e-15	65	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
3593	GM_82_B2_C01_T7	g3097320	BLASTN	481	1e-14	67	Glycine max gene for Bd 30K, complete cds
3594	GM_82_B2_C03_MR	g3777527	BLASTX	235	2e-17	38	(AF053008) gag-pol polyprotein [Glycine max]
3595	GM_82_B2_D09_MR	g2244839	BLASTX	265	4e-21	35	(Z97337) hypothetical protein [Arabidopsis thaliana]
3596	GM_82_B2_D11_MR	g3777527	BLASTX	624	6e-59	87	(AF053008) gag-pol polyprotein [Glycine max]
3597	GM_82_B2_E01_T7	g2522227	BLASTX	158	2e-10	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3598	GM_82_B2_E03_MR	g2623299	BLASTX	319	2e-27	54	(AC002409) hypothetical protein [Arabidopsis thaliana]
3599	GM_82_B2_E05_T7	g3449329	BLASTN	448	3e-13	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; MDH9, complete sequence [Arabidopsis thaliana]
3600	GM_82_B2_G03_MR	g3777527	BLASTX	512	6e-47	88	(AF053008) gag-pol polyprotein [Glycine max]
3601	GM_82_B2_G03_T7	g3450889	BLASTX	228	9e-31	67	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
3602	GM_82_B2_G04_T7	g99922	BLASTX	287	2e-31	63	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3603	GM_82_B2_G05_T7	g3645899	BLASTX	220	2e-19	54	(U68408) 5' end not determined experimentally [Zea mays]
3604	GM_82_B2_G07_MR	g3142328	BLASTN	853	1e-31	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB007466) reverse transcriptase-like protein [Vicia faba]
3605	GM_82_B2_G08_T7	g2522228	BLASTX	242	5e-24	58	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
3606	GM_82_B2_G09_MR	g3250687	BLASTX	306	2e-26	44	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
3607	GM_82_B2_G11_MR	g505129	BLASTN	373	7e-10	66	Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene.
3608	GM_82_B2_H02_T7	g308769	BLASTN	350	9e-10	60	G.max mRNA for putative cytochrome P450, clone CP7
3609	GM_82_B2_H10_T7	g3334666	BLASTN	939	2e-36	89	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
3610	GM_82_B2_H11_MR	g3845197	BLASTN	367	1e-09	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
3611	GM_82_B2_H12_MR	g3426334	BLASTN	458	1e-13	61	S.tuberosum mRNA for protein involved in starch metabolism
3612	GM_83_A1_A03_MR	g3287269	BLASTN	484	7e-15	67	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
3613	GM_83_A1_A05_MR	g3779030	BLASTX	161	3e-11	38	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
3614	GM_83_A1_A05_T7	g2708743	BLASTX	100	3e-09	31	(D85597) polyprotein [Oryza australiensis]
3615	GM_83_A1_A06_T7	g2443320	BLASTX	299	2e-24	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3616	GM_83_A1_A11_MR	g1769898	BLASTX	141	7e-18	46	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3617	GM_83_A1_A11_T7	g99922	BLASTX	371	2e-33	58	(AF059674) putative gag protein [Nicotiana tabacum]
3618	GM_83_A1_B01_T7	g3930515	BLASTX	117	4e-12	47	

3619	GM_83_A1_B04_T7	g3777527	BLASTX	191	9e-13	43	(AF053008) gag-pol polyprotein [Glycine max]
3620	GM_83_A1_B11_MR	g2586082	BLASTX	268	5e-21	44	(U72725) retrofit [Oryza longistaminata]
3621	GM_83_A1_C01_T7	g3650039	BLASTX	158	9e-10	44	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
3622	GM_83_A1_C05_MR	g1346261	BLASTX	315	5e-27	60	GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR) gi1015319 gnl PID d1011751 (D67088) glutamyl-tRNA reductase [Cucumis sativus]
3623	GM_83_A1_C05_T7	g4115938	BLASTX	115	6e-10	71	(AF118223) contains similarity several bacterial glutathione-regulated potassium efflux system proteins [Arabidopsis thaliana]
3624	GM_83_A1_D02_MR	g3097320	BLASTN	382	3e-10	72	Glycine max gene for Bd 30K, complete cds
3625	GM_83_A1_D04_MR	g4063760	BLASTX	321	3e-38	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3626	GM_83_A1_D05_MR	g1346261	BLASTX	424	5e-39	71	GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR) gi1015319 gnl PID d1011751 (D67088) glutamyl-tRNA reductase [Cucumis sativus]
3627	GM_83_A1_D05_T7	g4115930	BLASTN	346	6e-16	76	Arabidopsis thaliana BAC T4B21
3628	GM_83_A1_D12_MR	g507910	BLASTN	529	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
3629	GM_83_A1_E09_T7	g2462134	BLASTX	344	2e-30	50	(Y13368) reverse transcriptase [Beta vulgaris]
3630	GM_83_A1_E11_MR	g18559	BLASTN	728	6e-26	77	G.max gene for catalase
3631	GM_83_A1_E12_MR	g100484	BLASTX	350	2e-30	61	hypothetical protein - garden snapdragon
3632	GM_83_A1_F02_MR	g1142702	BLASTN	975	2e-37	93	Glycine max satellite STR120-A.4
3633	GM_83_A1_F05_MR	g2842478	BLASTX	218	3e-16	48	(AL021749) receptor protein kinase like protein [Arabidopsis thaliana]
3634	GM_83_A1_F05_T7	g2924653	BLASTN	361	3e-09	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]
3635	GM_83_A1_F07_MR	g3810596	BLASTX	189	7e-13	37	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3636	GM_83_A1_F09_MR	g4063756	BLASTN	377	5e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3637	GM_83_A1_G05_MR	g4063760	BLASTX	401	4e-39	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3638	GM_83_A1_G05_T7	g507910	BLASTN	402	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3639	GM_83_A1_G07_MR	g1769898	BLASTX	105	2e-12	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3640	GM_83_A1_H07_T7	g3097320	BLASTN	687	4e-24	83	Glycine max gene for Bd 30K, complete cds
3641	GM_83_A1_H09_T7	g18559	BLASTN	636	8e-22	80	G.max gene for catalase
3642	GM_83_A1_H10_MR	g3142328	BLASTN	601	2e-36	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3643	GM_83_A2_A04_T7	g3036785	BLASTN	379	4e-10	66	Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A1.H2B.1A.H4.H2A.1b.H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island
3644	GM_83_A2_A05_T7	g1680686	BLASTX	402	3e-36	67	(U51330) rust resistance kinase Lr10 [Triticum aestivum]

3645	GM_83_A2_A08_T7	g3928116	BLASTN	351	8e-09	59	, complete sequence [Homo sapiens]
3646	GM_83_A2_B07_T7	g3142328	BLASTN	699	1e-24	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3647	GM_83_A2_C02_MR	g4063756	BLASTN	663	7e-23	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3648	GM_83_A2_C05_MR	g1769898	BLASTX	504	2e-47	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3649	GM_83_A2_C11_MR	g1480927	BLASTN	644	2e-22	83	Glycine max cdc2 protein kinase (cdc2(1)) nonprocessed pseudogene
3650	GM_83_A2_C12_MR	g2827621	BLASTX	171	9e-18	43	(AL021636) putative protein [Arabidopsis thaliana]
3651	GM_83_A2_D05_MR	g3687234	BLASTX	192	5e-13	53	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
3652	GM_83_A2_D08_MR	g505129	BLASTN	390	1e-10	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
3653	GM_83_A2_D12_MR	g4063760	BLASTX	248	5e-19	42	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3654	GM_83_A2_E04_T7	g18559	BLASTN	352	6e-09	74	G.max gene for catalase
3655	GM_83_A2_E10_T7	g1742955	BLASTX	233	1e-17	65	(Z71446) CLC-b chloride channel protein [Arabidopsis thaliana]
3656	GM_83_A2_F04_T7	g3142328	BLASTN	1006	1e-38	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
3657	GM_83_A2_F10_T7	g3319362	BLASTX	231	3e-17	43	(AJ004901) resistance protein [Glycine max]
3658	GM_83_A2_G02_MR	g3452140	BLASTX	179	4e-13	43	(AF053008) gag-pol polyprotein [Glycine max]
3659	GM_83_A2_G05_T7	g3777527	BLASTX	550	5e-51	90	(AF053008) gag-pol polyprotein [Glycine max]
3660	GM_83_A2_G10_MR	g3777527	BLASTX	759	2e-73	93	(AF053008) gag-pol polyprotein [Glycine max]
3661	GM_83_A2_H05_T7	g3777527	BLASTX	492	8e-45	93	(AF053008) gag-pol polyprotein [Glycine max]
3662	GM_83_B1_A08_T7	g18559	BLASTN	796	5e-29	76	G.max gene for catalase
3663	GM_83_B1_B03_MR	g3097320	BLASTN	1076	1e-41	80	Glycine max gene for Bd 30K, complete cds
3664	GM_83_B1_B04_T7	g3777527	BLASTX	515	3e-47	94	(AF053008) gag-pol polyprotein [Glycine max]
3665	GM_83_B1_B06_MR	g507910	BLASTN	612	5e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
3666	GM_83_B1_B11_MR	g669002	BLASTN	1655	4e-69	97	Glycine max calnexin mRNA, complete cds.
3667	GM_83_B1_B12_T7	g3176806	BLASTN	478	2e-15	65	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
3668	GM_83_B1_C11_MR	g507910	BLASTN	348	4e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
3669	GM_83_B1_C11_T7	g507910	BLASTN	352	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3670	GM_83_B1_D08_T7	g1710587	BLASTX	172	8e-23	87	60S ACIDIC RIBOSOMAL PROTEIN P0 gi 1196897 (L46848) acidic ribosomal protein P0 [Glycine max]
3671	GM_83_B1_D09_MR	g3097320	BLASTN	791	9e-29	75	Glycine max gene for Bd 30K, complete cds
3672	GM_83_B1_D12_T7	g1769899	BLASTX	265	4e-22	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3673	GM_83_B1_F06_MR	g3695395	BLASTX	158	1e-09	35	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]

3674	GM_83_B1_F07_MR	g20886	BLASTN	446	3e-13	64	Pea S2 organ specific gene
3675	GM_83_B1_G02_MR	g2129618	BLASTX	181	6e-12	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3676	GM_83_B1_G04_T7	g2656024	BLASTN	378	5e-10	71	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6
3677	GM_83_B1_G11_T7	g18559	BLASTN	865	3e-32	78	G.max gene for catalase
3678	GM_83_B1_H03_MR	g3097320	BLASTN	1103	6e-43	82	Glycine max gene for Bd 30K, complete cds
3679	GM_83_B1_H08_T7	g2815075	BLASTN	393	1e-10	62	Caenorhabditis elegans cosmid Y38H8A, complete sequence [Caenorhabditis elegans]
3680	GM_83_B1_H12_MR	g3283026	BLASTX	211	2e-15	39	putative transposase [Arabidopsis thaliana]
3681	GM_83_B2_A01_MR	g4063756	BLASTN	389	1e-10	65	Arabidopsis thaliana chromosome II BAC T9J8 genomic sequence, complete sequence [Arabidopsis thaliana]
3682	GM_83_B2_A02_MR	g4063760	BLASTX	174	4e-11	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3683	GM_83_B2_A06_MR	g226407	BLASTX	268	5e-21	38	retrotransposon del1-46 [Lilium henryi]
3684	GM_83_B2_A06_T7	g1769899	BLASTX	256	3e-21	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3685	GM_83_B2_A08_MR	g507910	BLASTN	478	5e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3686	GM_83_B2_A08_T7	g507910	BLASTN	600	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3687	GM_83_B2_A11_T7	g3142328	BLASTN	903	6e-34	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3688	GM_83_B2_B01_MR	g507910	BLASTN	427	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
3689	GM_83_B2_B03_T7	g3426334	BLASTN	574	6e-19	63	Pisum sativum pectin methyltransferase (rcpme1) gene, complete cds (AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
3690	GM_83_B2_B07_T7	g3033389	BLASTX	161	7e-10	36	Glycine max gene for Bd 30K, complete cds
3691	GM_83_B2_B08_T7	g3097320	BLASTN	353	6e-09	73	(Y12321) open reading frame 2 [Brassica oleracea]
3692	GM_83_B2_B09_MR	g2462936	BLASTX	181	3e-26	51	(AC003028) putative diphenol oxidase [Arabidopsis thaliana]
3693	GM_83_B2_B09_T7	g3335357	BLASTX	212	8e-24	70	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
3694	GM_83_B2_C01_T7	g3461840	BLASTX	228	1e-16	40	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3695	GM_83_B2_C05_T7	g3810596	BLASTX	238	5e-18	34	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976)
3696	GM_83_B2_C11_T7	g99726	BLASTX	102	7e-12	42	orf 3 [Arabidopsis thaliana]
3697	GM_83_B2_D08_MR	g2160155	BLASTN	340	2e-18	67	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
3698	GM_83_B2_D12_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3699	GM_83_B2_E04_MR	g4006831	BLASTX	206	2e-14	35	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
3700	GM_83_B2_E04_T7	g2995405	BLASTX	228	5e-17	35	(Y12432) polyprotein [Ananas comosus]
3701	GM_83_B2_E06_MR	g1480927	BLASTN	1007	4e-39	84	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
3702	GM_83_B2_F12_T7	g18559	BLASTN	860	6e-32	76	G.max gene for catalase
3703	GM_83_B2_F06_MR	g3645899	BLASTX	342	4e-29	49	(U68408) 5' end not determined experimentally [Zea mays]

3704	GM_83_B2_G01_T7	g2341032	BLASTX	207	5e-15	61	(AC000104) EST gb ATTS0956 comes from this gene [Arabidopsis thaliana]
3705	GM_83_B2_G03_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3706	GM_83_B2_G04_MR	g507910	BLASTN	621	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3707	GM_83_B2_G12_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3708	GM_83_B2_H03_MR	g18559	BLASTN	819	4e-30	71	G.max gene for catalase
3709	GM_83_B2_H07_T7	g3395436	BLASTX	218	2e-17	49	(AC004683) unknown protein [Arabidopsis thaliana]
3710	GM_83_B2_H09_T7	g3097320	BLASTN	472	2e-14	75	Glycine max gene for Bd 30K. complete cds
3711	GM_83_B2_H12_T7	g3928116	BLASTN	400	5e-11	67	, complete sequence [Homo sapiens]
3712	GM_84_A1_A02_T7	g3777527	BLASTX	693	3e-66	92	(AF053008) gag-pol polyprotein [Glycine max]
3713	GM_84_A1_A03_T7	g2997694	BLASTX	254	5e-21	38	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
3714	GM_84_A1_A08_MR	g3142328	BLASTN	972	4e-37	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Y12432) polyprotein [Ananas comosus]
3715	GM_84_A1_A09_MR	g2995405	BLASTX	401	1e-35	62	Arabidopsis thaliana BAC F8M12
3716	GM_84_A1_A10_T7	g3513725	BLASTN	437	1e-12	77	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3717	GM_84_A1_A11_T7	g3810596	BLASTX	118	4e-10	53	retrovirus-related copia polyprotein - fruit fly (Drosophila simulans) (fragments)
3718	GM_84_A1_C04_T7	g345511	BLASTX	325	2e-27	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3719	GM_84_A1_D03_T7	g3810596	BLASTX	202	5e-19	57	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
3720	GM_84_A1_D10_MR	g130582	BLASTX	357	1e-30	44	(TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
3721	GM_84_A1_D10_T7	g1707019	BLASTX	290	7e-25	58	(U78721) hypothetical protein [Arabidopsis thaliana]
3722	GM_84_A1_F01_T7	g18559	BLASTN	1127	4e-44	76	G.max gene for catalase
3723	GM_84_A1_F07_T7	g4063760	BLASTX	214	2e-15	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3724	GM_84_A1_E08_MR	g3859610	BLASTN	537	3e-17	65	Arabidopsis thaliana BAC T9E19
3725	GM_84_A1_E10_T7	g508826	BLASTN	259	4e-11	70	Drosophila melanogaster Oregon-R mitochondrial A+T region.
3726	GM_84_A1_E11_T7	g3204134	BLASTX	201	3e-14	70	(AJ006771) beta-galactosidase [Cicer arietinum]
3727	GM_84_A1_F01_MR	g1666236	BLASTX	202	3e-15	32	(U76261) unknown [Hordeum vulgare]
3728	GM_84_A1_F01_T7	g3777527	BLASTX	257	8e-20	41	(AF053008) gag-pol polyprotein [Glycine max]
3729	GM_84_A1_F05_MR	g1184075	BLASTX	304	5e-25	43	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
3730	GM_84_A1_F06_T7	g905361	BLASTX	704	1e-68	95	(U22103) gag-protase polyprotein [Glycine max]
3731	GM_84_A1_F07_T7	g2522228	BLASTX	155	9e-10	34	(AB007466) reverse transcriptase-like protein [Vicia faba]
3732	GM_84_A1_F08_MR	g3193314	BLASTX	248	1e-19	61	(AF069299) contains similarity to Arabidopsis scarecrow (GB:U62798) [Arabidopsis thaliana]

3733	GM_84_A1_F08_T7	g2522230	BLASTX	218	3e-17	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
3734	GM_84_A1_F10_MR	g905361	BLASTX	383	4e-34	94	(U22103) gag-protease polyprotein [Glycine max]
3735	GM_84_A1_G03_T7	g4063760	BLASTX	533	2e-49	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3736	GM_84_A1_G07_T7	g3142328	BLASTN	998	3e-38	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3737	GM_84_A1_G09_MR	g1633043	BLASTN	603	2e-20	76	Lupinus angustifolius conglutin gamma gene, complete cds
3738	GM_84_A1_G10_MR	g3142328	BLASTN	794	5e-29	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3739	GM_84_A1_H01_T7	g18559	BLASTN	382	3e-10	70	G-max gene for catalase
3740	GM_84_A1_H08_T7	g18559	BLASTN	399	5e-11	78	G-max gene for catalase
3741	GM_84_A1_H09_MR	g507910	BLASTN	361	1e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3742	GM_84_A1_H09_T7	g3142328	BLASTN	1114	2e-43	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3743	GM_84_A1_H12_T7	g3142328	BLASTN	991	6e-38	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3744	GM_84_A2_A01_T7	g226407	BLASTX	196	2e-13	37	retrotransposon del1-46 [Lilium henryi]
3745	GM_84_A2_A04_MR	g3097320	BLASTN	430	2e-12	72	Glycine max gene for Bd 30K, complete cds
3746	GM_84_A2_A05_MR	g3243214	BLASTN	384	3e-10	67	Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
3747	GM_84_A2_A05_T7	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
3748	GM_84_A2_A10_MR	g1272349	BLASTX	188	3e-13	53	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
3749	GM_84_A2_A11_T7	g99729	BLASTX	127	5e-12	47	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
3750	GM_84_A2_B02_MR	g3645899	BLASTX	206	6e-19	52	(U68408) 5' end not determined experimentally [Zea mays]
3751	GM_84_A2_B06_MR	g2827663	BLASTX	163	3e-10	30	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]
3752	GM_84_A2_B06_T7	g2244839	BLASTX	169	4e-24	52	(Z97337) hypothetical protein [Arabidopsis thaliana]
3753	GM_84_A2_C01_T7	g2129618	BLASTX	200	5e-14	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3754	GM_84_A2_C07_T7	g3599418	BLASTN	353	6e-09	63	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
3755	GM_84_A2_C12_T7	g1778843	BLASTN	429	2e-12	66	Dictyostelium discoideum LimA (limA) mRNA, partial cds
3756	GM_84_A2_D01_MR	g18559	BLASTN	1077	8e-42	75	G-max gene for catalase
3757	GM_84_A2_D08_MR	g2462134	BLASTX	106	1e-12	42	(Y13368) reverse transcriptase [Beta vulgaris]
3758	GM_84_A2_E01_MR	g4063760	BLASTX	420	4e-43	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3759	GM_84_A2_E01_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3760	GM_84_A2_E02_T7	g3777527	BLASTX	815	2e-79	97	(AF053008) gag-pol polyprotein [Glycine max]

3761	GM_84_A2_F03_MR	g1236920	BLASTN	508	4e-16	64	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
3762	GM_84_A2_E05_MR	g1272349	BLASTX	181	2e-12	55	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
3763	GM_84_A2_E07_T7	g3777527	BLASTX	257	9e-20	52	(AF053008) gag-pol polyprotein [Glycine max]
3764	GM_84_A2_F03_MR	g2760839	BLASTX	195	1e-13	35	(AC003105) putative receptor kinase [Arabidopsis thaliana]
3765	GM_84_A2_F04_T7	g122106	BLASTX	289	9e-25	93	HISTONE H4 gi 70771 pir HSM4 histone H4 - maize gi 81642 pir S06904 histone H4 - Arabidopsis thaliana gi 2119028 pir S60475 histone H4 - garden pea gi 21795 (X00043) histone H4 [Triticum aestivum] gi 166740 (M17132) histone H4 [Arabidopsis thaliana] gi 166742 (M17133) histone H4 [Arabidopsis thaliana] gi 168499 (M36659) histone H4 (H4C13) [Zea mays] gi 168501 (M13370) histone H4 [Zea mays] gi 168503 (M13377) histone H4 [Zea mays] gi 498898 (U10042) histone H4 homolog [Pisum sativum] gi 1806285 gnl PID e263432 (Z79638) histone H4 homologue [Sesbania rostrata] gi 225838 prf 1314298A histone H4 [Arabidopsis thaliana]
3766	GM_84_A2_F07_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3767	GM_84_A2_F09_MR	g3097320	BLASTN	438	9e-13	70	Glycine max gene for Bd 30K, complete cds
3768	GM_84_A2_F09_T7	g3451069	BLASTX	192	4e-13	63	(AL031326) hypothetical protein [Arabidopsis thaliana]
3769	GM_84_A2_F11_T7	g3777527	BLASTX	184	9e-15	40	(AF053008) gag-pol polyprotein [Glycine max]
3770	GM_84_A2_G03_MR	g2129618	BLASTX	227	7e-17	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3771	GM_84_A2_G08_MR	g3845108	BLASTN	386	2e-10	63	Plasmodium falciparum chromosome 2, section 13 of 73 of the complete sequence
3772	GM_84_A2_H02_T7	g2618603	BLASTN	545	1e-17	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]
3773	GM_84_A2_H06_MR	g3142328	BLASTN	978	2e-37	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3774	GM_84_A2_H09_MR	g507910	BLASTN	355	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3775	GM_84_A2_H09_T7	g3777527	BLASTX	573	2e-53	92	(AF053008) gag-pol polyprotein [Glycine max]
3776	GM_84_A2_H10_MR	g3142328	BLASTN	380	3e-10	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3777	GM_84_B1_A01_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3778	GM_84_B1_A01_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3779	GM_84_B1_A06_MR	g3097320	BLASTN	604	3e-20	76	Glycine max gene for Bd 30K, complete cds
3780	GM_84_B1_A08_MR	g3335331	BLASTN	303	4e-09	84	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]
3781	GM_84_B1_A08_T7	g3894193	BLASTX	219	7e-17	37	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

3782	GM_84_B1_A09_T7	g343760	BLASTN	250	3e-11	73	Yeast mitochondrial oxi3 gene, 3' end. ATPase subunit 3 (aap1) and ATPase subunit 6 (oli2) gene, complete cds.
3783	GM_84_B1_A10_MR	g1142701	BLASTN	1132	8e-45	82	Glycine max satellite STR120-A.3.
3784	GM_84_B1_A11_T7	g18559	BLASTN	401	4e-11	66	G.max gene for catalase
3785	GM_84_B1_B01_MR	g2443320	BLASTX	389	6e-34	49	(D85597) polyprotein [Oryza australiensis]
3786	GM_84_B1_B01_T7	g3097320	BLASTN	944	1e-35	73	Glycine max gene for Bd 30K, complete cds
3787	GM_84_B1_B03_T7	g3097320	BLASTN	492	3e-15	70	Glycine max gene for Bd 30K, complete cds
3788	GM_84_B1_B06_MR	g3426334	BLASTN	485	6e-15	62	Pisum sativum pectin methylesterase (rpmel) gene, complete cds
3789	GM_84_B1_B08_MR	g3068582	BLASTN	357	4e-09	61	Dictyostelium discoideum plasmid Ddp5, complete genome
3790	GM_84_B1_B08_T7	g99801	BLASTX	230	1e-17	61	chaperonine 60K alpha chain - rape plastid (fragment)
3791	GM_84_B1_B10_T7	g3777527	BLASTX	244	2e-18	42	(AF053008) gag-pol polyprotein [Glycine max]
3792	GM_84_B1_C01_MR	g18559	BLASTN	553	5e-18	73	G.max gene for catalase
3793	GM_84_B1_C04_MR	g629693	BLASTX	178	2e-12	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
3794	GM_84_B1_C07_MR	g18695	BLASTN	421	4e-12	85	Soybean nodulin 22 gene
3795	GM_84_B1_C10_T7	g3142328	BLASTN	648	2e-22	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U90439) unknown protein [Arabidopsis thaliana]
3796	GM_84_B1_D01_MR	g1871180	BLASTX	226	4e-18	76	(U68408) 5' end not determined experimentally [Zea mays]
3797	GM_84_B1_D02_MR	g3645899	BLASTX	398	4e-35	50	Soybean Tgm6 transposable element 3' end
3798	GM_84_B1_D03_T7	g18768	BLASTN	517	5e-17	73	(X98357) NADP-malate dehydrogenase [Chlamydomonas reinhardtii]
3799	GM_84_B1_D05_MR	g1770192	BLASTX	138	2e-29	70	G.max gene for catalase
3800	GM_84_B1_D07_T7	g18559	BLASTN	1026	2e-39	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3801	GM_84_B1_D10_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence
3802	GM_84_B1_D10_T7	g507910	BLASTN	376	2e-10	72	(Y12432) polyprotein [Ananas comosus]
3803	GM_84_B1_D11_MR	g2995405	BLASTX	284	5e-23	45	(AC004747) hypothetical protein [Arabidopsis thaliana]
3804	GM_84_B1_E02_MR	g3413707	BLASTX	344	7e-34	73	(AF031569) hypothetical protein [Zea mays]
3805	GM_84_B1_E05_T7	g2832245	BLASTX	138	1e-08	32	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3806	GM_84_B1_F06_T7	g3142328	BLASTN	923	7e-35	92	(AJ003197) adenine nucleotide translocator [Lupinus albus]
3807	GM_84_B1_E07_MR	g2780194	BLASTX	166	5e-11	44	(AL021637) Phosphoribosylanthranilate transferase [Arabidopsis thaliana]
3808	GM_84_B1_E07_T7	g2827662	BLASTX	247	3e-19	48	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]
3809	GM_84_B1_E11_MR	g2264306	BLASTN	349	1e-08	60	(U72725) retrofit [Oryza longistaminata]
3810	GM_84_B1_E11_T7	g2586082	BLASTX	202	5e-14	43	(AC002986) Contains repeats similar to RECA protein gb 1.26100 from Acinetobacter calcoaceticus. [Arabidopsis thaliana]
3811	GM_84_B1_E12_T7	g3152594	BLASTX	189	3e-13	42	(U22103) gag-protease polyprotein [Glycine max]
3812	GM_84_B1_F01_MR	g905361	BLASTX	424	9e-39	95	

3813	GM_84_B1_F02_MR	g1769898	BLASTX	303	2e-25	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3814	GM_84_B1_F02_T7	g2522227	BLASTX	180	5e-13	60	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3815	GM_84_B1_F05_T7	g13617	BLASTN	403	3e-11	61	S.douglasii gene for cytochrome b
3816	GM_84_B1_F08_MR	g507910	BLASTN	443	2e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3817	GM_84_B1_F08_T7	g507910	BLASTN	367	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3818	GM_84_B1_F09_T7	g2245044	BLASTX	121	2e-13	34	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
3819	GM_84_B1_G01_MR	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3820	GM_84_B1_G01_T7	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3821	GM_84_B1_G02_MR	g99922	BLASTX	577	3e-55	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3822	GM_84_B1_G02_T7	g2995405	BLASTX	198	9e-21	41	(Y12432) polyprotein [Ananas comosus]
3823	GM_84_B1_G03_MR	g1431738	BLASTN	713	2e-25	76	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
3824	GM_84_B1_G04_MR	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3825	GM_84_B1_G07_MR	g3142328	BLASTN	1066	2e-41	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3826	GM_84_B1_G08_MR	g18559	BLASTN	349	9e-09	71	G.max gene for catalase
3827	GM_84_B1_G10_MR	g2443320	BLASTX	366	2e-31	55	(D85597) polyprotein [Oryza australiensis]
3828	GM_84_B1_H01_MR	g99755	BLASTX	339	2e-29	46	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Tal-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
3829	GM_84_B1_H06_MR	g12628	BLASTN	417	5e-12	62	Aedes albopictus mit-gene for large ribosomal subunit RNA (LSU)
3830	GM_84_B1_H09_MR	g170080	BLASTN	355	4e-09	63	Soybean seed lectin gene transposable element tgm1.
3831	GM_84_B1_H10_T7	g3522933	BLASTX	169	1e-11	78	(AC004411) putative anion exchange protein 3 [Arabidopsis thaliana]
3832	GM_84_B1_H12_MR	g2462134	BLASTX	243	4e-19	35	(Y13368) reverse transcriptase [Beta vulgaris]
3833	GM_84_B2_A01_MR	g3645899	BLASTX	215	8e-25	51	(U68408) 5' end not determined experimentally [Zea mays]
3834	GM_84_B2_A03_MR	g18559	BLASTN	472	2e-14	67	G.max gene for catalase
3835	GM_84_B2_A03_T7	g3845197	BLASTN	424	4e-12	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
3836	GM_84_B2_A05_MR	g3142328	BLASTN	660	7e-23	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3837	GM_84_B2_B01_T7	g2995405	BLASTX	289	3e-30	71	(Y12432) polyprotein [Ananas comosus]
3838	GM_84_B2_B03_T7	g3688808	BLASTX	148	9e-09	52	(AF084104) AcsA [Bacillus firmus]
3839	GM_84_B2_B04_T7	g2443320	BLASTX	362	4e-31	49	(D85597) polyprotein [Oryza australiensis]
3840	GM_84_B2_B05_MR	g3264544	BLASTN	420	6e-12	62	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]

3841	GM_84_B2_B06_MR	g1666236	BLASTX	207	7e-16	36	(U76261) unknown [Hordeum vulgare]
3842	GM_84_B2_B07_MR	g4063760	BLASTX	388	6e-34	55	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3843	GM_84_B2_B08_MR	g18695	BLASTN	545	7e-18	70	Soybean nodulin 22 gene
3844	GM_84_B2_B08_T7	g2245109	BLASTX	162	7e-16	88	(Z97343) carboxyl-terminal proteinase homolog [Arabidopsis thaliana]
3845	GM_84_B2_B12_MR	g2995405	BLASTX	415	4e-37	57	(Y12432) polyprotein [Ananas comosus]
3846	GM_84_B2_C06_T7	g467491	BLASTN	397	1e-11	69	Chlorella vulgaris genomic DNA, telomeric repeat
3847	GM_84_B2_C08_T7	g18559	BLASTN	1017	4e-39	76	G.max gene for catalase
3848	GM_84_B2_C09_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3849	GM_84_B2_C09_T7	g905361	BLASTX	669	5e-65	94	(U22103) gag-protease polyprotein [Glycine max]
3850	GM_84_B2_C11_T7	g3319362	BLASTX	167	1e-19	52	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
3851	GM_84_B2_C12_MR	g100484	BLASTX	227	5e-17	48	hypothetical protein - garden snapdragon
3852	GM_84_B2_D02_T7	g99726	BLASTX	115	1e-16	50	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
3853	GM_84_B2_D08_MR	g905361	BLASTX	353	8e-31	96	(U22103) gag-protease polyprotein [Glycine max]
3854	GM_84_B2_D12_T7	g1666236	BLASTX	199	7e-15	33	(U76261) unknown [Hordeum vulgare]
3855	GM_84_B2_E01_T7	g507910	BLASTN	362	9e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3856	GM_84_B2_E02_MR	g3650039	BLASTX	241	1e-18	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
3857	GM_84_B2_E03_MR	g1769898	BLASTX	394	2e-35	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3858	GM_84_B2_E03_T7	g3777527	BLASTX	353	5e-30	50	(AF053008) gag-pol polyprotein [Glycine max]
3859	GM_84_B2_E05_T7	g3142328	BLASTN	970	5e-37	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3860	GM_84_B2_E09_T7	g2764526	BLASTN	673	2e-23	66	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
3861	GM_84_B2_E10_MR	g4063760	BLASTX	406	8e-36	58	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3862	GM_84_B2_E11_T7	g2129618	BLASTX	176	2e-11	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3863	GM_84_B2_E12_MR	g18559	BLASTN	952	4e-36	75	G.max gene for catalase
3864	GM_84_B2_F12_MR	g3142328	BLASTN	782	2e-28	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3865	GM_84_B2_G01_MR	g4063760	BLASTX	296	4e-24	57	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
3866	GM_84_B2_G04_MR	g507910	BLASTN	433	6e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3867	GM_84_B2_G04_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3868	GM_84_B2_G08_MR	g1236920	BLASTN	405	2e-11	66	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.

3869	GM_84_B2_G10_MR	g1769899	BLASTX	214	2e-19	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3870	GM_84_B2_G11_T7	g3142330	BLASTX	523	2e-49	86	(U96295) envelope-like [Glycine max]
3871	GM_84_B2_H12_T7	g170029	BLASTN	380	4e-10	79	Glycine max cv. Dare nodulin 26 gene fragment
3872	GM_85_A1_A05_MR	g3142330	BLASTX	580	1e-55	83	(U96295) envelope-like [Glycine max]
3873	GM_85_A1_A09_T7	g2995405	BLASTX	265	5e-21	46	(Y12432) polyprotein [Ananas comosus]
3874	GM_85_A1_A12_MR	g4063760	BLASTX	194	3e-13	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3875	GM_85_A1_B03_MR	g4063760	BLASTX	300	1e-24	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3876	GM_85_A1_B04_MR	g1039432	BLASTN	432	1e-12	65	Glycine max cellulase gene, partial cds.
3877	GM_85_A1_B04_T7	g2182286	BLASTN	353	7e-09	61	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
3878	GM_85_A1_B05_MR	g2522228	BLASTX	215	7e-34	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
3879	GM_85_A1_B06_MR	g505129	BLASTN	384	2e-10	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
3880	GM_85_A1_B07_MR	g2335067	BLASTN	317	2e-09	63	Human BAC clone GS200K05 from 7q21-q22, complete sequence [Homo sapiens]
3881	GM_85_A1_B08_MR	g3660471	BLASTX	167	1e-10	84	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
3882	GM_85_A1_B09_T7	g1236920	BLASTN	368	1e-09	62	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
3883	GM_85_A1_B11_T7	g531389	BLASTX	145	4e-09	41	(U12626) copia-like retrotransposon Hopscotch polypeptide [Zea mays]
3884	GM_85_A1_B12_T7	g1616609	BLASTX	248	2e-20	55	(Y08641) PR10-1 protein [Medicago truncatula]
3885	GM_85_A1_C01_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3886	GM_85_A1_C01_T7	g507910	BLASTN	403	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3887	GM_85_A1_C03_MR	g4063760	BLASTX	165	4e-19	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3888	GM_85_A1_C03_T7	g1480927	BLASTN	473	2e-14	73	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
3889	GM_85_A1_C05_MR	g2244855	BLASTX	194	8e-18	58	(Z97337) hypothetical protein [Arabidopsis thaliana]
3890	GM_85_A1_C06_MR	g4063760	BLASTX	425	7e-38	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3891	GM_85_A1_C06_T7	g507910	BLASTN	565	6e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
3892	GM_85_A1_C11_MR	g3176659	BLASTX	209	4e-15	62	(AC004393) Strong similarity to receptor kinase gb M80238 from A. thaliana. [Arabidopsis thaliana]
3893	GM_85_A1_D01_MR	g18559	BLASTN	621	8e-31	77	G.max gene for catalase
3894	GM_85_A1_D03_MR	g3650035	BLASTX	165	3e-10	36	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
3895	GM_85_A1_D04_MR	g100484	BLASTX	211	6e-31	54	hypothetical protein - garden snapdragon
3896	GM_85_A1_D04_T7	g99922	BLASTX	435	3e-40	63	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3897	GM_85_A1_D08_T7	g1468969	BLASTX	104	3e-09	52	(D30666) brain acyl-CoA synthase II [Rattus norvegicus]

3898	GM_85_A1_D12_MR	g507910	BLASTN	594	3e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
3899	GM_85_A1_E01_T7	g4063760	BLASTX	260	1e-21	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3900	GM_85_A1_E02_T7	g18693	BLASTN	455	1e-14	66	Soybean mRNA for Nodulin-21.
3901	GM_85_A1_E04_MR	g3241926	BLASTN	577	5e-19	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]
3902	GM_85_A1_E05_T7	g3513451	BLASTX	135	3e-09	58	(U78090) potassium channel regulator 1 [Rattus norvegicus]
3903	GM_85_A1_E07_MR	g4063760	BLASTX	516	1e-47	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3904	GM_85_A1_E09_MR	g2462744	BLASTX	134	1e-09	36	(AC002292) Hypothetical protein [Arabidopsis thaliana]
3905	GM_85_A1_E12_MR	g18559	BLASTN	1037	5e-40	76	G-max gene for catalase
3906	GM_85_A1_F01_MR	g1142703	BLASTN	295	7e-17	77	Glycine max satellite STR120-B.1.
3907	GM_85_A1_F03_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3908	GM_85_A1_F04_MR	g99922	BLASTX	236	4e-19	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA): pid:e150225 [Glycine max]
3909	GM_85_A1_G04_MR	g2129472	BLASTX	123	3e-13	72	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine gi 1100225 (L32561) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
3910	GM_85_A1_G04_T7	g3810596	BLASTX	359	5e-31	49	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3911	GM_85_A1_G10_T7	g2443320	BLASTX	154	6e-09	32	(D85597) polyprotein [Oryza australiensis]
3912	GM_85_A1_H01_T7	g4092471	BLASTN	540	2e-17	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
3913	GM_85_A1_H05_MR	g3599418	BLASTN	366	1e-09	74	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
3914	GM_85_A1_H07_T7	g3097320	BLASTN	451	2e-13	70	Glycine max gene for Bd 30K, complete cds
3915	GM_85_A1_H08_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence
3916	GM_85_A1_H10_T7	g1778105	BLASTX	269	1e-22	81	(U64893) expansin [Pinus taeda]
3917	GM_85_A2_A04_MR	g3097320	BLASTN	379	4e-10	71	Glycine max gene for Bd 30K, complete cds
3918	GM_85_A2_A05_MR	g1142701	BLASTN	1301	2e-52	85	Glycine max satellite STR120-A.3.
3919	GM_85_A2_A06_MR	g3746069	BLASTX	118	4e-10	38	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
3920	GM_85_A2_A07_MR	g3097320	BLASTN	1075	1e-41	79	Glycine max gene for Bd 30K, complete cds
3921	GM_85_A2_A10_T7	g1167523	BLASTX	270	3e-21	41	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
3922	GM_85_A2_B03_T7	g1666236	BLASTX	104	1e-12	46	(U76261) unknown [Hordeum vulgare]
3923	GM_85_A2_B04_MR	g507910	BLASTN	398	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3924	GM_85_A2_B04_T7	g4063760	BLASTX	269	3e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3925	GM_85_A2_B05_MR	g2708743	BLASTX	183	5e-12	30	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
3926	GM_85_A2_B05_T7	g3021268	BLASTX	191	9e-24	45	(AL022347) putative protein [Arabidopsis thaliana]
3927	GM_85_A2_B06_T7	g2443320	BLASTX	193	4e-13	36	(D85597) polyprotein [Oryza australiensis]
3928	GM_85_A2_C07_T7	g3510505	BLASTX	161	3e-15	45	(AF030881) pol polyprotein [Fugu rubripes]
3929	GM_85_A2_C08_MR	g1666236	BLASTX	109	7e-14	33	(U76261) unknown [Hordeum vulgare]

3930	GM_85_A2_C09_MR	g2842482	BLASTX	188	4e-14	57	(AL021749) protein phosphatase 2C-like protein [Arabidopsis thaliana]
3931	GM_85_A2_C10_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3932	GM_85_A2_C10_T7	g4063760	BLASTX	237	8e-18	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3933	GM_85_A2_C12_MR	g2842482	BLASTX	195	9e-15	58	(AL021749) protein phosphatase 2C-like protein [Arabidopsis thaliana]
3934	GM_85_A2_D02_T7	g2190263	BLASTX	101	1e-11	58	(D86387) A-type cyclin [Catharanthus roseus]
3935	GM_85_A2_D03_T7	g507910	BLASTN	401	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3936	GM_85_A2_D05_MR	g3047060	BLASTN	371	2e-10	67	Arabidopsis thaliana BAC F7N22
3937	GM_85_A2_D05_T7	g3810596	BLASTX	151	9e-09	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3938	GM_85_A2_D07_MR	g3378649	BLASTN	352	4e-09	74	M.sativa mRNA translated from abscisic activated gene
3939	GM_85_A2_D07_T7	g857393	BLASTX	111	2e-11	48	(D50868) mitotic cyclin a1-type [Glycine max]
3940	GM_85_A2_D09_T7	g2443320	BLASTX	204	3e-14	51	(D85597) polyprotein [Oryza australiensis]
3941	GM_85_A2_D10_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3942	GM_85_A2_D12_MR	g170606	BLASTN	743	4e-27	66	Broad bean (V.faba) BamHI repetitive element. 1750 bp family.
3943	GM_85_A2_E01_MR	g2462936	BLASTX	361	2e-32	49	(Y12321) open reading frame 2 [Brassica oleracea]
3944	GM_85_A2_E02_MR	g4063760	BLASTX	256	7e-20	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3945	GM_85_A2_E02_T7	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3946	GM_85_A2_E08_MR	g4063760	BLASTX	494	3e-45	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3947	GM_85_A2_E08_T7	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3948	GM_85_A2_E09_MR	g2429543	BLASTX	163	6e-10	37	Glycine max BSR-101 satellite SB92 genomic sequence. (AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350)
3949	GM_85_A2_E11_MR	g2443320	BLASTX	296	5e-24	49	[Caenorhabditis elegans]
3950	GM_85_A2_E12_MR	g3777526	BLASTN	508	6e-16	87	(D85597) polyprotein [Oryza australiensis]
3951	GM_85_A2_F02_MR	g2129618	BLASTX	170	8e-11	41	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
3952	GM_85_A2_F03_T7	g4033838	BLASTX	286	4e-28	70	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3953	GM_85_A2_F05_MR	g2129618	BLASTX	182	4e-12	40	(Y18550) sigma-like factor [Arabidopsis thaliana]
3954	GM_85_A2_F05_T7	g18559	BLASTN	840	5e-31	75	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3955	GM_85_A2_F08_MR	g2924781	BLASTX	146	7e-16	45	G.max gene for catalase
3956	GM_85_A2_F09_MR	g3845084	BLASTN	362	3e-09	65	(AC002334) putative cellulose synthase [Arabidopsis thaliana]
3957	GM_85_A2_G03_MR	g3142328	BLASTN	805	2e-29	82	Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence
3958	GM_85_A2_G07_MR	g507910	BLASTN	344	6e-09	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
							Glycine max BSR-101 satellite SB92 genomic sequence.

3959	GM_85_A2_H02_MR	g3763850	BLASTN	640	6e-22	66	Glycine max GmENOD93 gene for early nodulin, complete cds
3960	GM_85_A2_H03_MR	g3142328	BLASTN	1243	2e-49	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3961	GM_85_A2_H08_MR	g18559	BLASTN	814	7e-30	72	G.max gene for catalase
3962	GM_85_A2_H09_MR	g18559	BLASTN	823	3e-30	75	G.max gene for catalase
3963	GM_85_B1_A04_MR	g2464905	BLASTX	197	5e-15	53	(Z99708) minor allergen [Arabidopsis thaliana]
3964	GM_85_B1_A08_T7	g100484	BLASTX	365	6e-32	53	hypothetical protein - garden snapdragon
3965	GM_85_B1_B02_T7	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3966	GM_85_B1_C01_T7	g2129618	BLASTX	154	4e-09	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3967	GM_85_B1_C02_T7	g3142328	BLASTN	619	5e-21	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3968	GM_85_B1_C07_MR	g3645899	BLASTX	389	4e-34	56	(U68408) 5' end not determined experimentally [Zea mays]
3969	GM_85_B1_F01_T7	g2522228	BLASTX	193	3e-16	50	(AB007466) reverse transcriptase-like protein [Vicia faba]
3970	GM_85_B1_F05_T7	g3777526	BLASTN	448	3e-13	91	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
3971	GM_85_B1_F06_MR	g1769898	BLASTX	153	1e-16	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3972	GM_85_B1_F09_T7	g4063756	BLASTN	482	1e-14	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3973	GM_85_B1_G03_T7	g3080532	BLASTX	111	2e-11	64	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
3974	GM_85_B1_G05_MR	g4038056	BLASTX	321	5e-27	48	(AC005897) putative transposon [Arabidopsis thaliana]
3975	GM_85_B1_G06_MR	g3386614	BLASTX	146	1e-09	77	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]
3976	GM_85_B1_G10_MR	g4006831	BLASTX	191	6e-13	40	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
3977	GM_85_B1_G11_MR	g3319366	BLASTX	104	2e-09	41	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
3978	GM_85_B1_H12_T7	g2190544	BLASTX	148	4e-09	84	(AC001229) Similar to Saccharomyces hypothetical protein P9642.2 (gb U40828). [Arabidopsis thaliana]
3979	GM_85_B2_A04_MR	g18559	BLASTN	675	5e-36	79	G.max gene for catalase
3980	GM_85_B2_A07_MR	g1171583	BLASTN	354	6e-09	61	P.falciparum complete gene map of plastid-like DNA (IR-A)
3981	GM_85_B2_A12_MR	g2462756	BLASTX	184	2e-12	67	(AC002292) putative receptor kinase [Arabidopsis thaliana]
3982	GM_85_B2_A12_T7	g3777527	BLASTX	699	6e-67	90	(AF053008) gag-pol polyprotein [Glycine max]
3983	GM_85_B2_B04_MR	g3810596	BLASTX	231	2e-17	34	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3984	GM_85_B2_B05_T7	g3097320	BLASTN	1022	3e-39	78	Glycine max gene for Bd 30K, complete cds
3985	GM_85_B2_B07_T7	g3777527	BLASTX	647	2e-61	87	(AF053008) gag-pol polyprotein [Glycine max]
3986	GM_85_B2_B10_T7	g4063756	BLASTN	559	3e-18	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3987	GM_85_B2_B11_MR	g2462756	BLASTX	183	2e-12	70	(AC002292) putative receptor kinase [Arabidopsis thaliana]
3988	GM_85_B2_B11_T7	g3777527	BLASTX	753	1e-72	96	(AF053008) gag-pol polyprotein [Glycine max]

3989	GM_85_B2_B12_T7	g3426033	BLASTN	730	6e-26	71	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]
3990	GM_85_B2_C06_T7	g3810595	BLASTX	130	3e-16	33	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
3991	GM_85_B2_C12_MR	g4063760	BLASTX	495	2e-45	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3992	GM_85_B2_D01_T7	g3243214	BLASTN	463	7e-14	69	Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
3993	GM_85_B2_D02_T7	g4063760	BLASTX	514	2e-47	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3994	GM_85_B2_D03_MR	g3142328	BLASTN	1062	4e-41	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3995	GM_85_B2_D04_T7	g2129618	BLASTX	264	7e-21	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3996	GM_85_B2_E02_T7	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3997	GM_85_B2_E03_MR	g905361	BLASTX	153	3e-09	34	(U22103) gag-protease polyprotein [Glycine max]
3998	GM_85_B2_E06_MR	g3695395	BLASTX	250	1e-19	45	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
3999	GM_85_B2_F01_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4000	GM_85_B2_F01_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4001	GM_85_B2_F05_MR	g3021696	BLASTN	387	2e-10	62	Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, complete sequence [Homo sapiens]
4002	GM_85_B2_F08_MR	g886130	BLASTX	304	2e-26	60	(U28148) putative pectinesterase [Medicago sativa]
4003	GM_85_B2_G02_MR	g2367431	BLASTX	395	6e-36	50	(AF000403) putative cytochrome P450 [Lotus japonicus]
4004	GM_85_B2_G05_T7	g2995405	BLASTX	311	6e-26	46	(Y12432) polyprotein [Ananas comosus]
4005	GM_85_B2_G07_MR	g1785729	BLASTN	366	2e-09	62	A.thaliana mitochondrial genome, part B
4006	GM_85_B2_G09_T7	g4063760	BLASTX	382	3e-33	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4007	GM_85_B2_G12_MR	g4079614	BLASTN	592	1e-19	67	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]
4008	GM_85_B2_H01_MR	g18559	BLASTN	770	7e-28	72	G.max gene for catalase
4009	GM_85_B2_H03_MR	g1769899	BLASTX	164	2e-11	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4010	GM_85_B2_H04_MR	g3777527	BLASTX	192	7e-13	42	(AF053008) gag-pol polyprotein [Glycine max]
4011	GM_85_B2_H04_T7	g3097320	BLASTN	778	4e-44	82	Glycine max gene for Bd 30K, complete cds
4012	GM_85_B2_H05_MR	g4056485	BLASTX	196	8e-14	48	(AC005896) hypothetical protein [Arabidopsis thaliana]
4013	GM_85_B2_H08_T7	g3097320	BLASTN	453	2e-13	75	Glycine max gene for Bd 30K, complete cds
4014	GM_86_A2_A03_MR	g4063760	BLASTX	142	2e-19	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4015	GM_86_A2_A04_MR	g3142328	BLASTN	700	1e-24	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4016	GM_86_A2_A08_T7	g4063760	BLASTX	158	2e-09	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4017	GM_86_A2_A09_MR	g18559	BLASTN	983	2e-37	75	G.max gene for catalase
4018	GM_86_A2_B03_MR	g3859610	BLASTN	691	3e-24	66	Arabidopsis thaliana BAC T9E19

4019	GM_86_A2_B07_MR	g507910	BLASTN	536	1e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4020	GM_86_A2_B08_MR	g3820757	BLASTN	383	2e-10	60	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
4021	GM_86_A2_C02_T7	g100484	BLASTX	149	7e-15	52	hypothetical protein - garden snapdragon
4022	GM_86_A2_C05_MR	g4063760	BLASTX	292	1e-23	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4023	GM_86_A2_C09_T7	g3377855	BLASTX	233	8e-19	77	(AF076274) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zfr.hmm, score: 14.43) [Arabidopsis thaliana]
4024	GM_86_A2_D03_MR	g3810596	BLASTX	183	3e-12	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4025	GM_86_A2_D03_T7	g2281094	BLASTX	167	9e-18	67	(AC002333) molybdenum cofactor biosynthesis protein E isolog [Arabidopsis thaliana]
4026	GM_86_A2_D07_MR	g4050011	BLASTN	427	3e-12	70	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
4027	GM_86_A2_D09_MR	g507910	BLASTN	574	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4028	GM_86_A2_D09_T7	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4029	GM_86_A2_E03_MR	g4056466	BLASTX	155	6e-10	37	(AC005990) F508.39 [Arabidopsis thaliana]
4030	GM_86_A2_E08_MR	g507910	BLASTN	403	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4031	GM_86_A2_E10_T7	g13520	BLASTN	248	5e-11	67	Two yeast mitochondrial genes for transfer RNA.
4032	GM_86_A2_F01_MR	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4033	GM_86_A2_F01_T7	g4063756	BLASTN	410	2e-11	65	Arabidopsis thaliana chromosome II BAC T9f-8 genomic sequence, complete sequence [Arabidopsis thaliana]
4034	GM_86_A2_F07_MR	g3256035	BLASTX	315	2e-27	54	(Y14274) putative serine/threonine protein kinase [Sorghum bicolor]
4035	GM_86_A2_F11_MR	g3097320	BLASTN	726	8e-26	80	Glycine max gene for Bd 30K, complete cds
4036	GM_86_A2_G01_MR	g2961377	BLASTX	188	1e-12	38	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]
4037	GM_86_A2_G02_T7	g3355478	BLASTX	151	1e-09	37	(AC004218) hypothetical protein [Arabidopsis thaliana]
4038	GM_86_A2_G03_MR	g2995405	BLASTX	556	2e-52	69	(Y12432) polyprotein [Ananas comosus]
4039	GM_86_A2_G04_MR	g4158219	BLASTX	184	3e-13	53	(Y18623) amylogenin [Oryza sativa]
4040	GM_86_A2_G06_MR	g3097320	BLASTN	354	5e-09	72	Glycine max gene for Bd 30K, complete cds
4041	GM_86_A2_G09_MR	g2970554	BLASTN	384	3e-10	65	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
4042	GM_86_A2_H01_MR	g507910	BLASTN	504	4e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4043	GM_86_A2_H04_MR	g4038056	BLASTX	127	6e-12	43	(AC005897) putative transposon [Arabidopsis thaliana]
4044	GM_86_A2_H06_MR	g3645899	BLASTX	271	2e-21	47	(U68408) 5' end not determined experimentally [Zea mays]
4045	GM_86_A2_H08_MR	g3097320	BLASTN	1128	5e-44	81	Glycine max gene for Bd 30K, complete cds
4046	GM_86_A2_H09_MR	g1769897	BLASTX	237	2e-34	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4047	GM_86_B1_A01_MR	g1518625	BLASTN	362	6e-10	62	Cerataphis freycinetiae cytochrome oxidase I and II gene, mitochondrial genes encoding mitochondrial proteins, partial cds and tRNA-Leu gene, complete sequence
4048	GM_86_B1_A01_T7	g1418331	BLASTX	154	7e-11	46	(X05909) receptor like protein kinase [Arabidopsis thaliana]

4049	GM_86_B1_A06_MR	g505129	BLASTN	360	3e-09	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4050	GM_86_B1_A08_MR	g99922	BLASTX	241	7e-28	75	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA): pid:e150225 [Glycine max]
4051	GM_86_B1_A12_MR	g3695395	BLASTX	170	5e-11	43	(AF096372) contains similarity to reverse transcriptase (Pfam): PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
4052	GM_86_B1_B01_MR	g507910	BLASTN	502	4e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4053	GM_86_B1_B04_T7	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4054	GM_86_B1_B05_MR	g3142330	BLASTX	562	1e-53	93	(U96295) envelope-like [Glycine max]
4055	GM_86_B1_B07_MR	g507910	BLASTN	612	5e-21	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4056	GM_86_B1_C02_T7	g4140712	BLASTX	266	2e-22	63	(AF110183) putative integrase [Oryza sativa]
4057	GM_86_B1_C03_T7	g3777527	BLASTX	713	2e-68	98	(AF053008) gag-pol polypeptide [Glycine max]
4058	GM_86_B1_C05_MR	g226407	BLASTX	471	1e-42	53	retrotransposon del1-46 [Lilium henryi]
4059	GM_86_B1_C06_T7	g170606	BLASTN	425	2e-12	64	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
4060	GM_86_B1_D03_T7	g2443320	BLASTX	171	9e-11	35	(D85597) polypeptide [Oryza australiensis]
4061	GM_86_B1_D05_MR	g3142328	BLASTN	1054	8e-41	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF053008) gag-pol polypeptide [Glycine max]
4062	GM_86_B1_D07_MR	g3777527	BLASTX	679	8e-65	84	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4063	GM_86_B1_D08_MR	g2522230	BLASTX	247	3e-20	43	Glycine max BSR-101 satellite SB92 genomic sequence.
4064	GM_86_B1_D09_MR	g507910	BLASTN	529	3e-17	80	Glycine max gene for Bd 30K, complete cds
4065	GM_86_B1_D10_MR	g3097320	BLASTN	991	8e-38	79	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4066	GM_86_B1_D12_MR	g2129618	BLASTX	189	8e-13	36	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
4067	GM_86_B1_E02_MR	g3650039	BLASTX	257	2e-22	50	(AC005897) putative transposon [Arabidopsis thaliana]
4068	GM_86_B1_E02_T7	g4038056	BLASTX	314	3e-26	54	(AC004136) hypothetical protein [Arabidopsis thaliana]
4069	GM_86_B1_E03_T7	g3184285	BLASTX	189	1e-15	64	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4070	GM_86_B1_F01_T7	g3142328	BLASTN	1783	4e-74	94	G.max gene for catalase
4071	GM_86_B1_F06_T7	g18559	BLASTN	471	3e-14	67	retrotransposon del1-46 [Lilium henryi]
4072	GM_86_B1_F07_MR	g226407	BLASTX	299	2e-35	49	(AF053008) gag-pol polypeptide [Glycine max]
4073	GM_86_B1_G01_T7	g3777527	BLASTX	329	2e-27	53	(AF031569) hypothetical protein [Zea mays]
4074	GM_86_B1_G03_MR	g2832245	BLASTX	150	5e-10	31	Glycine max BSR-101 satellite SB92 genomic sequence.
4075	GM_86_B1_H02_MR	g507910	BLASTN	377	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4076	GM_86_B1_H02_T7	g507910	BLASTN	382	1e-10	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4077	GM_86_B1_H03_MR	g4063760	BLASTX	218	2e-20	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4078	GM_86_B1_H06_T7	g4063760	BLASTX	218	7e-16	46	(U96295) envelope-like [Glycine max]
4079	GM_86_B1_H09_T7	g3142330	BLASTX	676	1e-65	97	

4080	GM_86_B1_H11_MR	g2462058	BLASTX	205	1e-24	46	(Y13389) reverse transcriptase [Antirrhinum majus]
4081	GM_86_B2_A02_MR	g3142328	BLASTN	750	5e-27	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC003974) putative purple acid phosphatase [Arabidopsis thaliana]
4082	GM_86_B2_A03_T7	g2914696	BLASTX	164	1e-10	64	Glycine max gene for Bd 30K, complete cds
4083	GM_86_B2_A08_MR	g3097320	BLASTN	487	5e-15	68	(AF053008) gag-pol polyprotein [Glycine max]
4084	GM_86_B2_A10_T7	g3777527	BLASTX	312	1e-25	43	(D90730) Asparagine-tRNA ligase [Escherichia coli]
4085	GM_86_B2_B04_MR	g1651451	BLASTX	126	1e-18	75	Glycine max gene for Bd 30K, complete cds
4086	GM_86_B2_B05_T7	g3097320	BLASTN	483	8e-15	71	Glycine max satellite STR120-B.1.
4087	GM_86_B2_B12_T7	g1142703	BLASTN	271	5e-14	76	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabidopsis thaliana]
4088	GM_86_B2_C08_T7	g3193290	BLASTX	175	1e-11	45	(AL021637) leucine rich repeat-like protein (fragment) [Arabidopsis thaliana]
4089	GM_86_B2_C12_MR	g2832608	BLASTX	160	1e-10	40	Kunitz trypsin inhibitor precursor - soybean gi 510515 (X80039)
4090	GM_86_B2_D08_MR	g1071924	BLASTX	165	1e-14	50	Kunitz trypsin inhibitor [Glycine max]
4091	GM_86_B2_D10_T7	g2245004	BLASTX	225	5e-17	47	(Z97341) similarity to membrane transport protein [Arabidopsis thaliana]
4092	GM_86_B2_E04_MR	g13619	BLASTN	392	1e-11	63	Saccharomyces douglasii mtDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
4093	GM_86_B2_F03_MR	g226407	BLASTX	270	5e-29	45	retrotransposon del1-46 [Lilium henryi]
4094	GM_86_B2_F10_MR	g18559	BLASTN	896	1e-33	76	G.max gene for catalase
4095	GM_86_B2_G02_MR	g3142328	BLASTN	1237	4e-49	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4096	GM_86_B2_G02_T7	g136251	BLASTX	256	1e-20	73	TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR gi 99767 pir A31393 tryptophan synthase (EC 4.2.1.20) beta chain - Arabidopsis thaliana gi 166892 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]
4097	GM_86_B2_G04_T7	g3695403	BLASTX	179	1e-12	72	(AF096373) contains similarity to the pfkB family of carbohydrate kinases (Pfam: PF00294, E=1.6e-75) [Arabidopsis thaliana]
4098	GM_86_B2_G10_MR	g2501460	BLASTX	202	4e-14	52	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOL ESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gnl PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]
4099	GM_86_B2_H05_T7	g3777527	BLASTX	242	8e-22	73	(AF053008) gag-pol polyprotein [Glycine max]

4100	GM_86_B2_H08_MR	g3142328	BLASTN	1261	3e-50	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005311) putative reverse transcriptase [Arabidopsis thaliana]
4101	GM_86_B2_H11_T7	g3746069	BLASTX	164	5e-10	48	Glycine max cdc2 protein kinase (cdc2(1)) nonprocessed pseudogene
4102	GM_87_A1_A01_MR	g1480927	BLASTN	713	2e-25	91	Glycine max cv. Dare nodulin 26 gene fragment.
4103	GM_87_A1_A01_T7	g170029	BLASTN	413	1e-11	87	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
4104	GM_87_A1_A04_MR	g505129	BLASTN	364	2e-09	64	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Contain...
4105	GM_87_A1_A04_T7	g2769655	BLASTN	469	4e-14	66	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
4106	GM_87_A1_A07_MR	g2708743	BLASTX	243	2e-18	32	(AB007466) reverse transcriptase-like protein [Vicia faba]
4107	GM_87_A1_A09_MR	g2522228	BLASTX	424	5e-39	77	(AF076274) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
4108	GM_87_A1_B02_MR	g3377855	BLASTX	302	4e-48	73	(AC004255) T1F9.11 [Arabidopsis thaliana]
4109	GM_87_A1_B04_MR	g3056590	BLASTX	298	1e-24	59	(AF053008) gag-pol polyprotein [Glycine max]
4110	GM_87_A1_B05_T7	g3777527	BLASTX	308	3e-25	47	(Y12432) polyprotein [Ananas comosus]
4111	GM_87_A1_B07_MR	g2995405	BLASTX	127	9e-13	39	Glycine max BSR-101 satellite SB92 genomic sequence.
4112	GM_87_A1_B09_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4113	GM_87_A1_C03_T7	g507910	BLASTN	556	2e-18	79	hypothetical protein - garden snapdragon
4114	GM_87_A1_C08_MR	g100484	BLASTX	153	4e-09	42	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF053008) gag-pol polyprotein [Glycine max]
4115	GM_87_A1_C10_MR	g3142328	BLASTN	651	2e-22	70	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
4116	GM_87_A1_C10_T7	g3777527	BLASTX	596	2e-56	88	Glycine max gene for Bd 30K, complete cds
4117	GM_87_A1_C11_T7	g2522227	BLASTX	143	8e-09	47	(AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] gi 3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]
4118	GM_87_A1_D04_T7	g3097320	BLASTN	930	4e-35	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4119	GM_87_A1_D10_MR	g2642450	BLASTX	156	1e-09	63	(AC002337) hypothetical protein [Arabidopsis thaliana]
4120	GM_87_A1_D11_T7	g4063760	BLASTX	356	1e-30	53	(AB013599) MYB homologue [Perilla frutescens]
4121	GM_87_A1_E07_MR	g2275207	BLASTX	302	4e-26	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4122	GM_87_A1_E08_MR	g4115565	BLASTX	273	5e-23	53	(AL022347) putative protein [Arabidopsis thaliana]
4123	GM_87_A1_E11_T7	g4063760	BLASTX	374	2e-36	65	(Y07748) TMK [Oryza sativa]
4124	GM_87_A1_F04_MR	g3021268	BLASTX	431	2e-38	52	
4125	GM_87_A1_F04_T7	g1707642	BLASTX	217	7e-17	32	

4126	GM_87_A1_H01_MR	g3947439	BLASTX	151	7e-09	26	(AC005034) ge-rich sequence dna-binding factor [Homo sapiens]
4127	GM_87_A1_H03_MR	g220407	BLASTX	158	3e-09	32	retrotransposon del1-46 [Lilium henryi]
4128	GM_87_A1_H04_MR	g1666236	BLASTX	199	6e-15	32	(U76261) unknown [Hordeum vulgare]
4129	GM_87_A1_H04_T7	g3033398	BLASTX	202	4e-20	88	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]
4130	GM_87_A1_H05_MR	g3021268	BLASTX	373	3e-32	52	(AL022347) putative protein [Arabidopsis thaliana]
4131	GM_87_A1_H05_T7	g1707642	BLASTX	194	2e-13	30	(Y07748) TMK [Oryza sativa]
4132	GM_87_A1_H06_T7	g3777527	BLASTX	708	7e-68	95	(AF053008) gag-pol polyprotein [Glycine max]
4133	GM_87_A1_H10_MR	g1276977	BLASTX	154	3e-21	74	(U47143) nonsymbiotic hemoglobin [Glycine max]
4134	GM_87_A2_A01_T7	g2462058	BLASTX	160	4e-11	51	(Y13389) reverse transcriptase [Antirrhinum majus]
4135	GM_87_A2_A02_T7	g1769899	BLASTX	192	2e-14	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4136	GM_87_A2_A07_T7	g1769899	BLASTX	244	6e-20	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4137	GM_87_A2_A10_MR	g2443320	BLASTX	259	4e-20	43	(D85597) polyprotein [Oryza australiensis]
4138	GM_87_A2_A10_T7	g905361	BLASTX	199	4e-14	32	(U22103) gag-protease polyprotein [Glycine max]
4139	GM_87_A2_B03_MR	g507910	BLASTX	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
4140	GM_87_A2_B04_T7	g3746069	BLASTX	189	1e-12	41	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
4141	GM_87_A2_B05_MR	g14353	BLASTX	354	6e-09	60	Euglena gracilis Z Chloroplast DNA
4142	GM_87_A2_B05_T7	g2689221	BLASTX	189	4e-23	46	(Y10098) 7-ethoxycoumarin O-deethylase [Helianthus tuberosus]
4143	GM_87_A2_B06_MR	g2995405	BLASTX	170	7e-11	55	(Y12432) polyprotein [Ananas comosus]
4144	GM_87_A2_B08_T7	g507910	BLASTX	595	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4145	GM_87_A2_B10_T7	g507910	BLASTX	361	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4146	GM_87_A2_B12_T7	g3142379	BLASTX	184	3e-21	86	(AF053008) envelope-like [Glycine max]
4147	GM_87_A2_C03_MR	g4115565	BLASTX	298	1e-25	54	(AB013599) MYB homologue [Perilla frutescens]
4148	GM_87_A2_C04_MR	g3859610	BLASTX	379	4e-10	69	Arabidopsis thaliana BAC T9E19
4149	GM_87_A2_C04_T7	g2462134	BLASTX	161	3e-10	29	(Y13368) reverse transcriptase [Beta vulgaris]
4150	GM_87_A2_C06_T7	g507910	BLASTX	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4151	GM_87_A2_C11_MR	g1769898	BLASTX	251	9e-20	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4152	GM_87_A2_D03_T7	g3142328	BLASTX	1952	8e-82	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4153	GM_87_A2_D04_MR	g507910	BLASTX	586	7e-20	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4154	GM_87_A2_D05_MR	g1040717	BLASTX	411	2e-12	64	D-polychroa microsatellite sequence (clone Dp chl F3)
4155	GM_87_A2_D06_T7	g3097320	BLASTX	1092	2e-42	78	Glycine max gene for Bd 30K, complete cds
4156	GM_87_A2_D08_MR	g507910	BLASTX	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4157	GM_87_A2_D08_T7	g507910	BLASTX	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4158	GM_87_A2_E01_MR	g2462058	BLASTX	174	2e-12	50	(Y13389) reverse transcriptase [Antirrhinum majus]
4159	GM_87_A2_E04_MR	g507910	BLASTX	636	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
4160	GM_87_A2_E04_T7	g507910	BLASTX	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4161	GM_87_A2_E06_MR	g3426334	BLASTX	348	1e-08	62	Pisum sativum pectin methyltransferase (repme1) gene, complete cds

4162	GM_87_A2_E12_MR	g1345132	BLASTX	140	5e-09	37	(U47029) ERECTA [Arabidopsis thaliana] gi 1389566 gnl PID d1012536 (D83257) receptor protein kinase [Arabidopsis thaliana] gi 3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]
4163	GM_87_A2_F02_T7	g3777527	BLASTX	382	4e-33	77	(AF053008) gag-pol polyprotein [Glycine max]
4164	GM_87_A2_F07_MR	g3142328	BLASTN	722	1e-25	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005957) reverse transcriptase-like protein [Arabidopsis thaliana] (AC005561) putative POL3 protein [Arabidopsis thaliana] Figure 6. DNA sequence of three 3' apoB VNTR alleles. Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
4165	GM_87_A2_G01_MR	g4115365	BLASTX	275	8e-22	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4166	GM_87_A2_G01_T7	g4063760	BLASTX	552	9e-54	74	(D85597) polyprotein [Oryza australiensis]
4167	GM_87_A2_G02_MR	g340797	BLASTN	360	3e-10	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4168	GM_87_A2_G03_T7	g2264320	BLASTN	591	1e-19	65	(AF053008) gag-pol polyprotein [Glycine max] (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4169	GM_87_A2_H02_MR	g4063760	BLASTX	458	2e-41	57	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4170	GM_87_A2_H03_MR	g2443320	BLASTX	238	1e-27	46	Glycine max gene for Bd 30K, complete cds
4171	GM_87_A2_H06_T7	g4063760	BLASTX	394	1e-34	59	Glycine max BSR-101 satellite SB92 genomic sequence
4172	GM_87_A2_H07_MR	g3777527	BLASTX	244	2e-18	61	Glycine max cv. Dare nodulin 26 gene fragment
4173	GM_87_A2_H08_MR	g2522230	BLASTX	250	1e-23	42	Glycine max cv. Dare nodulin 26 gene fragment (AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4174	GM_87_A2_H10_T7	g3142328	BLASTN	910	3e-34	88	(AF053008) gag-pol polyprotein [Glycine max] Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MT120, complete sequence [Arabidopsis thaliana]
4175	GM_87_A2_H11_T7	g3097320	BLASTN	691	3e-24	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4176	GM_87_B1_A02_T7	g507910	BLASTN	417	3e-12	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4177	GM_87_B1_A03_MR	g170029	BLASTN	394	8e-11	80	(AF053008) gag-pol polyprotein [Glycine max]
4178	GM_87_B1_A09_T7	g3810596	BLASTX	179	9e-12	53	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MT120, complete sequence [Arabidopsis thaliana]
4179	GM_87_B1_B02_MR	g3777527	BLASTX	296	6e-24	91	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4180	GM_87_B1_B02_T7	g3128143	BLASTN	456	1e-13	62	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
4181	GM_87_B1_B08_MR	g4063760	BLASTX	233	2e-17	45	Terminal inverted repeat from Paramecium mitochondrion >gi 342968 gb J01432 PARMTDIN1 paramecium species 1 mitochondria dimer initiation region dna.
4182	GM_87_B1_B12_T7	g2541876	BLASTX	198	3e-14	43	(AC002328) F22O2.24 [Arabidopsis thaliana]
4183	GM_87_B1_C01_T7	g13373	BLASTN	400	6e-12	65	Glycine max BSR-101 satellite SB92 genomic sequence. (U76261) unknown [Hordeum vulgare]
4184	GM_87_B1_C02_MR	g3953479	BLASTX	296	4e-24	42	(AC000348) T7N9.20 [Arabidopsis thaliana]
4185	GM_87_B1_C07_T7	g507910	BLASTN	642	2e-22	84	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4186	GM_87_B1_C11_T7	g1666236	BLASTX	215	9e-17	39	S-locus-specific glycoprotein precursor - kale
4187	GM_87_B1_D03_MR	g2213600	BLASTX	194	1e-13	33	
4188	GM_87_B1_D04_MR	g1769898	BLASTX	350	4e-40	68	
4189	GM_87_B1_D04_T7	g81704	BLASTX	130	2e-14	43	

4190	GM_87_B1_D09_MR	g3810595	BLASTX	250	4e-19	43	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
4191	GM_87_B1_E05_T7	g3777527	BLASTX	749	3e-72	96	(AF053008) gag-pol polyprotein [Glycine max]
4192	GM_87_B1_E07_MR	g130398	BLASTX	193	3e-13	43	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE-TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
4193	GM_87_B1_E07_T7	g2522228	BLASTX	236	1e-18	53	(AB007466) reverse transcriptase-like protein [Vicia faba]
4194	GM_87_B1_E08_MR	g2618696	BLASTX	119	2e-16	44	(AC002510) hypothetical protein [Arabidopsis thaliana]
4195	GM_87_B1_E09_T7	g3687234	BLASTX	191	5e-13	52	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
4196	GM_87_B1_F03_T7	g441205	BLASTN	449	3e-20	71	Soybean lox1gm4 gene encoding lipxygenase L-4
4197	GM_87_B1_G02_MR	g507910	BLASTN	499	6e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4198	GM_87_B1_G05_MR	g507910	BLASTN	373	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4199	GM_87_B1_G06_MR	g3810596	BLASTX	202	3e-14	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4200	GM_87_B1_G11_T7	g2462134	BLASTX	354	1e-31	54	(Y13368) reverse transcriptase [Beta vulgaris]
4201	GM_87_B1_H01_MR	g3176800	BLASTN	220	4e-10	64	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 3' sequence
4202	GM_87_B1_H01_T7	g2914696	BLASTX	168	9e-14	45	(AC003974) putative purple acid phosphatase [Arabidopsis thaliana]
4203	GM_87_B1_H04_T7	g2443320	BLASTX	311	1e-25	51	(D85597) polyprotein [Oryza australiensis]
4204	GM_87_B1_H06_T7	g4063760	BLASTX	543	2e-50	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4205	GM_87_B1_H09_MR	g170606	BLASTN	841	1e-31	68	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
4206	GM_87_B1_H10_MR	g2864621	BLASTX	151	3e-09	30	hypothetical protein [Arabidopsis thaliana]
4207	GM_87_B1_H10_T7	g3645899	BLASTX	165	3e-10	50	(U68408) 5' end not determined experimentally [Zea mays]
4208	GM_87_B1_H11_MR	g170029	BLASTN	401	4e-11	81	Glycine max cv. Dare nodulin 26 gene fragment.
4209	GM_87_B1_H12_MR	g2497953	BLASTX	159	8e-10	53	MOLYBDOPTEIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) gi 1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]
4210	GM_87_B2_A01_T7	g4115377	BLASTX	273	4e-22	42	(AC005967) unknown protein [Arabidopsis thaliana]
4211	GM_87_B2_A02_MR	g1155261	BLASTX	577	3e-55	92	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]
4212	GM_87_B2_A06_T7	g2864621	BLASTX	152	2e-09	38	hypothetical protein [Arabidopsis thaliana]
4213	GM_87_B2_A07_MR	g4063760	BLASTX	240	3e-30	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4214	GM_87_B2_A11_T7	g3777527	BLASTX	711	3e-68	93	(AF053008) gag-pol polyprotein [Glycine max]
4215	GM_87_B2_B02_MR	g2583130	BLASTX	258	6e-20	41	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
4216	GM_87_B2_B03_T7	g1685003	BLASTX	274	1e-22	47	(U32643) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

4217	GM_87_B2_B05_MR	g1236920	BLASTN	367	1e-09	63	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and VarIp (varI) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
4218	GM_87_B2_B07_T7	g3142328	BLASTN	897	1e-33	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4219	GM_87_B2_C01_T7	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4220	GM_87_B2_C04_MR	g2073447	BLASTN	362	3e-09	62	L-japonicus gln1, pge1 & krm genes
4221	GM_87_B2_C08_MR	g507910	BLASTN	504	4e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4222	GM_87_B2_C08_T7	g507910	BLASTN	417	3e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4223	GM_87_B2_C09_T7	g3142328	BLASTN	887	3e-33	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4224	GM_87_B2_D03_MR	g4092470	BLASTN	392	1e-10	62	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
4225	GM_87_B2_D05_MR	g1785740	BLASTX	126	8e-11	31	(Y08502) orf170 [Arabidopsis thaliana]
4226	GM_87_B2_D06_MR	g1335862	BLASTX	243	3e-18	90	(U42608) clathrin heavy chain [Glycine max]
4227	GM_87_B2_D08_T7	g2827662	BLASTX	209	4e-15	55	(AL021637) Phosphoribosyltransferase [Arabidopsis thaliana]
4228	GM_87_B2_D11_MR	g507910	BLASTN	487	2e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4229	GM_87_B2_E01_T7	g100484	BLASTX	404	3e-36	55	hypothetical protein - garden snapdragon
4230	GM_87_B2_E03_T7	g3097320	BLASTN	484	7e-15	70	Glycine max gene for Bd 30K, complete cds
4231	GM_87_B2_E08_T7	g100484	BLASTX	362	1e-31	51	hypothetical protein - garden snapdragon
4232	GM_87_B2_E10_T7	g4063760	BLASTX	202	3e-15	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4233	GM_87_B2_E12_MR	g1234900	BLASTX	249	2e-20	90	(X92489) homeobox-leucine zipper protein [Glycine max]
4234	GM_87_B2_F02_T7	g18559	BLASTN	842	4e-31	72	G max gene for catalase
4235	GM_87_B2_F05_MR	g507910	BLASTN	569	4e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4236	GM_87_B2_F05_T7	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4237	GM_87_B2_F08_T7	g629693	BLASTX	255	4e-21	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
4238	GM_87_B2_F11_T7	g4092470	BLASTN	419	7e-12	62	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
4239	GM_87_B2_G02_MR	g3810596	BLASTX	219	5e-16	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4240	GM_87_B2_G05_MR	g4063760	BLASTX	238	6e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4241	GM_87_B2_H03_MR	g99755	BLASTX	332	1e-28	50	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
4242	GM_87_B2_H04_T7	g2982247	BLASTX	177	7e-13	48	(AF051206) probable thioredoxin H [Picea mariana]
4243	GM_87_B2_H11_T7	g3047060	BLASTN	393	1e-10	66	Arabidopsis thaliana BAC F7N22
4244	GM_88_A1_A04_MR	g2522228	BLASTX	306	2e-26	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
4245	GM_88_A1_A05_T7	g3461813	BLASTX	106	6e-16	61	(AC004138) putative sucrose/H+ symporter [Arabidopsis thaliana]

4246	GM_88_A1_A07_T7	g3025708	BLASTN	305	1e-09	64	Plasmodium falciparum subclone R5 variant surface antigen (var7b) gene, upstream regulatory region and partial cds
4247	GM_88_A1_A09_MR	g4063760	BLASTX	175	3e-11	33	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4248	GM_88_A1_B03_MR	g4063760	BLASTX	461	8e-42	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4249	GM_88_A1_B04_T7	g4063760	BLASTX	480	9e-44	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4250	GM_88_A1_B05_MR	g2244950	BLASTN	493	3e-15	71	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 5
4251	GM_88_A1_B07_T7	g4115365	BLASTX	175	2e-17	58	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
4252	GM_88_A1_B09_MR	g3142328	BLASTN	831	1e-30	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005897) putative transposon [Arabidopsis thaliana]
4253	GM_88_A1_C03_T7	g4038056	BLASTX	316	2e-26	43	(U22103) gag-protease polyprotein [Glycine max]
4254	GM_88_A1_D02_MR	g905361	BLASTX	158	9e-10	40	Glycine max satellite STR120-A.1.
4255	GM_88_A1_D08_MR	g1142699	BLASTN	300	5e-17	77	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
4256	GM_88_A1_D09_MR	g4150930	BLASTN	367	1e-09	60	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
4257	GM_88_A1_D11_MR	g4092470	BLASTN	374	7e-10	69	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Contain...
4258	GM_88_A1_E03_T7	g2769655	BLASTN	457	1e-13	63	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
4259	GM_88_A1_E06_MR	g1167523	BLASTX	180	1e-11	46	Glycine max BSR-101 satellite SB92 genomic sequence.
4260	GM_88_A1_E07_MR	g507910	BLASTN	395	3e-11	73	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-110, complete sequence [Plasmodium falciparum]
4261	GM_88_A1_E09_MR	g2673766	BLASTN	325	2e-11	65	S. gregaria mitochondrial control region DNA
4262	GM_88_A1_E10_MR	g1063404	BLASTN	375	1e-10	61	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
4263	GM_88_A1_E10_T7	g2961349	BLASTX	327	2e-27	54	Glycine max BSR-101 satellite SB92 genomic sequence.
4264	GM_88_A1_F02_T7	g507910	BLASTN	488	2e-15	77	60S RIBOSOMAL PROTEIN L7A gi 542158 pir S38360 ribosomal protein L7a - rice gi 303855 gnl PID d1002646 (D12631) ribosomal protein L7A [Oryza sativa]
4265	GM_88_A1_F06_T7	g548774	BLASTX	256	3e-21	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4266	GM_88_A1_G02_T7	g507910	BLASTN	426	1e-12	77	(U04785) lipoxigenase [Glycine max]
4267	GM_88_A1_G03_T7	g439857	BLASTX	286	3e-23	91	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4268	GM_88_A1_H03_MR	g4063760	BLASTX	204	3e-14	44	(U22103) gag-protease polyprotein [Glycine max]
4269	GM_88_A1_H03_T7	g905361	BLASTX	216	5e-16	36	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
4270	GM_88_A1_H05_T7	g1167523	BLASTX	213	4e-15	40	

4271	GM_88_A1_H07_MR	g3820976	BLASTN	463	7e-14	64	Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complet...
4272	GM_88_A2_A02_T7	g505129	BLASTN	301	4e-12	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4273	GM_88_A2_A04_T7	g1171591	BLASTN	417	8e-12	60	P.falciparum complete gene map of plastid-like DNA (IR-B) (AC005561) putative POL3 protein [Arabidopsis thaliana]
4274	GM_88_A2_A05_MR	g4063760	BLASTX	205	2e-14	35	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4275	GM_88_A2_A07_T7	g3142328	BLASTN	466	4e-14	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
4276	GM_88_A2_A08_T7	g2264320	BLASTN	463	5e-15	61	(AC005561) putative POL3 protein [Arabidopsis thaliana] hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4277	GM_88_A2_A09_MR	g4063760	BLASTX	271	2e-21	56	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U68408) 5' end not determined experimentally [Zea mays]
4278	GM_88_A2_A10_T7	g2129618	BLASTX	249	3e-19	46	G.max gene for catalase (AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4279	GM_88_A2_A11_T7	g3142328	BLASTN	745	9e-27	70	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
4280	GM_88_A2_B01_T7	g3645899	BLASTX	254	1e-32	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4281	GM_88_A2_B02_MR	g185559	BLASTN	973	4e-37	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4282	GM_88_A2_B10_MR	g3810596	BLASTX	223	2e-16	58	(AB004906) transposase [Ipomoea purpurea]
4283	GM_88_A2_B12_MR	g1946279	BLASTX	331	3e-29	53	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
4284	GM_88_A2_C02_MR	g4063760	BLASTX	612	7e-58	74	Glycine max satellite STR120-B.1.
4285	GM_88_A2_C04_T7	g507910	BLASTN	453	7e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4286	GM_88_A2_C06_MR	g4063770	BLASTX	142	3e-09	35	(AB004906) transposase [Ipomoea purpurea]
4287	GM_88_A2_C07_T7	g3599418	BLASTN	419	6e-12	91	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
4288	GM_88_A2_C09_MR	g1142703	BLASTN	294	7e-17	76	Glycine max satellite STR120-B.1.
4289	GM_88_A2_E02_T7	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4290	GM_88_A2_F05_MR	g1326016	BLASTX	296	4e-24	45	(U90262) calcium-dependent calmodulin-independent protein kinase
4291	GM_88_A2_F09_T7	g1899175	BLASTX	243	5e-19	79	CDPK [Cucurbita pepo]
4292	GM_88_A2_F12_MR	g1946279	BLASTX	173	9e-21	42	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
4293	GM_88_A2_F02_MR	g185559	BLASTN	523	1e-16	69	G.max gene for catalase
4294	GM_88_A2_F03_T7	g2522228	BLASTX	128	9e-11	53	(AB007466) reverse transcriptase-like protein [Vicia faba]
4295	GM_88_A2_F05_MR	g2335061	BLASTN	397	7e-11	62	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]

4324	GM_88_B1_E07_MR	g543905	BLASTX	290	8e-25	86	BRASSINOSTEROID-REGULATED PROTEIN BRU1 gi 347459 (L22162) brassinosteroid-regulated protein [Glycine max] (Y08010) lectin receptor kinase [Arabidopsis thaliana] (AC005561) putative POL3 protein [Arabidopsis thaliana] (AC002409) hypothetical protein [Arabidopsis thaliana] putative transposase [Arabidopsis thaliana] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U22533) NADP-malate dehydrogenase [Flaveria trinervia] (AL022347) putative protein [Arabidopsis thaliana] (Y08010) lectin receptor kinase [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. Soybean nodulin 22 gene hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum] Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens] (AF053008) gag-pol polyprotein [Glycine max] small auxin up RNA gene cluster: orf 6B [Glycine max=soybeans, cv. Wayne, Genomic; 665 nt] Glycine max BSR-101 satellite SB92 genomic sequence. Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana] (AC005897) putative transposon [Arabidopsis thaliana] Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds (Y13368) reverse transcriptase [Beta vulgaris] (AC003952) putative Tai-1-like reverse transcriptase [Arabidopsis thaliana] Homo sapiens allele 8 fragile site locus (FRA10B) minisatellite sequence Glycine max satellite STR120-A.2. Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens] (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba] (AB004906) transposase [Ipomoea purpurea] (U22103) gag-protease polyprotein [Glycine max] (U22103) gag-protease polyprotein [Glycine max]
4325	GM_88_B1_E09_MR	g1769898	BLASTX	185	1e-12	50	
4326	GM_88_B1_E12_T7	g4063760	BLASTX	616	3e-58	60	
4327	GM_88_B1_F01_T7	g2623296	BLASTX	191	5e-13	46	
4328	GM_88_B1_F02_T7	g3283026	BLASTX	212	2e-15	33	
4329	GM_88_B1_F05_MR	g3142328	BLASTN	476	1e-14	79	
4330	GM_88_B1_F09_MR	g726334	BLASTX	287	2e-50	87	
4331	GM_88_B1_F09_T7	g3021268	BLASTX	339	1e-28	45	
4332	GM_88_B1_F10_MR	g1769897	BLASTX	345	2e-30	56	
4333	GM_88_B1_G04_T7	g507910	BLASTN	348	4e-09	70	
4334	GM_88_B1_G08_MR	g18695	BLASTN	506	4e-16	87	
4335	GM_88_B1_G11_T7	g421955	BLASTX	333	2e-29	59	
4336	GM_88_B1_H06_T7	g3273387	BLASTN	457	1e-13	62	
4337	GM_88_B1_H10_MR	g3777527	BLASTX	119	2e-17	42	
4338	GM_88_B1_H12_T7	g255576	BLASTN	338	7e-09	95	
4339	GM_89_A1_A03_MR	g507910	BLASTN	526	4e-17	78	
4340	GM_89_A1_A05_MR	g4063756	BLASTN	544	2e-17	64	
4341	GM_89_A1_A08_T7	g4038056	BLASTX	267	3e-21	48	
4342	GM_89_A1_A10_T7	g3599418	BLASTN	795	5e-29	72	
4343	GM_89_A1_B03_T7	g2462134	BLASTX	215	2e-24	46	
4344	GM_89_A1_B06_MR	g2708743	BLASTX	140	5e-09	35	
4345	GM_89_A1_B07_MR	g3176788	BLASTN	364	3e-10	65	
4346	GM_89_A1_C02_MR	g1142700	BLASTN	775	2e-28	86	
4347	GM_89_A1_C04_T7	g4006838	BLASTN	413	1e-11	62	
4348	GM_89_A1_C05_MR	g2522230	BLASTX	248	2e-27	41	
4349	GM_89_A1_C07_MR	g4063770	BLASTX	151	7e-09	33	
4350	GM_89_A1_C08_MR	g905361	BLASTX	730	2e-71	96	
4351	GM_89_A1_C10_MR	g905361	BLASTX	701	2e-68	92	

4352	GM_89_A1_D01_T7	g4115365	BLASTX	223	3e-16	38	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
4353	GM_89_A1_D03_T7	g4038056	BLASTX	297	2e-24	46	(AC005897) putative transposon [Arabidopsis thaliana]
4354	GM_89_A1_D04_T7	g507910	BLASTN	419	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4355	GM_89_A1_D05_T7	g3142328	BLASTN	1002	2e-38	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4356	GM_89_A1_D06_MR	g3142328	BLASTN	603	3e-20	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
4357	GM_89_A1_D07_MR	g1514643	BLASTX	120	1e-14	85	(X96932) PS60 gene product [Nicotiana tabacum]
4358	GM_89_A1_D08_MR	g1255951	BLASTX	152	3e-09	40	(AF053008) gag-pol polyprotein [Glycine max]
4359	GM_89_A1_D09_MR	g3777527	BLASTX	249	6e-19	58	G.max N-20t gene
4360	GM_89_A1_D11_MR	g18683	BLASTN	526	7e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4361	GM_89_A1_D12_MR	g507910	BLASTN	494	1e-15	78	(AC004557) F17L21.23 [Arabidopsis thaliana]
4362	GM_89_A1_E02_MR	g3935180	BLASTX	258	6e-20	47	A. majus TAM1 gene for TNPI and TNP2.
4363	GM_89_A1_E02_T7	g16056	BLASTN	385	2e-10	59	S.douglasii mitochondrial ATP subunit 9 gene, complete CDS
4364	GM_89_A1_E04_MR	g396249	BLASTN	435	6e-13	62	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
4365	GM_89_A1_E05_MR	g1480927	BLASTN	1143	2e-45	83	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4366	GM_89_A1_E05_T7	g1769897	BLASTX	213	8e-16	42	Saccharomyces cerevisiae mitochondrion origin of replication (ori3 and ori4).
4367	GM_89_A1_E06_T7	g559278	BLASTN	451	2e-13	61	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
4368	GM_89_A1_E08_MR	g3319362	BLASTX	192	3e-13	41	Glycine max gene for Bd 30K, complete cds
4369	GM_89_A1_E09_T7	g3097320	BLASTN	532	5e-17	70	(AF110183) putative integrase [Oryza sativa]
4370	GM_89_A1_F05_MR	g4140712	BLASTX	318	8e-28	47	(Y12432) polyprotein [Ananas comosus]
4371	GM_89_A1_F07_MR	g2995405	BLASTX	443	4e-40	55	(U76261) unknown [Hordeum vulgare]
4372	GM_89_A1_G02_MR	g1666236	BLASTX	146	7e-14	31	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4373	GM_89_A1_G10_MR	g4063760	BLASTX	361	5e-31	67	G.max gene for catalase
4374	GM_89_A1_H01_MR	g18559	BLASTN	1428	9e-58	87	(Y12321) open reading frame 2 [Brassica oleracea]
4375	GM_89_A1_H01_T7	g2462936	BLASTX	245	5e-25	48	Glycine max BSR-101 satellite SB92 genomic sequence.
4376	GM_89_A1_H06_MR	g507910	BLASTN	557	1e-18	80	probable integrase - common tobacco (fragment) gi 530742
4377	GM_89_A1_H08_MR	g629693	BLASTX	157	4e-10	52	(X80830) integrase [Nicotiana tabacum]
4378	GM_89_A1_H08_T7	g2443320	BLASTX	241	7e-22	48	(D85597) polyprotein [Oryza australiensis]
4379	GM_89_A1_H09_MR	g4050011	BLASTN	581	3e-19	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
4380	GM_89_A1_H10_MR	g3582436	BLASTX	153	1e-21	68	(AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
4381	GM_89_A1_H12_T7	g4126312	BLASTN	416	9e-12	64	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]

4382	GM_89_A2_A05_T7	g18702	BLASTN	365	3e-10	68	Soybean nodulin-24 gene 5' end (U76261) unknown [Hordeum vulgare]
4383	GM_89_A2_A06_MR	g1666236	BLASTX	302	4e-26	34	(AL023094) Homeodomain - like protein [Arabidopsis thaliana]
4384	GM_89_A2_A07_MR	g3096930	BLASTX	216	4e-16	67	G.max gene for catalase
4385	GM_89_A2_A09_T7	g18559	BLASTN	1345	5e-54	74	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4386	GM_89_A2_B02_MR	g2522230	BLASTX	267	4e-29	41	(AF053008) envelope-like [Glycine max]
4387	GM_89_A2_B02_T7	g3142379	BLASTX	291	7e-25	85	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
4388	GM_89_A2_B06_MR	g130582	BLASTX	353	4e-30	45	REVERSE TRANSCRIPTASE ; ENDONUCLEASE (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4389	GM_89_A2_B10_MR	g2213632	BLASTX	164	1e-10	50	(AC000103) F21J9.24 [Arabidopsis thaliana]
4390	GM_89_A2_B11_MR	g130582	BLASTX	163	7e-10	41	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
4391	GM_89_A2_B12_MR	g2924653	BLASTN	396	2e-11	69	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4392	GM_89_A2_C01_MR	g507910	BLASTN	684	3e-24	86	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]
4393	GM_89_A2_C03_T7	g1666236	BLASTX	212	2e-16	30	Glycine max BSR-101 satellite SB92 genomic sequence.
4394	GM_89_A2_C08_T7	g2982452	BLASTX	132	8e-11	70	(U76261) unknown [Hordeum vulgare]
4395	GM_89_A2_D02_MR	g2443320	BLASTX	177	2e-18	32	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
4396	GM_89_A2_D05_MR	g2995405	BLASTX	485	1e-44	65	(D85597) polyprotein [Oryza australiensis]
4397	GM_89_A2_D07_T7	g2104945	BLASTN	562	2e-34	71	(Y12432) polyprotein [Ananas comosus]
4398	GM_89_A2_D08_MR	g3142328	BLASTN	1240	3e-77	88	Glycine max copia-like retrotransposon Tgm, complete sequence
4399	GM_89_A2_D12_T7	g3426334	BLASTN	375	6e-10	65	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete cds
4400	GM_89_A2_E01_T7	g4050011	BLASTN	444	5e-13	65	Pisum sativum pectin methylesterase (repme1) gene, complete cds
4401	GM_89_A2_E05_MR	g3201608	BLASTN	360	3e-09	67	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
4402	GM_89_A2_E06_T7	g905361	BLASTX	619	2e-62	85	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence.
4403	GM_89_A2_E10_T7	g18559	BLASTN	544	1e-17	66	(U22103) gag-protease polyprotein [Glycine max]
4404	GM_89_A2_E11_MR	g3777527	BLASTX	744	9e-72	95	G.max gene for catalase
4405	GM_89_A2_F01_MR	g3777527	BLASTX	450	2e-40	80	(AF053008) gag-pol polyprotein [Glycine max]
4406	GM_89_A2_F03_T7	g18559	BLASTN	349	9e-09	69	(AF053008) gag-pol polyprotein [Glycine max]

4407	GM_89_A2_F07_MR	g170605	BLASTN	575	2e-19	64	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
4408	GM_89_A2_G01_T7	g3377802	BLASTX	203	3e-20	74	(AF075597) Similar to sucrose synthase: T2H3.8 [Arabidopsis thaliana]
4409	GM_89_A2_G03_T7	g2244950	BLASTN	356	8e-18	84	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment
4410	GM_89_A2_G04_MR	g1619300	BLASTX	119	2e-09	40	No. 5
4411	GM_89_A2_G04_T7	g3033389	BLASTX	186	2e-12	30	(X95269) LRR protein [Lycopersicon esculentum]
4412	GM_89_A2_G05_T7	g2501766	BLASTX	172	2e-11	77	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
4413	GM_89_A2_G07_MR	g4115365	BLASTX	252	2e-19	38	(U69174) calmodulin-like domain protein kinase isoenzyme gamma [Glycine max]
4414	GM_89_A2_G09_T7	g421955	BLASTX	342	2e-30	62	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
4415	GM_89_A2_H01_MR	g303900	BLASTN	425	3e-12	69	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387)
4416	GM_89_A2_H07_MR	g3250687	BLASTX	246	3e-25	43	ORF4 [Solanum tuberosum]
4417	GM_90_A1_A04_MR	g507910	BLASTN	580	1e-19	82	Soybean gene for ubiquitin, complete cds
4418	GM_90_A1_A04_T7	g905361	BLASTX	527	5e-50	70	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
4419	GM_90_A1_A05_T7	g4063770	BLASTX	202	3e-14	39	Glycine max BSR-101 satellite SB92 genomic sequence.
4420	GM_90_A1_A08_T7	g100484	BLASTX	244	7e-19	44	(U22103) gag-protease polyprotein [Glycine max]
4421	GM_90_A1_A10_T7	g3193284	BLASTX	294	3e-24	40	(AB004906) transposase [Ipomoea purpurea]
4422	GM_90_A1_A12_MR	g3142328	BLASTN	723	9e-26	91	hypothetical protein - garden snapdragon
4423	GM_90_A1_A12_T7	g507910	BLASTN	356	2e-09	72	(AF069298) No definition line found [Arabidopsis thaliana]
4424	GM_90_A1_B02_T7	g3157938	BLASTX	162	3e-10	62	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4425	GM_90_A1_B03_MR	g507910	BLASTN	539	1e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4426	GM_90_A1_B03_T7	g507910	BLASTN	536	1e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4427	GM_90_A1_B04_MR	g2760172	BLASTN	444	5e-13	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
4428	GM_90_A1_B07_MR	g2995405	BLASTX	357	7e-31	64	MUB3, complete sequence [Arabidopsis thaliana]
4429	GM_90_A1_C07_MR	g3894383	BLASTX	166	3e-15	41	(Y12432) polyprotein [Ananas comosus]
4430	GM_90_A1_D01_MR	g3928097	BLASTX	146	3e-09	50	(AF053993) disease resistance protein [Lycopersicon esculentum]
4431	GM_90_A1_D01_T7	g2522228	BLASTX	157	5e-10	29	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]
4432	GM_90_A1_D03_MR	g3695395	BLASTX	248	2e-19	48	(AB007466) reverse transcriptase-like protein [Vicia faba]
4433	GM_90_A1_D04_MR	g3193221	BLASTN	583	2e-19	92	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
4434	GM_90_A1_D10_MR	g18559	BLASTN	450	2e-13	70	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
							G.max gene for catalase

4435	GM_90_A1_E01_T7	g3426047	BLASTX	134	3e-10	51	(AC005168) putative DNA-binding protein [Arabidopsis thaliana]
4436	GM_90_A1_E06_T7	g3426334	BLASTN	351	7e-09	63	Pisum sativum pectin methyltransferase (rcpme1) gene, complete cds
4437	GM_90_A1_E09_T7	g4063760	BLASTX	419	3e-37	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4438	GM_90_A1_E10_T7	g4063760	BLASTX	543	2e-50	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4439	GM_90_A1_F01_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
4440	GM_90_A1_F01_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4441	GM_90_A1_F05_T7	g4139266	BLASTX	151	1e-09	55	(AF112444) L-asparaginase [Lupinus luteus]
4442	GM_90_A1_F07_T7	g1294787	BLASTN	387	1e-10	65	Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS.
4443	GM_90_A1_F09_MR	g507910	BLASTN	486	2e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4444	GM_90_A1_F11_T7	g4038056	BLASTX	330	6e-28	46	(AC005897) putative transposon [Arabidopsis thaliana]
4445	GM_90_A1_G01_T7	g1769897	BLASTX	455	6e-47	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4446	GM_90_A1_G02_T7	g2129618	BLASTX	211	4e-15	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4447	GM_90_A1_G03_MR	g3777527	BLASTX	318	3e-26	86	(AF053008) gag-pol polyprotein [Glycine max]
4448	GM_90_A1_G04_T7	g99922	BLASTX	511	3e-48	70	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
4449	GM_90_A1_G09_MR	g3779023	BLASTX	155	1e-10	36	(AC005171) probable splicing factor [Arabidopsis thaliana]
4450	GM_90_A1_H03_T7	g4140712	BLASTX	200	3e-15	36	(AF110183) putative integrase [Oryza sativa]
4451	GM_90_A1_H04_T7	g2129618	BLASTX	247	5e-19	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4452	GM_90_A1_H06_MR	g2522228	BLASTX	198	2e-14	78	(AB007466) reverse transcriptase-like protein [Vicia faba]
4453	GM_90_A1_H08_MR	g3777527	BLASTX	220	7e-16	53	(AF053008) gag-pol polyprotein [Glycine max]
4454	GM_90_A1_H09_T7	g2129618	BLASTX	198	8e-14	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4455	GM_90_A2_A02_MR	g1769898	BLASTX	104	6e-10	69	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4456	GM_90_A2_A05_T7	g4063760	BLASTX	132	5e-11	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4457	GM_90_A2_A06_MR	g2367675	BLASTX	233	2e-17	35	(AF017040) Pol [Dictyostelium discoideum]
4458	GM_90_A2_A11_MR	g3810596	BLASTX	184	3e-12	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4459	GM_90_A2_B01_MR	g3236259	BLASTX	161	7e-11	65	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
4460	GM_90_A2_B03_MR	g2146735	BLASTX	268	6e-22	84	glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (clone E:5) - Arabidopsis thaliana (fragment) gi 1166405 (X84229) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
4461	GM_90_A2_B05_T7	g505129	BLASTN	350	7e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4462	GM_90_A2_B07_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
4463	GM_90_A2_B10_MR	g3142328	BLASTN	2447	3e-105	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

4464	GM_90_A2_C01_T7	g3645899	BLASTX	206	1e-14	45	(U68408) 5' end not determined experimentally [Zea mays]
4465	GM_90_A2_C02_MR	g2252836	BLASTX	287	2e-23	41	(AF013293) contains weak similarity to <i>S. cerevisiae</i> BOB1 protein (PIR:S45444) [Arabidopsis thaliana]
4466	GM_90_A2_C07_MR	g18559	BLASTN	1053	1e-40	75	G.max gene for catalase
4467	GM_90_A2_C09_MR	g507910	BLASTN	462	3e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4468	GM_90_A2_C10_T7	g4063760	BLASTX	221	4e-16	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4469	GM_90_A2_D03_MR	g4063760	BLASTX	266	6e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4470	GM_90_A2_D06_T7	g3047068	BLASTX	204	2e-14	35	(AF058825) similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
4471	GM_90_A2_D07_T7	g3142328	BLASTN	744	1e-26	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4472	GM_90_A2_D09_T7	g507910	BLASTN	407	9e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4473	GM_90_A2_D10_T7	g1666236	BLASTX	163	7e-11	29	(U76261) unknown [Hordeum vulgare]
4474	GM_90_A2_D11_MR	g3097320	BLASTN	657	1e-22	74	Glycine max gene for Bd 30K, complete cds
4475	GM_90_A2_D11_T7	g3282250	BLASTX	142	9e-11	55	(AF009337) CDPK-related protein kinase [Tradescantia virginiana]
4476	GM_90_A2_E02_MR	g340797	BLASTN	500	1e-16	64	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
4477	GM_90_A2_E06_MR	g3482916	BLASTX	162	7e-12	43	(AC003970) Hypothetical protein [Arabidopsis thaliana]
4478	GM_90_A2_F01_T7	g4063760	BLASTX	249	3e-21	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4479	GM_90_A2_F02_T7	g3080427	BLASTX	166	1e-20	61	(AL022604) putative protein [Arabidopsis thaliana]
4480	GM_90_A2_F08_T7	g531389	BLASTX	102	5e-09	42	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
4481	GM_90_A2_G06_T7	g3021409	BLASTX	157	2e-12	60	(Y12781) transducin (beta) like 1 protein [Homo sapiens]
4482	GM_90_A2_G08_MR	g431164	BLASTX	127	4e-13	86	(D21823) ORF [Lilium longiflorum]
4483	GM_90_A2_G11_MR	g905361	BLASTX	428	3e-39	96	(U22103) gag-protease polyprotein [Glycine max]
4484	GM_90_A2_G12_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4485	GM_90_A2_H04_MR	g507910	BLASTN	515	1e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4486	GM_90_A2_H04_T7	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4487	GM_90_A2_H06_MR	g1769898	BLASTX	190	4e-26	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4488	GM_90_A2_H09_MR	g4063760	BLASTX	202	5e-15	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4489	GM_90_A2_IH11_MR	g1142703	BLASTN	267	1e-11	72	Glycine max satellite STR120-B.1.
4490	GM_90_B1_A03_MR	g3204107	BLASTN	508	5e-17	69	Cicer arietinum mRNA for putative cytidine or deoxycytidylate deaminase, partial.
4491	GM_90_B1_A03_T7	g4063760	BLASTX	273	1e-21	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4492	GM_90_B1_A10_MR	g3777527	BLASTX	343	6e-29	71	(AF053008) gag-pol polyprotein [Glycine max]
4493	GM_90_B1_A11_MR	g4063770	BLASTX	188	2e-15	34	(AB004906) transposase [Ipomoea purpurea]
4494	GM_90_B1_A12_MR	g905361	BLASTX	266	2e-21	94	(U22103) gag-protease polyprotein [Glycine max]
4495	GM_90_B1_B02_MR	g4063760	BLASTX	457	3e-43	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4496	GM_90_B1_B02_T7	g1871192	BLASTX	378	2e-33	50	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

4497	GM_90_B1_B05_T7	g3142328	BLASTN	1832	3e-76	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4498	GM_90_B1_B07_T7	g2828827	BLASTN	491	4e-15	61	Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) g...
4499	GM_90_B1_B09_T7	g4063760	BLASTX	255	9e-20	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4500	GM_90_B1_C03_MR	g3289984	BLASTN	359	3e-09	63	Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence [Homo sapiens]
4501	GM_90_B1_C05_MR	g507910	BLASTN	484	3e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4502	GM_90_B1_C05_T7	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4503	GM_90_B1_C10_MR	g4063756	BLASTN	601	4e-20	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
4504	GM_90_B1_C10_T7	g3142379	BLASTX	298	1e-25	46	(AF053008) envelope-like [Glycine max]
4505	GM_90_B1_D02_T7	g1769898	BLASTX	460	7e-43	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4506	GM_90_B1_D10_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4507	GM_90_B1_D10_T7	g507910	BLASTN	368	5e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4508	GM_90_B1_D11_MR	g3777527	BLASTX	251	3e-19	35	(AF053008) gag-pol polypeptide [Glycine max]
4509	GM_90_B1_D12_T7	g2586082	BLASTX	136	3e-10	50	(U72725) retrofit [Oryza longistaminata]
4510	GM_90_B1_E01_T7	g18559	BLASTN	1664	1e-68	90	G.max gene for catalase
4511	GM_90_B1_E02_T7	g507910	BLASTN	341	8e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4512	GM_90_B1_E03_MR	g13767	BLASTN	358	5e-10	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSL.MTIG05 Yeast (T. glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
4513	GM_90_B1_E03_T7	g3746069	BLASTX	205	2e-14	31	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
4514	GM_90_B1_E04_T7	g1142703	BLASTN	317	1e-17	78	Glycine max satellite STR120-B.1.
4515	GM_90_B1_E10_MR	g18559	BLASTN	1191	5e-47	72	G.max gene for catalase
4516	GM_90_B1_E11_T7	g2979574	BLASTN	419	7e-12	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
4517	GM_90_B1_E12_T7	g1666236	BLASTX	174	4e-12	29	(U76261) unknown [Hordeum vulgare]
4518	GM_90_B1_F10_T7	g18559	BLASTN	997	3e-38	70	G.max gene for catalase
4519	GM_90_B1_F12_MR	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4520	GM_90_B1_F12_T7	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4521	GM_90_B1_G06_MR	g3645899	BLASTX	228	4e-21	45	(U68408) 5' end not determined experimentally [Zea mays]
4522	GM_90_B1_G08_MR	g507910	BLASTN	486	2e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4523	GM_90_B1_G10_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4524	GM_90_B1_G10_T7	g4063760	BLASTX	288	3e-23	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4525	GM_90_B1_H02_MR	g3461846	BLASTX	356	9e-40	56	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]

4526	GM_90_B1_H12_MR	g3142328	BLASTN	887	3e-33	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4527	GM_90_B2_A02_MR	g3777527	BLASTX	739	3e-71	95	(AF053008) gag-pol polyprotein [Glycine max]
4528	GM_90_B2_A04_T7	g4038056	BLASTX	347	9e-30	46	(AC005897) putative transposon [Arabidopsis thaliana]
4529	GM_90_B2_A06_MR	g3645899	BLASTX	374	2e-32	60	(U68408) 5' end not determined experimentally [Zea mays]
4530	GM_90_B2_A08_MR	g629693	BLASTX	363	1e-32	61	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
4531	GM_90_B2_A10_MR	g18737	BLASTN	368	1e-09	69	Glycine max RPRP3 gene for repetitive proline-rich protein 3
4532	GM_90_B2_A12_T7	g2911048	BLASTX	201	7e-15	54	(AL021961) hypothetical protein [Arabidopsis thaliana]
4533	GM_90_B2_B02_MR	g507910	BLASTN	435	5e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4534	GM_90_B2_B02_T7	g507910	BLASTN	555	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4535	GM_90_B2_C10_MR	g3810596	BLASTX	139	1e-13	33	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4536	GM_90_B2_D04_T7	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4537	GM_90_B2_D05_MR	g505129	BLASTN	363	2e-09	71	Winged bean DNA: Kunitz chymotrypsin inhibitor-3 gene homologous region
4538	GM_90_B2_D05_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
4539	GM_90_B2_D06_MR	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4540	GM_90_B2_D06_T7	g4063760	BLASTX	481	7e-44	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4541	GM_90_B2_D08_MR	g4063760	BLASTX	303	7e-25	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4542	GM_90_B2_D09_T7	g2959736	BLASTX	306	1e-26	80	(Y13651) homologous to GATA-binding transcription factors [Arabidopsis thaliana]
4543	GM_90_B2_D12_T7	g4038056	BLASTX	379	3e-33	52	(AC005897) putative transposon [Arabidopsis thaliana]
4544	GM_90_B2_E01_MR	g1628038	BLASTN	400	5e-11	62	Caenorhabditis elegans cosmid K09G1, complete sequence [Caenorhabditis elegans]
4545	GM_90_B2_E06_MR	g507910	BLASTN	413	5e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4546	GM_90_B2_E06_T7	g3097320	BLASTN	509	5e-16	80	Glycine max gene for Bd 30K, complete cds
4547	GM_90_B2_E07_T7	g3549661	BLASTX	344	1e-30	51	(AL031394) hypothetical protein [Arabidopsis thaliana]
4548	GM_90_B2_F05_MR	g1652066	BLASTX	188	2e-13	45	(D90902) Na/H antiporter [Synechocystis sp.]
4549	GM_90_B2_F05_T7	g170083	BLASTN	388	8e-11	69	Soybean (clone E15) urease (ure) gene, exons 2,3 and 4 and partial cds.
4550	GM_90_B2_F06_T7	g18559	BLASTN	463	6e-14	75	G-max gene for catalase
4551	GM_90_B2_G01_MR	g3810596	BLASTX	159	1e-09	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4552	GM_90_B2_G01_T7	g340697	BLASTN	464	2e-19	71	Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA.
4553	GM_90_B2_G08_MR	g3930515	BLASTX	122	4e-12	38	(AF059674) putative gag protein [Nicotiana tabacum]
4554	GM_90_B2_G09_MR	g2995405	BLASTX	477	8e-44	66	(Y12432) polyprotein [Ananas comosus]
4555	GM_90_B2_G09_T7	g3452140	BLASTX	231	1e-18	47	(AJ004901) resistance protein [Glycine max]
4556	GM_90_B2_G12_MR	g507910	BLASTN	561	1e-18	83	Glycine max BSR-101 satellite SB92 genomic sequence.
4557	GM_90_B2_H05_MR	g18559	BLASTN	974	4e-37	76	G-max gene for catalase
4558	GM_90_B2_H06_T7	g905361	BLASTX	694	1e-67	95	(U22103) gag-protease polyprotein [Glycine max]

4559	GM_90_B2_H07_MR	g507910	BLASTN	353	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4560	GM_90_B2_H08_T7	g4092471	BLASTN	446	4e-13	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
4561	GM_90_B2_H10_MR	g1076755	BLASTX	411	8e-37	78	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
4562	GM_91_A1_A09_T7	g3157910	BLASTX	196	6e-19	67	(AF003551) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Zea mays]
4563	GM_91_A1_A12_T7	g3142328	BLASTN	1094	1e-42	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
4564	GM_91_A1_B03_T7	g3695395	BLASTX	211	2e-15	45	(Y15367) MtN19 [Medicago truncatula]
4565	GM_91_A1_B06_MR	g2598589	BLASTX	250	3e-20	48	G.max gene for catalase
4566	GM_91_A1_B08_T7	g18559	BLASTN	972	5e-37	75	(Z92770) fadE2 [Mycobacterium tuberculosis]
4567	GM_91_A1_C04_T7	g1877279	BLASTX	121	9e-09	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4568	GM_91_A1_C10_T7	g4063760	BLASTX	300	2e-24	43	pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 gi 8702 (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster]
4569	GM_91_A1_D05_T7	g85105	BLASTX	177	2e-11	38	Glycine max BSR-101 satellite SB92 genomic sequence.
4570	GM_91_A1_D09_MR	g507910	BLASTN	349	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4571	GM_91_A1_D09_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
4572	GM_91_A1_E02_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4573	GM_91_A1_E07_T7	g1666236	BLASTX	224	7e-18	32	(U76261) unknown [Hordeum vulgare]
4574	GM_91_A1_E10_T7	g2522228	BLASTX	566	4e-54	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
4575	GM_91_A1_E11_T7	g1785739	BLASTX	149	2e-12	43	(Y08502) orf240b [Arabidopsis thaliana]
4576	GM_91_A1_F05_MR	g3510505	BLASTX	116	6e-10	41	(AF030881) pol polyprotein [Fugu rubripes]
4577	GM_91_A1_F06_MR	g3777527	BLASTX	415	1e-36	100	(AF053008) gag-pol polyprotein [Glycine max]
4578	GM_91_A1_F10_T7	g2129618	BLASTX	212	3e-15	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4579	GM_91_A1_F11_T7	g3645899	BLASTX	203	2e-19	53	(U68408) 5' end not determined experimentally [Zea mays]
4580	GM_91_A1_G02_MR	g100484	BLASTX	221	2e-16	42	hypothetical protein - garden snapdragon
4581	GM_91_A1_G09_MR	g2961349	BLASTX	153	7e-09	50	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
4582	GM_91_A1_G09_T7	g1369955	BLASTN	383	3e-10	63	Caenorhabditis elegans cosmid B0564, complete sequence [Caenorhabditis elegans]
4583	GM_91_A1_H01_T7	g507910	BLASTN	715	1e-25	88	Glycine max BSR-101 satellite SB92 genomic sequence.
4584	GM_91_A1_H02_MR	g4159704	BLASTN	437	1e-12	71	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence [Arabidopsis thaliana]
4585	GM_91_A1_H05_T7	g3695395	BLASTX	155	2e-14	44	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]

4586	GM_91_A1_H08_MR	g3327389	BLASTX	165	8e-22	79	(AC004483) putative DNA replication licensing factor, mcm5 [Arabidopsis thaliana]
4587	GM_91_A1_H08_T7	g557882	BLASTX	343	2e-30	62	(U13923) putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family [Solanum pimpinellifolium] gi 1809263 (U59317) serine/threonine protein kinase Fen [Lycopersicon pimpinellifolium] gi 1096880 prf 2112354B Fen gene [Lycopersicon esculentum] gi 1098334 prf 2115395A Fen gene [Lycopersicon esculentum] (Y08010) lectin receptor kinase [Arabidopsis thaliana] Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region Glycine max gene for Bd 30K, complete cds Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region (AC005561) putative POL3 protein [Arabidopsis thaliana] Pisum sativum genomic DNA encoding the complete Ty3/cypsy-like retroelement Cyclops-2 (U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays] (U72725) retrofit [Oryza longistaminata] Glycine max BSR-101 satellite SB92 genomic sequence (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba] (AC005561) putative POL3 protein [Arabidopsis thaliana] (D85597) polyprotein [Oryza australiensis] (AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana] (Y08010) lectin receptor kinase [Arabidopsis thaliana] (AC005897) putative transposon [Arabidopsis thaliana] (AC005561) putative POL3 protein [Arabidopsis thaliana] (Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus] (AI031394) putative protein [Arabidopsis thaliana] (D85597) polyprotein [Oryza australiensis] (AC003981) F22O13.26 [Arabidopsis thaliana] L-japonicus gln1, pge1 & krm genes (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana] Glycine max satellite STR120-A.4.
4588	GM_91_B1_A02_T7	g1769899	BLASTX	311	4e-27	59	
4589	GM_91_B1_A04_T7	g505129	BLASTN	453	1e-13	66	
4590	GM_91_B1_A06_T7	g3097320	BLASTN	488	5e-15	72	
4591	GM_91_B1_A07_T7	g505129	BLASTN	353	5e-09	70	
4592	GM_91_B1_A10_T7	g4063760	BLASTX	254	1e-31	48	
4593	GM_91_B1_B01_T7	g2764526	BLASTN	398	7e-16	65	
4594	GM_91_B1_B11_T7	g531389	BLASTX	227	4e-26	49	
4595	GM_91_B1_C01_T7	g2586082	BLASTX	236	1e-25	47	
4596	GM_91_B1_C08_T7	g507910	BLASTN	686	2e-24	86	
4597	GM_91_B1_C09_T7	g2522230	BLASTX	134	1e-10	36	
4598	GM_91_B1_C12_T7	g4063760	BLASTX	249	4e-19	60	
4599	GM_91_B1_D05_T7	g2443320	BLASTX	218	1e-15	40	
4600	GM_91_B1_D08_T7	g3810596	BLASTX	158	1e-09	39	
4601	GM_91_B1_E10_T7	g1769898	BLASTX	402	2e-36	60	
4602	GM_91_B1_F10_T7	g4038056	BLASTX	266	4e-21	46	
4603	GM_91_B1_F12_T7	g4063760	BLASTX	495	2e-45	72	
4604	GM_91_B1_H12_T7	g1946279	BLASTX	270	5e-26	51	
4605	GM_91_B2_A02_MR	g3549672	BLASTX	158	2e-18	91	
4606	GM_91_B2_A03_T7	g2443320	BLASTX	269	3e-21	37	
4607	GM_91_B2_A05_MR	g3063464	BLASTX	248	6e-20	80	
4608	GM_91_B2_A08_MR	g2073447	BLASTN	369	1e-09	63	
4609	GM_91_B2_B06_MR	g3319362	BLASTX	267	4e-21	47	
4610	GM_91_B2_B07_MR	g1142702	BLASTN	1080	3e-42	95	

4611	GM_91_B2_B08_T7	g3777527	BLASTX	304	8e-25	43	(AF053008) gag-pol polyprotein [Glycine max]
4612	GM_91_B2_B09_MR	g3645899	BLASTX	272	1e-21	46	(U68408) 5' end not determined experimentally [Zea mays]
4613	GM_91_B2_B11_T7	g3645899	BLASTX	214	2e-15	48	(U68408) 5' end not determined experimentally [Zea mays]
4614	GM_91_B2_C06_MR	g3962377	BLASTX	663	2e-64	96	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]
4615	GM_91_B2_C07_MR	g1142701	BLASTN	1351	1e-54	87	Glycine max satellite STR120-A.3.
4616	GM_91_B2_C08_MR	g2129618	BLASTX	238	4e-18	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4617	GM_91_B2_D01_MR	g3097320	BLASTN	1149	5e-45	79	Glycine max gene for Bd 30K, complete cds
4618	GM_91_B2_D03_T7	g508442	BLASTN	365	1e-09	60	Cucurbita maxima (clone gPC13-1B) phloem protein 2 (PP2) gene, complete cds.
4619	GM_91_B2_D06_MR	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
4620	GM_91_B2_D06_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence
4621	GM_91_B2_D07_MR	g128771	BLASTX	99	3e-11	59	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5.
4622	GM_91_B2_D08_T7	g4063760	BLASTX	449	2e-40	64	CHLOROPLAST gi 100110 pir S08494 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - fava bean chloroplast gi 11555 (X14804) ndhF gene product (AA 1-746) [Vicia faba] gi 12390 (X51471) NADH dehydrogenase [Vicia faba] gi 552971 (M36832) NADH dehydrogenase (ndhF) [Vicia faba]
4623	GM_91_B2_D09_T7	g3641837	BLASTX	183	3e-12	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4624	GM_91_B2_D10_MR	g1769898	BLASTX	363	5e-32	55	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]
4625	GM_91_B2_F08_MR	g3142328	BLASTN	2018	7e-85	95	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4626	GM_91_B2_E09_T7	g3513745	BLASTX	252	3e-19	34	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
4627	GM_91_B2_F03_MR	g3845197	BLASTN	467	4e-14	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
4628	GM_91_B2_F03_T7	g3894157	BLASTX	251	2e-19	38	(AC005312) putative protein kinase, 3' partial [Arabidopsis thaliana]
4629	GM_91_B2_F05_T7	g507910	BLASTN	619	2e-21	85	Glycine max BSR-101 satellite SB92 genomic sequence.
4630	GM_91_B2_F07_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4631	GM_91_B2_F11_MR	g3097836	BLASTN	407	2e-11	62	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
4632	GM_91_B2_G04_MR	g3426334	BLASTN	350	8e-09	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
4633	GM_91_B2_G05_T7	g4092471	BLASTN	381	4e-10	64	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]

4634	GM_91_B2_G06_MR	g117519	BLASTX	489	6e-46	94	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE) gi 99945 pir A39597 phytoene dehydrogenase (EC 1.3.-.-) - soybean gi 170044 (M64704) phytoene desaturase [Glycine max]
4635	GM_91_B2_G08_MR	g2764526	BLASTN	655	1e-22	68	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
4636	GM_91_B2_G08_T7	g100484	BLASTX	228	8e-24	52	hypothetical protein - garden snapdragon
4637	GM_91_B2_G09_T7	g2564051	BLASTN	380	7e-11	75	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]
4638	GM_91_B2_G11_T7	g3142328	BLASTN	1794	1e-74	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF053008) gag-pol polyprotein [Glycine max]
4639	GM_91_B2_H01_MR	g3777527	BLASTX	773	7e-75	96	Pneumocystis carinii genes for MSG99 and MSG100, complete cds (AC005560) unknown protein [Arabidopsis thaliana]
4640	GM_91_B2_H03_T7	g559718	BLASTN	354	6e-09	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4641	GM_91_B2_H04_MR	g3785989	BLASTX	190	3e-13	63	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
4642	GM_91_B2_H07_MR	g505129	BLASTN	371	8e-10	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4643	GM_91_B2_H08_MR	g3650039	BLASTX	301	4e-25	43	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4644	GM_91_B2_H10_MR	g4063760	BLASTX	174	4e-11	41	Glycine max gene for Bd 30K, complete cds
4645	GM_91_B2_H11_MR	g3142328	BLASTN	794	5e-29	88	MITOCHONDRIAL LON PROTEASE HOMOLOG 2
4646	GM_92_A2_A07_MR	g3097320	BLASTN	1330	3e-53	83	PRECURSOR >gi 1848291 (U88087) LON protease homolog [Arabidopsis thaliana]
4647	GM_92_A2_A09_MR	g3914007	BLASTX	157	5e-11	85	Oncorhynchus kisutch growth hormone 1 gene, intron C, complete sequence
4648	GM_92_A2_A10_MR	g2735745	BLASTN	344	7e-09	60	G-max gene for catalase
4649	GM_92_A2_B04_MR	g18559	BLASTN	467	4e-14	67	PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR gi
4650	GM_92_A2_B04_T7	g464900	BLASTX	221	6e-18	39	539008 pir S39476 kinase-like transmembrane protein TMKL1 precursor - Arabidopsis thaliana gi 313190 (X72863) TMKL1 gene product [Arabidopsis thaliana]
4651	GM_92_A2_B05_T7	g3142328	BLASTN	1205	1e-47	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC001229) Similar to Saccharomyces hypothetical protein P9642.2 (gb U40828), [Arabidopsis thaliana]
4652	GM_92_A2_B06_T7	g2190544	BLASTX	158	4e-10	72	Broad bean (V.faba) BamHI repetitive element, 900 bp family: Melanoplus sanguinipes entomopoxvirus, complete genome A.thaliana RH1, TCI, G14587-5, G14587-6, and PRI.1 genes
4653	GM_92_A2_B08_MR	g170602	BLASTN	490	3e-16	67	
4654	GM_92_A2_C05_MR	g4049647	BLASTN	398	6e-11	63	
4655	GM_92_A2_C08_MR	g2326340	BLASTN	351	8e-09	61	

4656	GM_92_A2_C11_MR	g4182	BLASTN	588	1e-19	85	2 micron plasmid of yeast (circularly closed). >gi 172190 gb J01347 YSCPLASM S.cerevisiae 2 micron circle plasmid, complete genome.
4657	GM_92_A2_D01_MR	g1666236	BLASTX	151	1e-09	32	(U76261) unknown [Hordeum vulgare]
4658	GM_92_A2_D08_T7	g905361	BLASTX	545	7e-52	82	(U22103) gag-protease polyprotein [Glycine max]
4659	GM_92_A2_D09_T7	g840618	BLASTN	348	7e-09	65	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
4660	GM_92_A2_D10_T7	g1769898	BLASTX	228	4e-32	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4661	GM_92_A2_D11_MR	g1167523	BLASTX	266	8e-21	40	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
4662	GM_92_A2_E02_T7	g3097320	BLASTN	367	1e-09	75	Glycine max gene for Bd 30K, complete cds
4663	GM_92_A2_E07_T7	g3142328	BLASTN	1971	1e-82	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]
4664	GM_92_A2_E08_MR	g2947063	BLASTX	151	4e-13	35	Glycine max gene for Bd 30K, complete cds
4665	GM_92_A2_F05_MR	g3097320	BLASTN	916	2e-34	70	Glycine max gene for Bd 30K, complete cds
4666	GM_92_A2_F09_MR	g3097320	BLASTN	423	4e-12	69	(AF053008) gag-pol polyprotein [Glycine max]
4667	GM_92_A2_G02_MR	g3777527	BLASTX	179	2e-11	32	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4668	GM_92_A2_G03_T7	g3142328	BLASTN	1391	4e-56	78	G max gene for catalase
4669	GM_92_A2_G05_MR	g18559	BLASTN	542	2e-17	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
4670	GM_92_A2_G08_MR	g3142328	BLASTN	898	1e-33	85	(AF075598) No definition line found [Arabidopsis thaliana]
4671	GM_92_A2_H01_T7	g2522227	BLASTX	151	1e-09	46	Glycine max BSR-101 satellite SB92 genomic sequence.
4672	GM_92_A2_H03_T7	g3377834	BLASTX	192	2e-13	33	(AC004450) hypothetical protein [Arabidopsis thaliana]
4673	GM_92_A2_H05_MR	g507910	BLASTN	346	5e-09	72	(Y12432) polyprotein [Ananas comosus]
4674	GM_92_A2_H06_MR	g3763929	BLASTX	268	1e-21	70	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]
4675	GM_92_A2_H10_MR	g2995405	BLASTX	319	8e-27	51	Glycine max BSR-101 satellite SB92 genomic sequence.
4676	GM_92_B1_A01_T7	g2961377	BLASTX	163	6e-10	34	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005897) putative transposon [Arabidopsis thaliana]
4677	GM_92_B1_A02_T7	g507910	BLASTN	455	6e-14	73	G max gene for catalase
4678	GM_92_B1_A11_T7	g3142328	BLASTN	1185	9e-47	79	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4679	GM_92_B1_B01_T7	g4038056	BLASTX	377	5e-33	48	retrotransposon dell-46 [Lilium henryi]
4680	GM_92_B1_B03_MR	g18559	BLASTN	1027	2e-39	73	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4681	GM_92_B1_B05_MR	g2129618	BLASTX	179	9e-12	44	(AB007466) reverse transcriptase-like protein [Vicia faba]
4682	GM_92_B1_C04_MR	g226407	BLASTX	339	1e-28	45	(U64926) NTGP5 [Nicotiana tabacum]
4683	GM_92_B1_C05_MR	g2522230	BLASTX	171	3e-12	37	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4684	GM_92_B1_C05_T7	g2522228	BLASTX	366	7e-33	53	
4685	GM_92_B1_C12_T7	g4097587	BLASTX	185	1e-13	65	
4686	GM_92_B1_D02_MR	g1769898	BLASTX	226	4e-17	42	

4687	GM_92_B1_D03_MR	g1890143	BLASTN	347	1e-08	64	A.egypti DNA, copia-like transposable element ZebedeeII
4688	GM_92_B1_D05_T7	g2462936	BLASTX	253	2e-23	41	(Y12321) open reading frame 2 [Brassica oleracea]
4689	GM_92_B1_D09_T7	g18695	BLASTN	370	7e-10	68	Soybean nodulin 22 gene
4690	GM_92_B1_D11_MR	g18559	BLASTN	913	2e-34	75	G.max gene for catalase
4691	GM_92_B1_D11_T7	g2961349	BLASTX	197	1e-28	52	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
4692	GM_92_B1_E01_T7	g3097320	BLASTN	1221	3e-48	84	Glycine max gene for Bd 30K, complete cds
4693	GM_92_B1_E02_T7	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4694	GM_92_B1_E04_T7	g507910	BLASTN	353	2e-09	84	Glycine max BSR-101 satellite SB92 genomic sequence.
4695	GM_92_B1_E06_T7	g507910	BLASTN	410	6e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4696	GM_92_B1_F01_T7	g508826	BLASTN	415	9e-12	60	Drosophila melanogaster Oregon-R mitochondrial A+T region
4697	GM_92_B1_F07_T7	g99922	BLASTX	693	1e-67	85	hypothetical protein - soybean gi 930025 (X13528) ORF (3.34 AA); pid:c150225 [Glycine max]
4698	GM_92_B1_F10_MR	g3212869	BLASTX	335	6e-29	77	(AC004005) unknown protein [Arabidopsis thaliana]
4699	GM_92_B1_G02_MR	g3142289	BLASTX	234	4e-18	55	(AC002411) Strong similarity to beta-keto-Coa synthase gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
4700	GM_92_B1_G02_T7	g3142328	BLASTN	1094	1e-42	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
4701	GM_92_B1_G04_MR	g2367675	BLASTX	194	2e-13	33	(AF017040) Pol [Dictyostelium discoideum]
4702	GM_92_B1_G05_MR	g3560170	BLASTX	230	3e-24	71	(AL031525) 26s protease regulatory subunit S10b [Schizosaccharomyces pombe]
4703	GM_92_B1_G05_T7	g102489	BLASTX	114	4e-14	54	vacuolar proton pump homolog - Caenorhabditis elegans gi 6961 (Z11115) cDNA EST yk307a1.5 comes from this gene; cDNA EST yk469d12.5 comes from this gene; cDNA EST yk499g12.5 comes from this gene [Caenorhabditis elegans]
4704	GM_92_B1_G08_MR	g3377855	BLASTX	278	6e-35	59	(AF076274) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf- CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
4705	GM_92_B1_H03_T7	g18559	BLASTN	320	4e-10	76	G.max gene for catalase
4706	GM_92_B1_H05_T7	g2129618	BLASTX	171	6e-11	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4707	GM_92_B1_H09_MR	g2746847	BLASTX	179	2e-13	38	(AF040649) contains similarity to helicases [Caenorhabditis elegans]
4708	GM_92_B1_H09_T7	g18559	BLASTN	544	1e-17	71	G.max gene for catalase
4709	GM_94_A1_B08_T7	g3142328	BLASTN	948	5e-36	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
4710	GM_94_A1_B09_T7	g3560029	BLASTN	427	2e-12	65	Schistosoma intercalatum ribosomal intergenic spacer DNA (2169 bp)
4711	GM_94_A1_C03_MR	g507910	BLASTN	366	6e-10	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4712	GM_94_A1_C04_T7	g3777527	BLASTX	520	8e-48	91	(AF053008) gag-pol polyprotein [Glycine max]
4713	GM_94_A1_C07_MR	g507910	BLASTN	387	7e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.

4714	GM_94_A1_C07_T7	g507910	BLASTN	363	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4715	GM_94_A1_C12_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4716	GM_94_A1_D03_T7	g2462134	BLASTX	323	5e-28	45	(Y13368) reverse transcriptase [Beta vulgaris]
4717	GM_94_A1_E02_MR	g2244747	BLASTN	355	5e-09	72	Arabidopsis thaliana DNA chromosome 4, ESSA 1 contig fragment
4718	GM_94_A1_F08_MR	g18559	BLASTN	399	5e-11	73	No. 0
4719	GM_94_A1_F08_MR	g4063760	BLASTX	175	3e-11	36	G.max gene for catalase
4720	GM_94_A1_H12_MR	g18559	BLASTN	631	1e-21	74	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
4721	GM_94_A2_A01_MR	g4050011	BLASTN	559	3e-18	70	G.max gene for catalase
4722	GM_94_A2_A03_T7	g3142328	BLASTN	471	3e-14	88	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
4723	GM_94_A2_A06_MR	g3777527	BLASTX	665	3e-63	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF053008) gag-pol polyprotein [Glycine max]
4724	GM_94_A2_A11_MR	g3777527	BLASTX	679	8e-65	92	(AF053008) gag-pol polyprotein [Glycine max]
4725	GM_94_A2_A11_T7	g1769898	BLASTX	241	4e-28	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4726	GM_94_A2_A12_T7	g2522227	BLASTX	160	1e-10	43	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
4727	GM_94_A2_B03_T7	g18559	BLASTN	966	9e-37	75	G.max gene for catalase
4728	GM_94_A2_B06_MR	g507910	BLASTN	557	1e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence
4729	GM_94_A2_B06_T7	g507910	BLASTN	615	4e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence
4730	GM_94_A2_B08_MR	g507910	BLASTN	362	9e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence
4731	GM_94_A2_B09_MR	g4092471	BLASTN	520	2e-16	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
4732	GM_94_A2_B11_MR	g3930515	BLASTX	115	4e-09	46	(AF059674) putative gag protein [Nicotiana tabacum]
4733	GM_94_A2_C01_T7	g2522228	BLASTX	442	6e-41	57	(AB007466) reverse transcriptase-like protein [Vicia faba]
4734	GM_94_A2_C02_MR	g1916643	BLASTX	269	1e-22	54	(U71604) desacetoxymyosin 4-hydroxylase [Catharanthus roseus]
4735	GM_94_A2_C03_MR	g2443320	BLASTX	369	8e-32	45	(D85597) polyprotein [Oryza australiensis]
4736	GM_94_A2_C03_T7	g18559	BLASTN	607	2e-20	71	G.max gene for catalase
4737	GM_94_A2_C05_T7	g09922	BLASTX	279	1e-23	62	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
4738	GM_94_A2_C06_MR	g2708743	BLASTX	258	6e-20	43	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
4739	GM_94_A2_C08_MR	g2443320	BLASTX	351	7e-30	58	(D85597) polyprotein [Oryza australiensis]
4740	GM_94_A2_C12_MR	g320565	BLASTX	298	1e-25	55	transposon TAI-1 KAS-1 - Arabidopsis thaliana (fragment)
4741	GM_94_A2_D03_MR	g2129618	BLASTX	265	6e-21	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4742	GM_94_A2_D04_MR	g1769898	BLASTX	399	4e-42	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4743	GM_94_A2_D07_T7	g3142379	BLASTX	304	2e-26	67	(AF053008) envelope-like [Glycine max]
4744	GM_94_A2_D09_MR	g4006829	BLASTX	270	3e-22	70	(AC005970) putative protein kinase [Arabidopsis thaliana]

4745	GM_94_A2_D10_T7	g1666236	BLASTX	170	1e-11	28	(U76261) unknown [Hordeum vulgare]
4746	GM_94_A2_D12_MR	g100484	BLASTX	379	2e-33	62	hypothetical protein - garden snapdragon
4747	GM_94_A2_E07_MR	g505129	BLASTN	380	3e-10	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4748	GM_94_A2_F02_MR	g13767	BLASTN	367	2e-10	59	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
4749	GM_94_A2_F02_T7	g3763998	BLASTN	344	4e-10	63	Plasmodium falciparum MAL3P4, complete sequence [Plasmodium falciparum]
4750	GM_94_A2_F05_T7	g2129618	BLASTX	196	1e-13	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] (X98422) delta-1-pyrroline-5-carboxylate synthase [Medicago sativa] RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4751	GM_94_A2_F06_MR	g1781040	BLASTX	172	3e-12	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4752	GM_94_A2_F06_T7	g130582	BLASTX	178	2e-11	32	Glycine max BSR-101 satellite SB92 genomic sequence.
4753	GM_94_A2_F07_MR	g507910	BLASTN	624	1e-21	83	RAC-LIKE GTP BINDING PROTEIN RHO1 gi 477010 pir A47525 ras-related small GTP-binding protein Rho1Ps - garden pea gi 1263170 (L19093) GTP-binding protein [Pisum sativum]
4754	GM_94_A2_F07_T7	g507910	BLASTN	416	3e-12	77	METALLOTHIONEIN-LIKE PROTEIN B gi 480753 pir S37240 metallothionein-like protein - white clover gi 403329 (Z26493) metallothionein-like protein [Trifolium repens]
4755	GM_94_A2_F10_MR	g2500199	BLASTX	130	1e-16	93	Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence
4756	GM_94_A2_F11_MR	g1171046	BLASTX	180	3e-13	60	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) gi 1083259 pir JC4073 TCP-1 containing cytosolic chaperonin (CCT) theta chain - mouse gi 695625 (Z37164) CCTtheta, theta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]
4757	GM_94_A2_G02_T7	g3845307	BLASTN	350	9e-09	63	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]
4758	GM_94_A2_G03_MR	g1174621	BLASTX	219	8e-22	54	HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION gi 626631 pir S46811 hypothetical protein YHR074w - yeast (Saccharomyces cerevisiae) gi 500832 (U10556) Yhr074wp [Saccharomyces cerevisiae]
4759	GM_94_A2_G03_T7	g3894211	BLASTN	483	9e-15	65	
4760	GM_94_A2_G08_MR	g731675	BLASTX	101	2e-11	58	

4761	GM_94_A2_G12_MR	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4762	GM_94_A2_H02_T7	g4063760	BLASTX	125	3e-11	50	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
4763	GM_94_A2_H11_T7	g4038056	BLASTX	191	4e-13	42	(AC005897) putative transposon [Arabidopsis thaliana]
4764	GM_94_B2_B01_MR	g100484	BLASTX	300	6e-25	60	hypothetical protein - garden snapdragon
4765	GM_94_B2_B06_MR	g2443320	BLASTX	237	2e-21	52	(D85597) polyprotein [Oryza australiensis]
4766	GM_94_B2_B10_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4767	GM_94_B2_C03_T7	g905361	BLASTX	209	3e-15	38	(U22103) gag-protease polyprotein [Glycine max]
4768	GM_94_B2_C06_T7	g2997694	BLASTX	182	2e-13	43	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
4769	GM_94_B2_C08_T7	g507910	BLASTN	621	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4770	GM_94_B2_D03_T7	g2995405	BLASTX	278	2e-22	45	(Y12432) polyprotein [Ananas comosus]
4771	GM_94_B2_D08_MR	g507910	BLASTN	410	6e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4772	GM_94_B2_D10_T7	g3097320	BLASTN	1185	1e-46	82	Glycine max gene for Bd 30K. complete cds
4773	GM_94_B2_D11_T7	g4038056	BLASTX	298	1e-24	54	(AC005897) putative transposon [Arabidopsis thaliana]
4774	GM_94_B2_E05_T7	g3097320	BLASTN	610	1e-20	74	Glycine max gene for Bd 30K. complete cds
4775	GM_94_B2_F05_MR	g130582	BLASTX	292	1e-23	56	Glycine max gene for Bd 30K. complete cds
4776	GM_94_B2_F09_MR	g3142328	BLASTN	1054	8e-41	93	RETROVIRUS-RELATED POL. POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE; (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4777	GM_94_B2_G04_T7	g2275215	BLASTX	219	2e-17	65	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4778	GM_94_B2_G11_T7	g4063760	BLASTX	299	3e-26	60	(AC002337) hypothetical protein [Arabidopsis thaliana]
4779	GM_94_B2_H05_MR	g2995405	BLASTX	161	7e-10	39	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
4780	GM_94_B2_H05_T7	g3688328	BLASTX	112	2e-14	44	(Y12432) polyprotein [Ananas comosus]
4781	GM_95_A2_A06_T7	g4006833	BLASTX	200	8e-14	38	(AJ228325) reverse transcriptase [Ginkgo biloba]
4782	GM_95_A2_B10_T7	g3645899	BLASTX	225	2e-28	63	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
4783	GM_95_A2_C05_MR	g3287465	BLASTN	372	9e-10	66	(U68408) 5' end not determined experimentally [Zea mays]
4784	GM_95_A2_D06_MR	g1769898	BLASTX	300	3e-33	54	Homo sapiens chromosome 17, clone hRPK.1003_J_3, complete sequence [Homo sapiens]
4785	GM_95_A2_E05_MR	g2586082	BLASTX	152	6e-12	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4786	GM_95_A2_F07_MR	g2462936	BLASTX	277	2e-23	38	(U72725) retrofit [Oryza longistaminata]
4787	GM_95_A2_G04_T7	g507910	BLASTN	547	4e-18	79	(Y12321) open reading frame 2 [Brassica oleracea]
4788	GM_95_B1_A01_T7	g2522228	BLASTX	329	6e-29	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4789	GM_95_B1_A02_T7	g3337381	BLASTN	361	3e-09	67	Glycine max CTT987SK-A-952F10. (AB007466) reverse transcriptase-like protein [Vicia faba]
4790	GM_95_B1_A03_MR	g3599418	BLASTN	1038	4e-40	88	Homo sapiens Chromosome 16 BAC clone CTT987SK-A-952F10. complete sequence [Homo sapiens]
							Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds

4791	GM_95_B1_B03_T7	g3080452	BLASTX	163	2e-10	57	(AL022605) putative L-ascorbate oxidase [Arabidopsis thaliana]
4792	GM_95_B1_B05_T7	g2443320	BLASTX	364	3e-31	50	(D85597) polyprotein [Oryza australiensis]
4793	GM_95_B1_B11_T7	g3777527	BLASTX	168	3e-10	31	(AF053008) gag-pol polyprotein [Glycine max]
4794	GM_95_B1_C01_T7	g209638	BLASTN	346	8e-09	63	Amsacta entomopoxvirus thymidine kinase gene, complete cds; Q1 ORF, complete cds; Q3 ORF, 5'end. >gi 1251579 gb 116671116671 ORF, complete cds; Q3 ORF, 5'end. >gi 3409364 gb 189424189424 Sequence 8 from patent US 5476781 >gi 3409364 gb 189424189424 Sequence 8 from patent US 5721352
4795	GM_95_B1_C02_MR	g4063760	BLASTX	129	2e-11	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4796	GM_95_B1_C02_T7	g18559	BLASTN	414	1e-11	66	Gmax gene for catalase
4797	GM_95_B1_C04_MR	g2245115	BLASTX	160	8e-10	57	(Z97343) unnamed protein product [Arabidopsis thaliana]
4798	GM_95_B1_C05_MR	g2522228	BLASTX	107	9e-09	27	(AB007466) reverse transcriptase-like protein [Vicia faba]
4799	GM_95_B1_C11_T7	g13773	BLASTN	441	7e-14	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
4800	GM_95_B1_C12_T7	g20854	BLASTN	419	4e-12	68	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr. -Asn. -Ala. -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
4801	GM_95_B1_D01_MR	g3006135	BLASTN	421	6e-12	70	Pea rbcS-3A gene for ribulose 1,5-bisphosphate carboxylase (RBC) small subunit
4802	GM_95_B1_D06_MR	g1169534	BLASTX	141	5e-16	96	Homo sapiens DNA sequence from BAC 363A12 on chromosome 22q11.2-12.2, complete sequence [Homo sapiens]
4803	GM_95_B1_E01_MR	g3777527	BLASTX	123	4e-09	28	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) gi 542019 pir S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean gi 433609 (Z28386) enolase [Ritcinus communis]
4804	GM_95_B1_E02_T7	g3264544	BLASTN	490	4e-15	64	(AF053008) gag-pol polyprotein [Glycine max]
4805	GM_95_B1_E04_T7	g1666236	BLASTX	219	3e-17	31	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
4806	GM_95_B1_E05_MR	g1173285	BLASTX	288	9e-25	68	(U76261) unknown [Hordeum vulgare]
4807	GM_95_B1_F01_T7	g3142328	BLASTN	923	8e-41	86	40S RIBOSOMAL PROTEIN S9 gi 1362936 pir S55917 ribosomal protein S9 - human gi 550023 (U14971) ribosomal protein S9 [Homo sapiens] gi 1096943 prf 2113200F ribosomal protein S9 [Homo sapiens]
4808	GM_95_B1_F03_T7	g2464905	BLASTX	164	2e-11	58	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Z99708) minor allergen [Arabidopsis thaliana]
4809	GM_95_B1_F04_T7	g1514643	BLASTX	232	2e-25	62	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
4810	GM_95_B1_F07_T7	g18768	BLASTN	370	2e-10	73	Soybean Tgm6 transposable element 3' end
4811	GM_95_B1_F08_T7	g90922	BLASTX	164	2e-23	82	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

4812	GM_95_B1_G06_T7	g3142328	BLASTN	909	3e-34	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4813	GM_95_B1_G11_T7	g507910	BLASTN	348	4e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4814	GM_95_B1_H02_MR	g2558662	BLASTX	176	2e-13	59	(AC002354) No definition line found [Arabidopsis thaliana]
4815	GM_95_B1_H06_T7	g4063760	BLASTX	337	2e-28	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4816	GM_95_B1_H10_T7	g288378	BLASTN	372	7e-10	68	Z.mays gene PG for polygalacturonase.
4817	GM_95_B1_H11_MR	g2208908	BLASTX	327	2e-28	54	(AB004809) phosphate transporter [Catharanthus roseus]
4818	GM_95_B2_A09_MR	g3777527	BLASTX	162	1e-09	35	(AF053008) gag-pol polyprotein [Glycine max]
4819	GM_95_B2_A09_T7	g3097320	BLASTN	403	3e-11	76	Glycine max gene for Bd 30K, complete cds
4820	GM_95_B2_A10_MR	g3096945	BLASTX	160	5e-11	58	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]
4821	GM_95_B2_A10_T7	g1944188	BLASTN	346	8e-09	72	Soybean DNA for nodulin 35, partial cds
4822	GM_95_B2_A12_T7	g3142328	BLASTN	1171	4e-46	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4823	GM_95_B2_B01_MR	g507910	BLASTN	446	1e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4824	GM_95_B2_B02_MR	g1813979	BLASTX	238	4e-32	70	(Y10860) hypothetical protein [Musa acuminata]
4825	GM_95_B2_B04_MR	g507910	BLASTN	582	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4826	GM_95_B2_B04_T7	g4063760	BLASTX	267	2e-36	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4827	GM_95_B2_B10_MR	g2129618	BLASTX	180	7e-12	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4828	GM_95_B2_B11_T7	g3264565	BLASTN	358	4e-09	62	Homo sapiens chromosome 17, clone hRPC.1037.O_7, complete sequence [Homo sapiens]
4829	GM_95_B2_B12_MR	g2443320	BLASTX	379	7e-33	48	(D85597) polyprotein [Oryza australiensis]
4830	GM_95_B2_C02_MR	g20854	BLASTN	468	3e-14	71	Pea rbcS-3A gene for ribulose 1,5-bisphosphate carboxylase (RBC) small subunit
4831	GM_95_B2_C02_T7	g18559	BLASTN	1046	2e-40	76	G-max gene for catalase
4832	GM_95_B2_C06_MR	g507910	BLASTN	343	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4833	GM_95_B2_D04_MR	g507910	BLASTN	591	4e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4834	GM_95_B2_D06_T7	g18559	BLASTN	527	7e-17	66	G-max gene for catalase
4835	GM_95_B2_D10_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4836	GM_95_B2_D10_T7	g507910	BLASTN	553	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4837	GM_95_B2_D11_T7	g1171583	BLASTN	415	1e-11	64	P.falciparum complete gene map of plastid-like DNA (IR-A)
4838	GM_95_B2_E01_T7	g1769898	BLASTX	233	7e-18	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4839	GM_95_B2_E04_MR	g507910	BLASTN	540	8e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4840	GM_95_B2_E04_T7	g507910	BLASTN	495	9e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4841	GM_95_B2_E06_T7	g3212846	BLASTN	451	2e-13	78	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]
4842	GM_95_B2_E10_MR	g1769898	BLASTX	222	7e-20	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4843	GM_95_B2_E11_T7	g2462134	BLASTX	150	5e-11	42	(Y13368) reverse transcriptase [Beta vulgaris]
4844	GM_95_B2_F01_T7	g507910	BLASTN	423	2e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.

4845	GM_95_B2_F03_T7	g2464905	BLASTX	220	2e-17	56	(Z99708) minor allergen [Arabidopsis thaliana]
4846	GM_95_B2_F06_T7	g18767	BLASTN	458	2e-14	73	Soybean Tgm6 transposable element 5' end
4847	GM_95_B2_F07_MR	g3402755	BLASTX	245	1e-18	36	(AL031187) putative transposable element [Arabidopsis thaliana]
4848	GM_95_B2_F09_MR	g2104945	BLASTN	536	3e-17	80	Glycine max copia-like retrotransposon Tgm, complete sequence
4849	GM_95_B2_H02_T7	g130405	BLASTX	220	5e-16	39	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
							(TRANSPONSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol
							polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi
							1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase
							[Drosophila melanogaster] gi 224319 prf 1101404B ORF 2
							[Drosophila melanogaster]
4850	GM_95_B2_H04_T7	g1184075	BLASTX	174	4e-11	34	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf
4851	GM_95_B2_H05_T7	g3650039	BLASTX	210	2e-15	36	2207203A Cf-2 gene [Lycopersicon esculentum]
							(AC005396) putative En/Spm transposon protein, 5' partial
							[Arabidopsis thaliana]
4852	GM_95_B2_H08_MR	g2160154	BLASTX	248	2e-19	34	(AC000375) F19K23.18 gene product [Arabidopsis thaliana]
4853	GM_95_B2_H08_T7	g342952	BLASTN	430	2e-13	60	paramesium species 1.168 mt dna dimer: replication init. region.
4854	GM_98_A2_A01_MR	g4063760	BLASTX	524	2e-48	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4855	GM_98_A2_A02_MR	g507910	BLASTN	501	5e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4856	GM_98_A2_A02_T7	g507910	BLASTN	474	8e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4857	GM_98_A2_A10_MR	g70616	BLASTX	157	9e-11	81	leghemoglobin c3 - soybean
4858	GM_98_A2_A12_MR	g3777527	BLASTX	480	2e-43	91	(AF053008) gag-pol polyprotein [Glycine max]
4859	GM_98_A2_B02_T7	g507910	BLASTN	588	6e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
4860	GM_98_A2_B03_T7	g3142328	BLASTN	1139	1e-44	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4861	GM_98_A2_B04_MR	g507910	BLASTN	673	8e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
4862	GM_98_A2_B08_MR	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4863	GM_98_A2_B08_T7	g507910	BLASTN	600	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4864	GM_98_A2_B12_T7	g2459440	BLASTX	131	8e-12	41	(AC002332) putative receptor kinase [Arabidopsis thaliana]
4865	GM_98_A2_C02_T7	g2588617	BLASTN	372	9e-10	65	Human BAC clone RG119H12 from 7p15, complete sequence
							[Homo sapiens]
4866	GM_98_A2_C03_T7	g4115365	BLASTX	192	6e-13	42	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
4867	GM_98_A2_C04_MR	g507910	BLASTN	577	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4868	GM_98_A2_C04_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4869	GM_98_A2_C06_MR	g3097320	BLASTN	757	3e-34	82	Glycine max gene for Bd 30K, complete cds
4870	GM_98_A2_C07_MR	g3327389	BLASTX	119	3e-11	66	(AC004483) putative DNA replication licensing factor, mem5
							[Arabidopsis thaliana]
4871	GM_98_A2_C08_T7	g3820757	BLASTN	380	2e-10	64	Caenorhabditis elegans cosmid Y53C12D, complete sequence
							[Caenorhabditis elegans]

4872	GM_98_A2_C10_T7	g3777527	BLASTX	178	2e-11	55	(AF053008) gag-pol polyprotein [Glycine max]
4873	GM_98_A2_C11_T7	g4049332	BLASTN	362	5e-10	71	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAH project)
4874	GM_98_A2_C12_MR	g1769898	BLASTX	200	2e-14	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4875	GM_98_A2_D03_MR	g218269	BLASTX	197	5e-15	87	(D12839) reverse transcriptase [Glycine max]
4876	GM_98_A2_D04_MR	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4877	GM_98_A2_D04_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4878	GM_98_A2_D06_MR	g531389	BLASTX	371	6e-32	53	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
4879	GM_98_A2_D11_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4880	GM_98_A2_D11_T7	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4881	GM_98_A2_D12_T7	g507910	BLASTN	347	4e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4882	GM_98_A2_E06_MR	g507910	BLASTN	364	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4883	GM_98_A2_E09_T7	g507910	BLASTN	494	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4884	GM_98_A2_E10_MR	g3947839	BLASTN	375	7e-10	60	Human DNA sequence from clone 569D19 on chromosome 22q13.1. Contains a novel gene similar to mouse Ras, Dexamethasone-induced 1 (Ras-related protein, RASD1, DEXRAS1) and the last exon of the MB gene for Myoglobin. Cont...
4885	GM_98_A2_F08_MR	g507910	BLASTN	657	4e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
4886	GM_98_A2_F10_MR	g4063760	BLASTX	436	5e-39	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4887	GM_98_A2_G01_MR	g3097320	BLASTN	369	1e-09	75	Glycine max gene for Bd 30K, complete cds
4888	GM_98_A2_G03_MR	g3810596	BLASTX	125	6e-12	61	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4889	GM_98_A2_G04_MR	g2832611	BLASTN	288	7e-10	74	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAH project)
4890	GM_98_A2_G08_T7	g3777527	BLASTX	590	3e-55	95	(AF053008) gag-pol polyprotein [Glycine max]
4891	GM_98_A2_G09_MR	g1769898	BLASTX	537	5e-51	80	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4892	GM_98_A2_G12_MR	g3142328	BLASTN	755	3e-27	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4893	GM_98_A2_H03_MR	g130582	BLASTX	422	2e-37	52	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4894	GM_98_A2_H09_MR	g3142328	BLASTN	802	2e-29	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4895	GM_98_A2_H10_T7	g3063438	BLASTN	482	1e-14	71	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]
4896	GM_98_A2_H11_T7	g507910	BLASTN	394	3e-11	78	Glycine max BSR-101 satellite SB92 genomic sequence.

4897	GM_98_B1_A01_MR	g3142328	BLASTN	785	1e-28	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC004255) TIF9.15 [Arabidopsis thaliana]
4898	GM_98_B1_A08_MR	g3056594	BLASTX	199	5e-14	56	(Z75513) reverse transcriptase [Oryza sativa]
4899	GM_98_B1_B03_MR	g1419120	BLASTX	233	8e-19	58	Glycine max BSR-101 satellite SB92 genomic sequence.
4900	GM_98_B1_B05_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4901	GM_98_B1_B05_T7	g507910	BLASTN	370	4e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4902	GM_98_B1_B09_T7	g507910	BLASTN	514	1e-16	83	(Z97340) strong similarity to ZK688.3 protein - Caenorhabditis elegans [Arabidopsis thaliana]
4903	GM_98_B1_C01_MR	g2244952	BLASTX	224	9e-25	76	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
4904	GM_98_B1_C01_T7	g2642431	BLASTX	270	3e-21	50	(AF053008) gag-pol polyprotein [Glycine max]
4905	GM_98_B1_C03_MR	g3777527	BLASTX	318	6e-28	81	paramesicium species 5.311 mt dna dimer: replication init. region.
4906	GM_98_B1_C07_T7	g342964	BLASTN	535	4e-18	66	(AF053008) gag-pol polyprotein [Glycine max]
4907	GM_98_B1_C09_MR	g3777527	BLASTX	177	3e-11	37	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA);
4908	GM_98_B1_D02_MR	g99922	BLASTX	391	1e-57	81	pid:e150225 [Glycine max]
4909	GM_98_B1_D11_MR	g2982452	BLASTX	266	5e-21	43	(A1022223) receptor protein kinase - like protein [Arabidopsis thaliana]
4910	GM_98_B1_E02_MR	g2522230	BLASTX	171	3e-12	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4911	GM_98_B1_E02_T7	g2522230	BLASTX	190	3e-14	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4912	GM_98_B1_E03_MR	g3970803	BLASTX	117	3e-12	37	(AJ130841) caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa]
4913	GM_98_B1_F05_T7	g4063760	BLASTX	152	9e-09	29	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4914	GM_98_B1_F08_MR	g342964	BLASTN	419	7e-13	63	paramesicium species 5.311 mt dna dimer: replication init. region.
4915	GM_98_B1_E10_T7	g2522228	BLASTX	161	2e-10	51	(AB007466) reverse transcriptase-like protein [Vicia faba]
4916	GM_98_B1_G02_T7	g2160161	BLASTX	167	7e-11	36	(AC000132) F21M12.7 gene product [Arabidopsis thaliana]
4917	GM_98_B1_G04_T7	g2586082	BLASTX	179	6e-20	60	(U72725) retrofit [Oryza longistaminata]
4918	GM_98_B1_H06_MR	g2522230	BLASTX	200	3e-18	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4919	GM_98_B1_H09_T7	g1362091	BLASTX	178	4e-12	84	cellulase (EC 3.2.1.4) precursor - tomato gi 924622 (U20590) endo-1,4-beta-glucanase precursor [Solanum lycopersicum]
4920	GM_98_B2_A06_T7	g905361	BLASTX	893	9e-89	90	(U22103) gag-protease polyprotein [Glycine max]
4921	GM_98_B2_A08_T7	g507910	BLASTN	398	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4922	GM_98_B2_A10_T7	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.

4923	GM_98_B2_A12_T7	g130582	BLASTX	189	1e-19	51	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4924	GM_98_B2_B03_T7	g3386598	BLASTX	404	5e-37	75	(AC004665) putative cytochrome p450 [Arabidopsis thaliana]
4925	GM_98_B2_B08_T7	g2129618	BLASTX	293	6e-24	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4926	GM_98_B2_C07_T7	g4063760	BLASTX	310	2e-27	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4927	GM_98_B2_C08_T7	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
4928	GM_98_B2_C09_T7	g13581	BLASTN	331	9e-09	59	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
4929	GM_98_B2_C10_T7	g3142328	BLASTN	1730	1e-71	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF110183) putative integrase [Oryza sativa]
4930	GM_98_B2_F01_T7	g4140712	BLASTX	164	2e-11	45	Arabidopsis thaliana (clone NING6) reverse transcriptase (Ta27) pseudogene, partial cds
4931	GM_98_B2_F07_T7	g976282	BLASTN	377	6e-11	60	putative transposase [Arabidopsis thaliana]
4932	GM_98_B2_F01_T7	g3283026	BLASTX	298	1e-24	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4933	GM_98_B2_F04_T7	g4063760	BLASTX	513	3e-47	56	P.falciparum 3.8 gene for putative serine kinase (partial) and GBP130 gene for glycophorin binding protein (partial)
4934	GM_98_B2_F08_T7	g9837	BLASTN	446	3e-13	62	(X94624) acyl-CoA synthetase [Brassica napus]
4935	GM_98_B2_F09_T7	g1617270	BLASTX	233	6e-32	68	(X98316) peroxidase [Arabidopsis thaliana] gi 1429223 gnl PID e252638 (X99096) peroxidase [Arabidopsis thaliana]
4936	GM_98_B2_F11_T7	g1402910	BLASTX	191	2e-25	76	(AF053008) gag-pol polypeptide [Glycine max]
4937	GM_98_B2_F12_T7	g3777527	BLASTX	269	2e-24	45	(AB007466) reverse transcriptase-like protein [Vicia faba]
4938	GM_98_B2_G07_T7	g2522228	BLASTX	168	3e-11	53	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polypeptide (gb U12626). [Arabidopsis thaliana]
4939	GM_98_B2_G08_T7	g2194136	BLASTX	234	2e-17	32	(U55874) asparagine synthetase [Glycine max]
4940	GM_98_B2_H02_T7	g1305549	BLASTX	203	6e-27	74	Saccharomyces cerevisiae complete mitochondrial genome
4941	GM_98_B2_H04_T7	g4160362	BLASTN	366	3e-13	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4942	GM_98_B2_H08_T7	g1769897	BLASTX	219	7e-20	39	G.max gene for catalase
4943	GM_99_A2_A03_MR	g18559	BLASTN	1027	2e-39	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4944	GM_99_A2_A05_MR	g3142328	BLASTN	1102	5e-43	92	Glycine max gene for Bd 30K, complete cds
4945	GM_99_A2_A05_T7	g3097320	BLASTN	412	1e-11	75	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
4946	GM_99_A2_A06_MR	g3650039	BLASTX	289	8e-24	44	

4947	GM_99_A2_A07_MR	g2894590	BLASTN	371	8e-10	60	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-115, complete sequence [Plasmodium falciparum]
4948	GM_99_A2_A09_MR	g548488	BLASTX	208	1e-18	67	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) gi 166325 (L12019) polygalacturonase [Actinidia deliciosa]
4949	GM_99_A2_B03_T7	g2245073	BLASTN	403	4e-11	64	Arabidopsis thaliana DNA chromosome 4, ESSA 1 contig fragment No. 8
4950	GM_99_A2_B10_MR	g1769898	BLASTX	362	2e-39	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4951	GM_99_A2_B10_T7	g3142330	BLASTX	536	6e-51	80	(U96295) envelope-like [Glycine max]
4952	GM_99_A2_B11_T7	g4038056	BLASTX	315	2e-26	51	(AC005897) putative transposon [Arabidopsis thaliana]
4953	GM_99_A2_B12_T7	g2995405	BLASTX	421	8e-38	65	(Y12432) polyprotein [Ananas comosus]
4954	GM_99_A2_C02_T7	g4063760	BLASTX	571	2e-53	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4955	GM_99_A2_C03_T7	g4038056	BLASTX	314	3e-26	42	(AC005897) putative transposon [Arabidopsis thaliana]
4956	GM_99_A2_C08_MR	g421955	BLASTX	217	2e-26	60	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORE4 [Solanum tuberosum]
4957	GM_99_A2_D01_MR	g1165321	BLASTN	634	1e-29	91	Glycine max extensin (SbHRGP3) gene, complete cds
4958	GM_99_A2_D01_T7	g2085783	BLASTN	359	3e-09	58	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
4959	GM_99_A2_D03_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
4960	GM_99_A2_D03_T7	g4063760	BLASTX	277	4e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4961	GM_99_A2_D07_T7	g3142328	BLASTN	784	2e-28	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
4962	GM_99_A2_D08_MR	g3299824	BLASTN	473	3e-14	60	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]
4963	GM_99_A2_D08_T7	g2244876	BLASTX	421	5e-37	68	(Z97338) hypothetical protein [Arabidopsis thaliana]
4964	GM_99_A2_E01_MR	g3777527	BLASTX	223	4e-16	53	(AF053008) gag-pol polyprotein [Glycine max]
4965	GM_99_A2_E08_T7	g507910	BLASTN	575	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4966	GM_99_A2_E10_MR	g905361	BLASTX	181	3e-12	28	(U22103) gag-protease polyprotein [Glycine max]
4967	GM_99_A2_E11_MR	g1480927	BLASTN	462	5e-14	74	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
4968	GM_99_A2_F10_T7	g1480927	BLASTN	635	6e-22	96	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
4969	GM_99_A2_F12_MR	g507910	BLASTN	662	3e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
4970	GM_99_A2_G01_MR	g170029	BLASTN	388	1e-10	80	Glycine max cv. Dare nodulin 26 gene fragment.
4971	GM_99_A2_G01_T7	g2522230	BLASTX	297	1e-25	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4972	GM_99_A2_G02_MR	g4063760	BLASTX	176	3e-11	32	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4973	GM_99_A2_G03_MR	g2351064	BLASTN	676	2e-23	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22
4974	GM_99_A2_G04_MR	g3097320	BLASTN	982	2e-37	77	Glycine max gene for Bd 30K, complete cds

4975	GM_99_A2_G05_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4976	GM_99_A2_G05_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4977	GM_99_A2_G08_MR	g4115365	BLASTX	117	1e-13	36	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
4978	GM_99_A2_G09_MR	g3426334	BLASTN	535	3e-17	61	Pisum sativum pectin methyltransferase (rcpme1) gene, complete cds
4979	GM_99_A2_G10_MR	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4980	GM_99_A2_G11_MR	g1084429	BLASTX	235	5e-19	53	pectin esterase - Petunia inflata
4981	GM_99_A2_H05_T7	g100484	BLASTX	260	1e-20	46	hypothetical protein - garden snapdragon
4982	GM_99_A2_H07_MR	g507910	BLASTN	575	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4983	GM_99_A2_H07_T7	g507910	BLASTN	559	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4984	GM_99_A2_H08_MR	g4063760	BLASTX	364	7e-41	78	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4985	GM_99_A2_H09_MR	g4063760	BLASTX	191	5e-14	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4986	GM_99_A2_H11_MR	g507910	BLASTN	492	1e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4987	GM_99_A2_H11_T7	g507910	BLASTN	604	1e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
4988	GM_99_A2_H12_T7	g3283026	BLASTX	158	1e-09	34	putative transposase [Arabidopsis thaliana]
4989	GM_99_B1_C03_MR	g3142328	BLASTN	710	4e-25	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence.
4990	GM_99_B1_C04_MR	g509768	BLASTN	410	1e-11	62	Glycine max seed-specific low molecular weight sulfur-rich protein.
4991	GM_99_B1_D08_MR	g507910	BLASTN	605	1e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4992	GM_99_B1_D12_T7	g1666236	BLASTX	207	8e-16	30	(U76261) unknown [Hordeum vulgare]
4993	GM_99_B1_E01_T7	g2673901	BLASTN	351	8e-09	66	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete cds.
4994	GM_99_B1_F02_MR	g3097320	BLASTN	390	1e-10	68	Glycine max gene for Bd 30K, complete cds
4995	GM_99_B1_E06_T7	g3097320	BLASTN	710	4e-25	75	Glycine max gene for Bd 30K, complete cds
4996	GM_99_B1_F01_T7	g3021511	BLASTN	354	4e-09	67	N.tabacum mRNA for NADP-dependent isocitrate dehydrogenase
4997	GM_99_B1_F03_MR	g1217967	BLASTX	230	2e-17	72	(X96431) high affinity sulphate transporter [Hordeum vulgare]
4998	GM_99_B1_F03_T7	g2995405	BLASTX	359	4e-31	52	(Y12432) polyprotein [Ananas comosus]
4999	GM_99_B1_G02_T7	g3047066	BLASTX	134	2e-12	48	(AF058825) contains similarity to retrovirus-related POL polyproteins [Arabidopsis thaliana]
5000	GM_99_B1_G06_T7	g282964	BLASTX	230	5e-18	81	transforming protein (myb) homolog (clone myb.Ph3) - garden petunia gi 20563 (Z13996) protein 1 [Petunia hybrida]
5001	GM_99_B1_G07_MR	g3319362	BLASTX	186	2e-12	41	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
5002	GM_99_B1_G07_T7	g99755	BLASTX	346	3e-30	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
5003	GM_99_B1_G08_T7	g2443320	BLASTX	179	1e-11	33	(D85597) polyprotein [Oryza australiensis]
5004	GM_99_B1_G10_MR	g4063760	BLASTX	268	4e-21	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5005	GM_99_B1_H01_MR	g3176777	BLASTN	485	6e-16	63	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 3' sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5006	GM_99_B1_H08_MR	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5007	GM_99_B2_A02_MR	g2829133	BLASTX	179	3e-19	75	(AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]
5008	GM_99_B2_A08_T7	g3250687	BLASTX	317	1e-27	39	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
5009	GM_99_B2_A12_T7	g4063760	BLASTX	427	2e-39	61	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
5010	GM_99_B2_B03_MR	g2264320	BLASTN	979	3e-37	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; MX110, complete sequence [Arabidopsis thaliana]
5011	GM_99_B2_B05_T7	g3777526	BLASTN	478	1e-14	67	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
5012	GM_99_B2_B07_MR	g507910	BLASTN	581	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5013	GM_99_B2_B07_T7	g507910	BLASTN	492	1e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5014	GM_99_B2_B08_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5015	GM_99_B2_B08_T7	g507910	BLASTN	552	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence
5016	GM_99_B2_B09_T7	g3377824	BLASTX	125	3e-11	32	(AF075598) contains similarity to reverse transcriptases [Arabidopsis thaliana]
5017	GM_99_B2_B11_T7	g905361	BLASTX	218	3e-16	30	(U22103) gag-protease polyprotein [Glycine max]
5018	GM_99_B2_C01_MR	g905361	BLASTX	432	1e-39	97	(U22103) gag-protease polyprotein [Glycine max]
5019	GM_99_B2_C02_MR	g3142328	BLASTN	1271	1e-50	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5020	GM_99_B2_C03_MR	g4063760	BLASTX	290	2e-52	56	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
5021	GM_99_B2_C04_T7	g100484	BLASTX	152	5e-09	60	hypothetical protein - garden snapdragon
5022	GM_99_B2_C05_T7	g3142328	BLASTN	718	2e-25	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5023	GM_99_B2_C06_MR	g3097320	BLASTN	479	1e-14	71	Glycine max gene for Bd 30K, complete cds
5024	GM_99_B2_C06_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5025	GM_99_B2_C08_MR	g4049647	BLASTN	420	6e-12	61	Melanoplus sanguinipes entomopoxvirus, complete genome
5026	GM_99_B2_C09_MR	g505129	BLASTN	347	1e-08	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5027	GM_99_B2_C11_MR	g1666236	BLASTX	260	1e-21	33	(U76261) unknown [Hordeum vulgare]
5028	GM_99_B2_C11_T7	g3097320	BLASTN	1037	6e-40	76	Glycine max gene for Bd 30K, complete cds
5029	GM_99_B2_C12_MR	g3193221	BLASTN	455	1e-13	76	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
5030	GM_99_B2_D01_T7	g3645899	BLASTX	319	1e-35	44	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5031	GM_99_B2_D02_T7	g4049647	BLASTN	387	2e-10	60	Melanoplus sanguinipes entomopoxvirus, complete genome
5032	GM_99_B2_D04_MR	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5033	GM_99_B2_D04_T7	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5034	GM_99_B2_D08_T7	g507910	BLASTN	598	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5035	GM_99_B2_D09_T7	g2586082	BLASTX	195	5e-32	55	(U72725) retrofit [Oryza longistaminata]
5036	GM_99_B2_D11_MR	g2708743	BLASTX	168	2e-10	33	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
5037	GM_99_B2_F01_MR	g3599418	BLASTN	568	1e-18	91	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5038	GM_99_B2_F02_MR	g3777527	BLASTX	163	9e-10	57	(AF053008) gag-pol polyprotein [Glycine max]
5039	GM_99_B2_F04_T7	g4063760	BLASTX	163	6e-10	32	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5040	GM_99_B2_E05_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5041	GM_99_B2_E05_T7	g507910	BLASTN	367	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5042	GM_99_B2_E06_MR	g2961349	BLASTX	414	1e-46	44	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
5043	GM_99_B2_E06_T7	g3688328	BLASTX	147	7e-13	45	(AJ228325) reverse transcriptase [Cinkgo biloba]
5044	GM_99_B2_F08_MR	g4160362	BLASTN	350	9e-09	64	Saccharomyces cerevisiae complete mitochondrial genome
5045	GM_99_B2_E08_T7	g4115365	BLASTX	159	1e-11	56	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
5046	GM_99_B2_E12_T7	g3097320	BLASTN	1002	2e-38	76	Glycine max gene for Bd 30K, complete cds
5047	GM_99_B2_F03_MR	g3142328	BLASTN	690	3e-24	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5048	GM_99_B2_F04_MR	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5049	GM_99_B2_F04_T7	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5050	GM_99_B2_F06_T7	g1769899	BLASTX	401	1e-36	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5051	GM_99_B2_F10_MR	g1769897	BLASTX	366	8e-33	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5052	GM_99_B2_G01_MR	g3599418	BLASTN	457	1e-13	91	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5053	GM_99_B2_G03_T7	g4063756	BLASTN	432	2e-12	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5054	GM_99_B2_G04_MR	g507910	BLASTN	625	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5055	GM_99_B2_G08_MR	g18559	BLASTN	1360	1e-54	76	G.max gene for catalase
5056	GM_99_B2_G09_MR	g2088653	BLASTX	219	8e-17	67	(AF002109) HsIpro-1 related protein isolog [Arabidopsis thaliana]
5057	GM_99_B2_G10_T7	g3777527	BLASTX	761	1e-73	94	(AF053008) gag-pol polyprotein [Glycine max]
5058	GM_99_B2_G11_MR	g18559	BLASTN	1213	5e-48	75	G.max gene for catalase
5059	GM_99_B2_G12_MR	g3435286	BLASTX	148	4e-18	93	(AF082597) cytosolic glyceraldehyde-3-phosphate dehydrogenase [Leavenworthia crassa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5060	GM_99_B2_H03_MR	g507910	BLASTN	358	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5061	GM_99_B2_H03_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5062	GM_99_B2_H04_T7	g905361	BLASTX	851	3e-84	96	(U22103) gag-protease polyprotein [Glycine max]
5063	GM_99_B2_H06_MR	g170029	BLASTN	540	2e-17	66	Glycine max cv. Dare nodulin 26 gene fragment.
5064	GM_99_B2_H06_T7	g905361	BLASTX	750	1e-73	86	(U22103) gag-protease polyprotein [Glycine max]
5065	GM_99_B2_H08_T7	g1769898	BLASTX	223	1e-37	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5066	GM_99_B2_H11_MR	g3913366	BLASTX	387	4e-34	47	POTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR >gi 1597723 (U67422) CRINKLY4 precursor [Zea mays]
5067	GM_99_B2_H12_MR	g3777527	BLASTX	944	3e-93	96	(AF053008) gag-pol polyprotein [Glycine max]
5068	GM_100_A1_A03_MR	g3142328	BLASTN	442	5e-13	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5069	GM_100_A1_A07_MR	g100484	BLASTX	212	2e-15	51	hypothetical protein - garden snapdragon
5070	GM_100_A1_B04_MR	g3294511	BLASTN	420	6e-12	64	Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
5071	GM_100_A1_C01_MR	g2316016	BLASTX	160	2e-09	42	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
5072	GM_100_A1_C03_MR	g507910	BLASTN	361	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5073	GM_100_A1_C05_MR	g507910	BLASTN	558	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5074	GM_100_A1_D09_T7	g18559	BLASTN	684	6e-24	75	G.max gene for catalase
5075	GM_100_A1_E03_MR	g2995405	BLASTX	153	2e-16	61	(Y12432) polyprotein [Ananas comosus]
5076	GM_100_A1_E04_MR	g2369714	BLASTX	376	6e-33	86	(Z97178) elongation factor 2 [Beta vulgaris]
5077	GM_100_A1_E05_T7	g22490	BLASTX	154	2e-10	58	(X01380) ORF1 [Zea mays]
5078	GM_100_A1_F09_MR	g507910	BLASTN	340	9e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5079	GM_100_A1_F12_MR	g2769655	BLASTN	364	2e-09	61	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
5080	GM_100_A1_G09_MR	g2909782	BLASTN	382	3e-10	70	Affinity Sodium-Glucose Cotransporter. Cont...
5081	GM_100_A1_H07_MR	g3047098	BLASTX	186	3e-25	86	Arabidopsis thaliana MgATP-energized glutathione S-conjugate pump (MRP2) gene, complete cds
5082	GM_100_A1_H09_MR	g3777527	BLASTX	466	4e-42	85	(AF058826) similar to eukaryotic protein kinase domains (Plam: pkinae.hmm. score: 171.43) [Arabidopsis thaliana]
5083	GM_100_A2_A03_T7	g3097320	BLASTN	824	3e-30	79	(AF053008) gag-pol polyprotein [Glycine max]
5084	GM_100_A2_A05_T7	g2995405	BLASTX	416	3e-37	54	Glycine max gene for Bd 30K, complete cds
5085	GM_100_A2_A07_MR	g2443320	BLASTX	404	1e-35	52	(Y12432) polyprotein [Ananas comosus] (D85597) polyprotein [Oryza australiensis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
5086	GM_100_A2_A07_T7	g3979928	BLASTN	369	1e-09	61	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
5087	GM_100_A2_A08_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5088	GM_100_A2_A08_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5089	GM_100_A2_A09_T7	g1142701	BLASTN	1090	6e-43	82	Glycine max satellite STR120-A.3.
5090	GM_100_A2_A10_T7	g507910	BLASTN	501	5e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
5091	GM_100_A2_A11_MR	g3985949	BLASTN	412	1e-11	69	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]
5092	GM_100_A2_A12_MR	g100484	BLASTX	409	9e-37	54	hypothetical protein - garden snapdragon
5093	GM_100_A2_B02_MR	g3176798	BLASTN	473	4e-15	65	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
5094	GM_100_A2_B03_T7	g3645899	BLASTX	294	6e-24	56	(U68408) 5' end not determined experimentally [Zea mays]
5095	GM_100_A2_B04_MR	g3645899	BLASTX	249	3e-19	45	(U68408) 5' end not determined experimentally [Zea mays]
5096	GM_100_A2_B08_MR	g3142330	BLASTX	623	4e-60	87	(U96295) envelope-like [Glycine max]
5097	GM_100_A2_C02_T7	g3645899	BLASTX	290	1e-23	49	(U68408) 5' end not determined experimentally [Zea mays]
5098	GM_100_A2_C03_MR	g1171046	BLASTX	176	8e-13	58	METALLOTHIONEIN-LIKE PROTEIN B gi 480753 pir S37240 metallothionein-like protein - white clover gi 403329 (Z26493)
5099	GM_100_A2_C05_MR	g3935150	BLASTX	255	2e-20	62	metallothionein-like protein [Trifolium repens]
5100	GM_100_A2_C06_T7	g1666236	BLASTX	190	7e-14	33	(AC005106) T25N20.14 [Arabidopsis thaliana]
5101	GM_100_A2_C07_T7	g1076634	BLASTX	292	5e-25	45	(U76261) unknown [Hordeum vulgare] protein-serine/threonine kinase NPK15 - common tobacco gi 505146 gnl PID d1007109 (D31737) protein-serine/threonine kinase [Nicotiana tabacum]
5102	GM_100_A2_C08_T7	g3386621	BLASTX	236	4e-19	75	(AC004665) unknown protein [Arabidopsis thaliana]
5103	GM_100_A2_C10_MR	g2864621	BLASTX	149	3e-18	54	hypothetical protein [Arabidopsis thaliana]
5104	GM_100_A2_C11_T7	g4115365	BLASTX	133	4e-10	36	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
5105	GM_100_A2_D04_T7	g3169170	BLASTX	465	2e-43	67	(AC004401) putative chloroplast envelope Ca2+-ATPase, 5' partial [Arabidopsis thaliana]
5106	GM_100_A2_D05_MR	g507910	BLASTN	675	7e-24	85	Glycine max BSR-101 satellite SB92 genomic sequence.
5107	GM_100_A2_D07_MR	g3650035	BLASTX	190	7e-13	47	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
5108	GM_100_A2_E01_MR	g99726	BLASTX	128	3e-17	53	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
5109	GM_100_A2_E05_MR	g1335861	BLASTN	359	3e-09	78	Glycine max clathrin heavy chain mRNA, complete cds
5110	GM_100_A2_E10_T7	g1666236	BLASTX	206	1e-15	32	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5111	GM_100_A2_F02_T7	g507910	BLASTN	412	5e-12	79	Glycine max BSR-101 satellite SB92 genomic sequence.
5112	GM_100_A2_F03_T7	g2129618	BLASTX	257	4e-20	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5113	GM_100_A2_F06_MR	g905361	BLASTX	252	7e-20	41	(U22103) gag-protease polyprotein [Glycine max]
5114	GM_100_A2_F07_T7	g100484	BLASTX	254	6e-20	60	hypothetical protein - garden snapdragon
5115	GM_100_A2_F12_T7	g905361	BLASTX	223	9e-17	43	(U22103) gag-protease polyprotein [Glycine max]
5116	GM_100_A2_G01_T7	g3695395	BLASTX	265	3e-21	62	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5117	GM_100_A2_G04_MR	g4038056	BLASTX	151	7e-09	42	(AC005897) putative transposon [Arabidopsis thaliana]
5118	GM_100_A2_G04_T7	g629693	BLASTX	128	2e-13	42	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
5119	GM_100_A2_G07_T7	g2842490	BLASTX	380	2e-34	55	(AL021749) heat-shock protein [Arabidopsis thaliana]
5120	GM_100_A2_G10_MR	g3142328	BLASTN	831	1e-30	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5121	GM_100_A2_H03_T7	g3449319	BLASTN	401	9e-13	62	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQP15, complete sequence [Arabidopsis thaliana]
5122	GM_100_A2_H05_MR	g3935148	BLASTX	188	1e-29	70	(AC005106) T25N20.12 [Arabidopsis thaliana]
5123	GM_100_A2_H05_T7	g3142328	BLASTN	841	4e-31	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5124	GM_100_A2_H11_T7	g4063760	BLASTX	197	1e-13	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5125	GM_100_A2_H12_MR	g2146731	BLASTX	197	4e-14	88	FK506-binding protein - Arabidopsis thaliana gi 1354207 (U49453) rofl [Arabidopsis thaliana]
5126	GM_100_B1_A02_T7	g3426334	BLASTN	383	3e-10	61	Pisum sativum pectin methylesterase (repme1) gene, complete cds
5127	GM_100_B1_A03_MR	g2407790	BLASTX	154	3e-09	79	(AF019910) grr1 [Glycine max]
5128	GM_100_B1_A04_MR	g905361	BLASTX	432	1e-39	97	(U22103) gag-protease polyprotein [Glycine max]
5129	GM_100_B1_A05_T7	g1277164	BLASTX	213	1e-16	93	(U51853) cysteine proteinase inhibitor [Glycine max]
5130	GM_100_B1_A06_MR	g3142328	BLASTN	722	5e-52	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5131	GM_100_B1_A07_MR	g100484	BLASTX	365	6e-32	51	hypothetical protein - garden snapdragon
5132	GM_100_B1_A12_MR	g1666236	BLASTX	192	4e-14	30	(U76261) unknown [Hordeum vulgare]
5133	GM_100_B1_B01_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5134	GM_100_B1_B03_MR	g2522227	BLASTX	192	2e-14	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5135	GM_100_B1_B04_MR	g507910	BLASTN	382	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5136	GM_100_B1_B04_T7	g4063760	BLASTX	238	6e-18	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
5137	GM_100_B1_B06_T7	g1769897	BLASTX	311	2e-26	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5138	GM_100_B1_C01_T7	g1769899	BLASTX	361	2e-32	70	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5139	GM_100_B1_C05_MR	g507910	BLASTN	386	8e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5140	GM_100_B1_C07_MR	g3645899	BLASTX	242	1e-20	46	(U68408) 5' end not determined experimentally [Zea mays]
5141	GM_100_B1_D01_MR	g507910	BLASTN	604	1e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5142	GM_100_B1_D03_MR	g2129709	BLASTX	156	4e-09	34	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
5143	GM_100_B1_D04_T7	g4140712	BLASTX	194	1e-14	45	(AF110183) putative integrase [Oryza sativa]
5144	GM_100_B1_D05_MR	g507910	BLASTN	549	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
5145	GM_100_B1_D05_T7	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
5146	GM_100_B1_D08_MR	g3021285	BLASTX	137	5e-16	63	(AL022347) hypothetical protein [Arabidopsis thaliana] gi 3451058 gnl PID e1316745 (AL031326) hypothetical protein [Arabidopsis thaliana]
5147	GM_100_B1_D09_MR	g3171159	BLASTN	518	2e-16	65	Homo sapiens chromosome 21q22.3 PAC 211.13, complete sequence [Homo sapiens]
5148	GM_100_B1_D09_T7	g1769898	BLASTX	100	2e-11	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5149	GM_100_B1_E03_T7	g2842490	BLASTX	387	4e-35	56	(AL021749) heat-shock protein [Arabidopsis thaliana]
5150	GM_100_B1_E04_T7	g3142328	BLASTN	622	4e-21	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5151	GM_100_B1_E06_MR	g3426334	BLASTN	358	3e-09	66	Pisum sativum pectin methylesterase (rcpml) gene, complete cds
5152	GM_100_B1_E06_T7	g2522230	BLASTX	206	6e-16	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5153	GM_100_B1_E08_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5154	GM_100_B1_E08_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5155	GM_100_B1_F03_T7	g2443320	BLASTX	372	4e-32	52	(D85597) polypeptide [Oryza australiensis]
5156	GM_100_B1_F04_T7	g3426334	BLASTN	469	3e-14	62	Pisum sativum pectin methylesterase (rcpml) gene, complete cds
5157	GM_100_B1_F06_MR	g130582	BLASTX	231	4e-17	49	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
5158	GM_100_B1_F07_MR	g3777527	BLASTX	690	6e-66	95	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
5159	GM_100_B1_F11_MR	g1769897	BLASTX	203	4e-18	43	(AF053008) gag-pol polypeptide [Glycine max]
5160	GM_100_B1_F12_T7	g18559	BLASTN	793	6e-29	74	(Y08010) lectin receptor kinase [Arabidopsis thaliana] G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5161	GM_100_B1_G01_T7	g2564750	BLASTN	428	3e-12	64	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
5162	GM_100_B1_G02_MR	g1091678	BLASTX	274	5e-22	43	activator-like transposable element [Pennisetum glaucum]
5163	GM_100_B1_G03_MR	g13581	BLASTN	350	1e-09	60	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
5164	GM_100_B1_G04_MR	g4063760	BLASTX	551	2e-51	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5165	GM_100_B1_G04_T7	g507910	BLASTN	564	7e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5166	GM_100_B1_G05_T7	g3080401	BLASTX	351	3e-31	71	(AL022603) putative protein [Arabidopsis thaliana]
5167	GM_100_B1_G06_MR	g3860246	BLASTX	195	1e-14	36	(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]
5168	GM_100_B1_G06_T7	g3777526	BLASTN	1531	3e-62	89	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
5169	GM_100_B1_G08_T7	g2896804	BLASTN	394	9e-11	64	Human Chromosome 16 BAC clone CTT987SK-A-598D4, complete sequence [Homo sapiens]
5170	GM_100_B1_G11_MR	g3777527	BLASTX	269	5e-21	44	(AF053008) gag-pol polyprotein [Glycine max]
5171	GM_100_B1_G12_MR	g1142699	BLASTN	1450	3e-59	88	Glycine max satellite STR120-A.1.
5172	GM_100_B1_H04_MR	g2245104	BLASTX	185	3e-12	40	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
5173	GM_100_B1_H06_MR	g2443320	BLASTX	203	4e-14	41	(D85597) polyprotein [Oryza australiensis]
5174	GM_100_B1_H08_MR	g2462134	BLASTX	181	2e-12	31	(Y13368) reverse transcriptase [Beta vulgaris]
5175	GM_100_B1_H08_T7	g3328126	BLASTX	222	1e-17	67	(AF072691) putative basic helix-loop-helix DNA binding protein TCP2 [Arabidopsis thaliana]
5176	GM_100_B1_H12_T7	g3687234	BLASTX	201	5e-14	30	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
5177	GM_100_B2_A01_MR	g3142328	BLASTN	1414	3e-57	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5178	GM_100_B2_A03_MR	g505129	BLASTN	324	7e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5179	GM_100_B2_A08_MR	g2924781	BLASTX	283	8e-23	60	(AC002334) putative cellulose synthase [Arabidopsis thaliana]
5180	GM_100_B2_A10_T7	g2245104	BLASTX	168	1e-11	35	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
5181	GM_100_B2_A11_T7	g3695387	BLASTX	249	4e-19	63	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
5182	GM_100_B2_B02_MR	g3097320	BLASTN	658	9e-23	66	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5183	GM_100_B2_B05_T7	g3695303	BLASTX	233	2e-17	31	(AF096371) contains similarity to retroviral aspartyl proteases (Pfam: rvp.hmm, score: 11.80) [Arabidopsis thaliana]
5184	GM_100_B2_B06_MR	g3777527	BLASTX	117	8e-10	58	(AF053008) gag-pol polyprotein [Glycine max]
5185	GM_100_B2_B07_MR	g3097320	BLASTN	1271	2e-50	75	Glycine max gene for Bd 30K, complete cds
5186	GM_100_B2_B11_T7	g1170619	BLASTX	144	1e-13	62	KINESIN-LIKE PROTEIN A gi 479594 pir S34830 kinesin-related protein katA - Arabidopsis thaliana gi 303502 gnl PID d1002453 (D11371) kinesin-like motor protein heavy chain [Arabidopsis thaliana] gi 2911084 gnl PID e1253323 (AL021960) kinesin-related protein katA [Arabidopsis thaliana]
5187	GM_100_B2_B12_MR	g3142328	BLASTN	1379	1e-55	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF053008) gag-pol polyprotein [Glycine max]
5188	GM_100_B2_C01_MR	g3777527	BLASTX	381	5e-33	94	Glycine max BSR-101 satellite SB92 genomic sequence.
5189	GM_100_B2_C01_T7	g507910	BLASTN	380	1e-10	70	Speyeria mormonia large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
5190	GM_100_B2_C02_MR	g2895632	BLASTN	388	7e-11	58	Glycine max gene for Bd 30K, complete cds
5191	GM_100_B2_C06_MR	g3097320	BLASTN	432	2e-12	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5192	GM_100_B2_C06_T7	g3142379	BLASTX	337	7e-30	66	(AF053008) envelope-like [Glycine max]
5193	GM_100_B2_C07_MR	g3097320	BLASTN	469	3e-14	69	Glycine max gene for Bd 30K, complete cds
5194	GM_100_B2_C09_T7	g18634	BLASTN	349	8e-09	74	Soybean Gyl gene for glycinin subunit G1
5195	GM_100_B2_C10_MR	g3097320	BLASTN	449	3e-13	71	Glycine max gene for Bd 30K, complete cds
5196	GM_100_B2_C10_T7	g3142328	BLASTN	615	7e-21	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5197	GM_100_B2_C11_T7	g421955	BLASTX	152	1e-27	58	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
5198	GM_100_B2_D01_MR	g2735017	BLASTX	241	4e-22	66	(U82481) KI domain interacting kinase 1 [Zea mays]
5199	GM_100_B2_D02_T7	g3335226	BLASTX	175	9e-13	39	(AF077374) small proline-rich protein [Homo sapiens]
5200	GM_100_B2_D03_T7	g4063760	BLASTX	667	8e-64	69	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
5201	GM_100_B2_D05_MR	g3800955	BLASTN	394	9e-11	62	Caenorhabditis elegans cosmid F58E2
5202	GM_100_B2_D08_T7	g160298	BLASTN	483	6e-15	60	P.falciparum glutamic acid-rich protein gnen, complete cds.
5203	GM_100_B2_D09_MR	g3777527	BLASTX	790	1e-76	98	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
5204	GM_100_B2_D10_T7	g3059060	BLASTN	467	5e-14	60	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
5205	GM_100_B2_D12_MR	g507910	BLASTN	413	5e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5206	GM_100_B2_D12_T7	g2995405	BLASTX	312	4e-26	51	(Y12432) polyprotein [Ananas comosus]
5207	GM_100_B2_E03_MR	g4140712	BLASTX	597	2e-57	53	(AF110183) putative integrase [Oryza sativa]
5208	GM_100_B2_E05_T7	g2781364	BLASTX	149	2e-09	26	(AC003113) F24O1.20 [Arabidopsis thaliana]
5209	GM_100_B2_E06_T7	g3097320	BLASTN	920	1e-34	78	Glycine max gene for Bd 30K, complete cds
5210	GM_100_B2_E08_MR	g507910	BLASTN	352	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5211	GM_100_B2_E08_T7	g4063756	BLASTN	508	7e-16	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5212	GM_100_B2_E09_T7	g3378224	BLASTX	176	9e-13	73	(AJ001213) reverse transcriptase [Lycopersicon chilense]
5213	GM_100_B2_E11_T7	g3142328	BLASTN	2496	2e-107	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5214	GM_100_B2_E12_T7	g3142328	BLASTN	1186	8e-47	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5215	GM_100_B2_F02_MR	g3869063	BLASTN	367	1e-09	63	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17O22, complete sequence [Arabidopsis thaliana]
5216	GM_100_B2_F02_T7	g4038056	BLASTX	343	2e-29	38	(AC005897) putative transposon [Arabidopsis thaliana]
5217	GM_100_B2_F03_T7	g2688264	BLASTN	360	3e-09	60	Borrelia burgdorferi (section 28 of 70) of the complete genome
5218	GM_100_B2_F05_MR	g3845197	BLASTN	345	2e-10	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
5219	GM_100_B2_F06_MR	g1666236	BLASTX	298	1e-25	34	(U76261) unknown [Hordeum vulgare]
5220	GM_100_B2_F09_T7	g4063760	BLASTX	509	5e-48	56	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
5221	GM_100_B2_F11_T7	g2995405	BLASTX	295	9e-50	61	(Y12432) polyprotein [Ananas comosus]
5222	GM_100_B2_F12_MR	g3142328	BLASTN	1514	9e-62	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5223	GM_100_B2_G02_MR	g1666236	BLASTX	298	1e-25	34	(U76261) unknown [Hordeum vulgare]
5224	GM_100_B2_G03_T7	g99922	BLASTX	422	4e-60	82	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA), pid:e150225 [Glycine max]
5225	GM_100_B2_G05_T7	g3142328	BLASTN	1164	8e-46	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5226	GM_100_B2_G09_MR	g3738114	BLASTN	577	5e-19	66	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5227	GM_100_B2_G09_T7	g3941472	BLASTX	116	3e-13	47	(AF062890) putative transcription factor [Arabidopsis thaliana]
5228	GM_100_B2_G10_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5229	GM_100_B2_G12_MR	g2522228	BLASTX	459	1e-42	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
5230	GM_100_B2_H02_MR	g2245015	BLASTX	439	1e-40	56	(Z97341) unnamed protein product [Arabidopsis thaliana]
5231	GM_100_B2_H07_T7	g2995405	BLASTX	458	9e-42	72	(Y12432) polyprotein [Ananas comosus]
5232	GM_101_A1_B03_T7	g905361	BLASTX	168	8e-11	31	(U22103) gag-protease polyprotein [Glycine max]
5233	GM_101_A1_C04_T7	g226407	BLASTX	175	3e-24	46	retrotransposon del-46 [Lilium henryi]
5234	GM_101_A1_F02_T7	g3142328	BLASTN	464	5e-14	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5235	GM_101_A1_F03_T7	g3142328	BLASTN	878	8e-33	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5236	GM_101_A1_E12_T7	g507910	BLASTN	578	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
5237	GM_101_A1_F03_T7	g507910	BLASTN	610	6e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5238	GM_101_A1_F05_T7	g4063760	BLASTX	174	4e-11	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5239	GM_101_A1_F06_T7	g2462936	BLASTX	170	2e-23	48	(Y12321) open reading frame 2 [Brassica oleracea]
5240	GM_101_A1_F07_T7	g507910	BLASTN	358	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5241	GM_101_A1_F11_T7	g507910	BLASTN	352	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5242	GM_101_A1_G03_T7	g3548806	BLASTX	171	5e-11	42	(AC005313) unknown protein [Arabidopsis thaliana]
5243	GM_101_A1_G06_T7	g3142328	BLASTN	1441	2e-58	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5244	GM_101_B1_A01_T7	g2264320	BLASTN	546	1e-17	62	Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone: MX110, complete sequence [Arabidopsis thaliana]
5245	GM_101_B1_A06_MR	g3777527	BLASTX	619	3e-67	93	(AF053008) gag-pol polyprotein [Glycine max]
5246	GM_101_B1_A09_MR	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5247	GM_101_B1_A09_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5248	GM_101_B1_A12_MR	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5249	GM_101_B1_B03_MR	g505129	BLASTN	395	7e-11	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5250	GM_101_B1_B07_T7	g18559	BLASTN	1046	2e-40	75	G.max gene for catalase
5251	GM_101_B1_B08_MR	g2462134	BLASTX	246	1e-29	49	(Y13368) reverse transcriptase [Beta vulgaris]
5252	GM_101_B1_B08_T7	g629693	BLASTX	195	2e-18	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
5253	GM_101_B1_B09_MR	g3979928	BLASTN	373	8e-10	59	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
5254	GM_101_B1_B09_T7	g3513747	BLASTX	188	2e-12	46	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
5255	GM_101_B1_C02_MR	g2462134	BLASTX	343	2e-30	52	(Y13368) reverse transcriptase [Beta vulgaris]
5256	GM_101_B1_C02_T7	g2315153	BLASTX	264	2e-30	82	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
5257	GM_101_B1_C03_T7	g3193306	BLASTX	229	9e-19	31	(AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana]
5258	GM_101_B1_C10_MR	g2351073	BLASTN	461	9e-14	67	Arabidopsis thaliana genomic DNA: chromosome 5, P1 clone: MYJ24
5259	GM_101_B1_C12_MR	g3687828	BLASTN	380	4e-10	66	Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence [Homo sapiens]
5260	GM_101_B1_C12_T7	g1170878	BLASTX	176	7e-24	88	MALATE SYNTHASE, GLYOXYSOMAL (MS) gi 170026
5261	GM_101_B1_D01_MR	g3142328	BLASTN	493	2e-15	92	(L01629) malate synthase [Glycine max]
5262	GM_101_B1_D03_T7	g507910	BLASTN	600	2e-20	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5263	GM_101_B1_D04_T7	g4039114	BLASTN	625	2e-21	70	Glycine max BSR-101 satellite SB92 genomic sequence
5264	GM_101_B1_D06_T7	g3643603	BLASTX	413	9e-37	63	Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds
5265	GM_101_B1_D07_MR	g1666236	BLASTX	256	3e-21	34	Glycine max unknown protein [Arabidopsis thaliana]
5266	GM_101_B1_D09_T7	g3097320	BLASTN	924	8e-35	78	(U76261) unknown [Hordeum vulgare]
5267	GM_101_B1_D10_T7	g18559	BLASTN	918	8e-55	90	Glycine max gene for Bd 30K, complete cds
5268	GM_101_B1_D11_MR	g3142379	BLASTX	236	1e-18	55	G.max gene for catalase
5269	GM_101_B1_D11_T7	g421955	BLASTX	145	4e-18	52	(AF053008) envelope-like [Glycine max]
5270	GM_101_B1_E01_T7	g507910	BLASTN	557	1e-18	80	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387)
5271	GM_101_B1_E02_T7	g1488267	BLASTX	149	4e-09	75	ORF4 [Solanum tuberosum]
5272	GM_101_B1_E03_MR	g3319362	BLASTX	228	5e-23	55	Glycine max BSR-101 satellite SB92 genomic sequence
5273	GM_101_B1_E04_MR	g3777527	BLASTX	725	1e-69	91	(U57412) low affinity calcium antiporter CAX2 [Arabidopsis thaliana]
5274	GM_101_B1_E07_MR	g4150930	BLASTN	329	1e-08	61	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
							(AF053008) gag-pol polyprotein [Glycine max]
							Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5275	GM_101_B1_E08_MR	g1755156	BLASTX	473	3e-44	69	(U75189) germin-like protein [Arabidopsis thaliana] gi 1755158 (U75190) germin-like protein [Arabidopsis thaliana] gi 1755170 (U75196) germin-like protein [Arabidopsis thaliana] gi 1755172 (U75197) germin-like protein [Arabidopsis thaliana] gi 1755180 (U75201) germin-like protein [Arabidopsis thaliana] gi 1755190 (U75206) germin-like protein [Arabidopsis thaliana] gi 1934728 (U95035) germin-like protein [Arabidopsis thaliana] Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12 (U22103) gag-protease polypeptide [Glycine max] (AC005957) reverse transcriptase-like protein [Arabidopsis thaliana] RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum] Glycine max BSR-101 satellite SB92 genomic sequence. Tobacco chloroplast genome DNA S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2 Homo sapiens genomic DNA, 21q region, clone: S39BG29 (AC005897) putative transposon [Arabidopsis thaliana] Glycine max gene for Bd 30K, complete cds Glycine max BSR-101 satellite SB92 genomic sequence. Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13 (Y12432) polyprotein [Ananas comosus] (AC005561) putative POL3 protein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (U68408) 5' end not determined experimentally [Zea mays] Pisum sativum pectin methylesterase (rcpme1) gene, complete cds (AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana] (U76261) unknown [Hordeum vulgare] (AC002510) unknown protein [Arabidopsis thaliana]
5276	GM_101_B1_F08_T7	g2351069	BLASTN	577	5e-19	62	
5277	GM_101_B1_E09_MR	g905361	BLASTX	129	7e-14	41	
5278	GM_101_B1_E11_MR	g4115365	BLASTX	179	6e-15	47	
5279	GM_101_B1_E11_T7	g130582	BLASTX	283	1e-22	33	
5280	GM_101_B1_F01_T7	g507910	BLASTN	385	9e-11	73	
5281	GM_101_B1_F04_MR	g2924257	BLASTN	372	3e-18	70	
5282	GM_101_B1_F04_T7	g12212	BLASTN	1241	4e-67	89	
5283	GM_101_B1_F05_MR	g2579859	BLASTN	334	9e-09	63	
5284	GM_101_B1_F07_T7	g4038056	BLASTX	269	2e-21	50	
5285	GM_101_B1_F08_MR	g3097320	BLASTN	1343	8e-54	81	
5286	GM_101_B1_F09_MR	g507910	BLASTN	370	4e-10	71	
5287	GM_101_B1_F10_T7	g2656028	BLASTN	432	2e-12	61	
5288	GM_101_B1_F12_MR	g2995405	BLASTX	533	6e-50	60	
5289	GM_101_B1_G01_T7	g4063760	BLASTX	569	3e-53	59	
5290	GM_101_B1_G03_MR	g507910	BLASTN	409	7e-12	73	
5291	GM_101_B1_G04_MR	g3645899	BLASTX	187	2e-12	60	
5292	GM_101_B1_G05_MR	g3426334	BLASTN	372	8e-10	66	
5293	GM_101_B1_G07_T7	g3650039	BLASTX	105	4e-10	46	
5294	GM_101_B1_G09_MR	g1666236	BLASTX	107	7e-10	35	
5295	GM_101_B1_G10_MR	g2618689	BLASTX	149	6e-11	73	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
5296	GM_101_B1_G11_T7	g3142379	BLASTX	310	6e-27	67	(AF053008) envelope-like [Glycine max] (AC003671) Similar to ubiquitin ligase gb D63905 from <i>S. cerevisiae</i> . EST gb R65295 comes from this gene. [Arabidopsis thaliana]
5297	GM_101_B1_G12_T7	g3176690	BLASTX	157	9e-18	76	(Y13368) reverse transcriptase [Beta vulgaris] (X98929) SBT1 [Lycopersicon esculentum] gi 3687305 gnl PID e1299610 (AJ006378) subtilisin-like protease [Lycopersicon esculentum]
5298	GM_102_A1_A05_T7	g2462134	BLASTX	179	3e-12	35	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB007466) reverse transcriptase-like protein [Vicia faba]
5299	GM_102_A1_A12_T7	g1771160	BLASTX	222	7e-22	55	Medicago sativa aspartate aminotransferase (AAT1) gene, complete cds
5300	GM_102_A1_B07_MR	g3142328	BLASTN	798	4e-29	80	(Z97343) LTR retrotransposon [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence.
5301	GM_102_A1_B11_MR	g2522228	BLASTX	204	4e-15	78	retrotransposon del1-46 [Lilium henryi]
5302	GM_102_A1_C05_MR	g413725	BLASTN	410	1e-11	67	Glycine max BSR-101 satellite SB92 genomic sequence.
5303	GM_102_A1_C06_MR	g2245104	BLASTX	335	3e-29	58	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
5304	GM_102_A1_E03_T7	g507910	BLASTN	367	6e-10	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence.
5305	GM_102_A1_E04_T7	g226407	BLASTX	342	6e-29	54	Glycine max BSR-101 satellite SB92 genomic sequence.
5306	GM_102_A1_E10_MR	g507910	BLASTN	521	6e-17	77	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
5307	GM_102_A1_F03_T7	g2245104	BLASTX	164	6e-10	33	Glycine max BSR-101 satellite SB92 genomic sequence.
5308	GM_102_A1_F11_T7	g3142328	BLASTN	1085	3e-42	78	Glycine max BSR-101 satellite SB92 genomic sequence.
5309	GM_102_A1_G02_T7	g507910	BLASTN	353	2e-09	70	Arabidopsis thaliana mRNA for putative villin.
5310	GM_102_A1_G12_T7	g3093293	BLASTN	350	7e-09	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
5311	GM_102_A1_H02_MR	g2522228	BLASTX	153	1e-09	42	(U68408) 5' end not determined experimentally [Zea mays]
5312	GM_102_A1_H10_MR	g3645899	BLASTX	156	3e-09	43	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3
5313	GM_102_A1_H12_T7	g3171875	BLASTN	454	2e-13	64	(Dimethylamine Monooxygenase (N-Oxide 3, EC 1.14.1... (AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
5314	GM_102_A2_A03_T7	g3319345	BLASTX	169	1e-10	33	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5315	GM_102_A2_A04_T7	g4063760	BLASTX	491	6e-45	59	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
5316	GM_102_A2_A06_T7	g3337395	BLASTN	356	5e-09	60	Glycine max BSR-101 satellite SB92 genomic sequence.
5317	GM_102_A2_A12_MR	g507910	BLASTN	619	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5318	GM_102_A2_B04_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5319	GM_102_A2_B10_MR	g2522227	BLASTX	189	9e-17	34	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5320	GM_102_A2_C01_MR	g2462058	BLASTX	196	1e-18	56	(Y13389) reverse transcriptase [Antirrhinum majus]
5321	GM_102_A2_C02_T7	g507910	BLASTN	409	7e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5322	GM_102_A2_C05_MR	g3142328	BLASTN	756	3e-27	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5323	GM_102_A2_C05_T7	g3599418	BLASTN	381	3e-10	87	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5324	GM_102_A2_C07_MR	g507910	BLASTN	367	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5325	GM_102_A2_C07_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5326	GM_102_A2_C10_MR	g1419118	BLASTX	68	6e-11	81	(Z75512) reverse transcriptase [Oryza sativa]
5327	GM_102_A2_D04_MR	g18768	BLASTN	493	6e-16	74	Soybean Tgm6 transposable element 3' end
5328	GM_102_A2_D06_MR	g2443320	BLASTX	252	4e-20	39	(D85597) polypeptide [Oryza australiensis]
5329	GM_102_A2_D08_MR	g2522228	BLASTX	186	4e-13	51	(AB007466) reverse transcriptase-like protein [Vicia faba]
5330	GM_102_A2_D11_T7	g1666236	BLASTX	148	3e-09	26	(U76261) unknown [Hordeum vulgare]
5331	GM_102_A2_E01_MR	g99729	BLASTX	256	3e-21	45	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
5332	GM_102_A2_E01_T7	g3777527	BLASTX	107	8e-10	38	(AF053008) gag-pol polypeptide [Glycine max]
5333	GM_102_A2_E06_MR	g905361	BLASTX	390	6e-35	90	(U22103) gag-protease polypeptide [Glycine max]
5334	GM_102_A2_E08_MR	g408793	BLASTN	423	3e-12	72	Glycine soja chloroplast 3-omega fatty acid desaturase (Fad3) mRNA, complete cds.
5335	GM_102_A2_E10_MR	g3522939	BLASTX	185	9e-14	62	(AC004411) putative squamosa-promoter binding protein
5336	GM_102_A2_F01_T7	g99730	BLASTX	362	2e-32	50	[Arabidopsis thaliana] hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
5337	GM_102_A2_F05_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5338	GM_102_A2_F06_MR	g3142328	BLASTN	833	9e-31	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5339	GM_102_A2_F10_T7	g507910	BLASTN	583	1e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5340	GM_102_A2_F11_MR	g1142699	BLASTN	734	7e-27	83	Glycine max satellite STR120-A.1.
5341	GM_102_A2_F12_T7	g1490417	BLASTX	197	1e-13	49	(U45025) 89B helicase [Drosophila melanogaster]
5342	GM_102_A2_G07_T7	g2443320	BLASTX	354	3e-30	51	(D85597) polypeptide [Oryza australiensis]
5343	GM_102_A2_G11_T7	g3097320	BLASTN	467	4e-14	71	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5344	GM_102_A2_H02_T7	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5345	GM_102_A2_H05_MR	g507910	BLASTN	367	6e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5346	GM_102_A2_H06_T7	g3645899	BLASTX	273	9e-22	37	(U68408) 5' end not determined experimentally [Zea mays]
5347	GM_102_A2_H07_MR	g1167523	BLASTX	261	2e-20	53	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
5348	GM_102_A2_H08_T7	g3548808	BLASTX	457	1e-42	58	(AC005313) unknown protein [Arabidopsis thaliana]
5349	GM_102_A2_H10_T7	g4050011	BLASTN	561	2e-18	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
5350	GM_102_B1_A01_MR	g3097320	BLASTN	473	2e-14	71	Glycine max gene for Bd 30K, complete cds
5351	GM_102_B1_A02_MR	g905361	BLASTX	241	1e-18	34	(U22103) gag-protease polyprotein [Glycine max]
5352	GM_102_B1_A04_T7	g2194136	BLASTX	482	7e-44	55	(AC002062) Strong similarity to Zea mays retrotransposon Hopscoth polyprotein (gb U12626). [Arabidopsis thaliana]
5353	GM_102_B1_A06_MR	g1946355	BLASTX	138	1e-09	32	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
5354	GM_102_B1_A06_T7	g3426334	BLASTN	404	3e-11	59	Pisum sativum pectin methylesterase (rpme1) gene, complete cds
5355	GM_102_B1_A07_MR	g4160362	BLASTN	411	2e-11	60	Saccharomyces cerevisiae complete mitochondrial genome TY3-2 orfB
5356	GM_102_B1_A08_T7	g1326016	BLASTX	309	3e-28	38	(AC005897) putative transposon [Arabidopsis thaliana]
5357	GM_102_B1_A11_T7	g4038056	BLASTX	373	1e-32	49	Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence
5358	GM_102_B1_A12_MR	g3845100	BLASTN	278	1e-09	66	Glycine max BSR-101 satellite SB92 genomic sequence.
5359	GM_102_B1_B02_MR	g507910	BLASTN	701	5e-25	87	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5360	GM_102_B1_B03_MR	g1769898	BLASTX	160	2e-11	52	(Y12432) polyprotein [Ananas comosus]
5361	GM_102_B1_B10_T7	g2995405	BLASTX	166	2e-10	36	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5362	GM_102_B1_B11_T7	g505129	BLASTN	472	2e-14	63	receptor-like protein kinase precursor - Arabidopsis thaliana gi 166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
5363	GM_102_B1_B12_T7	g282881	BLASTX	398	2e-35	45	Drosophila melanogaster Oregon-R mitochondrial A+T region. Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5364	GM_102_B1_C01_T7	g508826	BLASTN	310	1e-15	62	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5365	GM_102_B1_C11_MR	g505129	BLASTN	287	2e-10	68	Glycine max gene for Bd 30K, complete cds
5366	GM_102_B1_C12_T7	g3142328	BLASTN	1786	3e-74	95	(AC005312) putative NAM (no apical meristem) protein [Arabidopsis thaliana]
5367	GM_102_B1_D02_MR	g3097320	BLASTN	1066	3e-41	79	
5368	GM_102_B1_D09_MR	g3894176	BLASTX	368	4e-33	85	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5369	GM_102_B1_D09_T7	g3377517	BLASTX	287	1e-28	50	(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
5370	GM_102_B1_D10_MR	g2129618	BLASTX	234	1e-17	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5371	GM_102_B1_E02_T7	g99729	BLASTX	178	1e-21	40	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Tal-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
5372	GM_102_B1_E04_MR	g130398	BLASTX	155	4e-09	53	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPONSON 297) gi 85089 pir B24872 retrovirus-related polypeptide homolog - fruit fly (Drosophila melanogaster) transposon 297 (AC005561) putative POL3 protein [Arabidopsis thaliana]
5373	GM_102_B1_E05_T7	g4063760	BLASTX	377	7e-35	54	Glycine max gene for Bd 30K, complete cds
5374	GM_102_B1_F11_MR	g3097320	BLASTN	881	7e-33	72	transposon copia - Arabidopsis thaliana (fragment)
5375	GM_102_B1_E12_MR	g320564	BLASTX	99	9e-09	48	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5376	GM_102_B1_F01_MR	g2129618	BLASTX	210	4e-15	33	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds (D85597) polyprotein [Oryza australiensis]
5377	GM_102_B1_F01_T7	g3599418	BLASTN	622	4e-21	82	(U66345) calreticulin [Arabidopsis thaliana]
5378	GM_102_B1_F03_T7	g2443320	BLASTX	239	5e-18	40	(AF058914) similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]
5379	GM_102_B1_F04_MR	g2052383	BLASTX	252	2e-20	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5380	GM_102_B1_F04_T7	g3047086	BLASTX	412	9e-37	45	Glycine max BSR-101 satellite SB92 genomic sequence
5381	GM_102_B1_F07_T7	g3142328	BLASTN	1455	4e-59	78	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
5382	GM_102_B1_F12_MR	g507910	BLASTN	371	4e-10	76	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS
5383	GM_102_B1_G01_MR	g2970554	BLASTN	378	5e-10	64	*** from contig 4-54, complete sequence [Plasmodium falciparum]
5384	GM_102_B1_G01_T7	g3273127	BLASTN	360	3e-09	61	Glycine max BSR-101 satellite SB92 genomic sequence
5385	GM_102_B1_G02_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence
5386	GM_102_B1_G02_T7	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence
5387	GM_102_B1_G04_T7	g3273123	BLASTN	370	1e-09	59	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS
5388	GM_102_B1_G05_T7	g559268	BLASTN	337	9e-09	64	*** from contig 4-58, complete sequence [Plasmodium falciparum]
5389	GM_102_B1_G12_T7	g1091678	BLASTX	174	2e-23	47	Saccharomyces cerevisiae mitochondrion DNA segment activator-like transposable element [Pennisetum glaucum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
5390	GM_102_B1_H07_MR	g33808101	BLASTX	241	9e-24	84	(AJ012165) chloroplast protease [Capsicum annuum]
5391	GM_102_B1_H09_MR	g4063760	BLASTX	157	2e-09	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5392	GM_102_B1_H09_T7	g507910	BLASTN	574	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5393	GM_102_B2_A01_T7	g2505865	BLASTX	301	3e-25	44	(Y12227) putative topoisomerase [Arabidopsis thaliana]
5394	GM_102_B2_A04_T7	g2764526	BLASTN	489	4e-15	61	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
5395	GM_102_B2_A07_MR	g3128138	BLASTN	681	1e-23	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFO20, complete sequence [Arabidopsis thaliana]
5396	GM_102_B2_A12_MR	g18559	BLASTN	1404	1e-56	81	G.max gene for catalase
5397	GM_102_B2_B02_MR	g3461840	BLASTX	154	7e-09	34	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
5398	GM_102_B2_B03_MR	g3319362	BLASTX	159	1e-09	36	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
5399	GM_102_B2_B04_T7	g2522228	BLASTX	619	5e-62	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
5400	GM_102_B2_B08_T7	g3845108	BLASTN	398	6e-11	63	Plasmodium falciparum chromosome 2, section 13 of 73 of the complete sequence
5401	GM_102_B2_B11_MR	g3142328	BLASTN	512	3e-16	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5402	GM_102_B2_B11_T7	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5403	GM_102_B2_C01_MR	g3142328	BLASTN	2385	2e-102	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5404	GM_102_B2_C01_T7	g505129	BLASTN	324	2e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5405	GM_102_B2_C02_MR	g18559	BLASTN	397	6e-11	66	G.max gene for catalase
5406	GM_102_B2_C04_MR	g18559	BLASTN	1105	4e-43	74	G.max gene for catalase
5407	GM_102_B2_C05_T7	g4063760	BLASTX	262	2e-20	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5408	GM_102_B2_C08_T7	g3097320	BLASTN	464	6e-14	70	Glycine max gene for Bd 30K, complete cds
5409	GM_102_B2_C09_T7	g3201541	BLASTX	152	2e-24	74	(AJ005077) TCSTR2 protein [Lycopersicon esculentum]
5410	GM_102_B2_C10_MR	g3845079	BLASTN	352	7e-09	59	Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence
5411	GM_102_B2_C10_T7	g2995405	BLASTX	367	1e-34	43	(Y12432) polyprotein [Ananas comosus]
5412	GM_102_B2_D02_MR	g2501498	BLASTX	203	9e-17	37	FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE) gi 1076656 pir S51767 glycosyl transferase - eggplant gi 607192 (X77369) glycosyl transferase [Solanum melongena]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5413	GM_102_B2_D02_T7	g2982576	BLASTN	439	8e-13	56	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from config 3-105, complete sequence [Plasmodium falciparum]
5414	GM_102_B2_D03_T7	g343624	BLASTN	453	1e-13	61	Leptomus sp. 9S and 12S ribosomal RNA genes.
5415	GM_102_B2_D05_T7	g1045530	BLASTN	395	6e-11	64	Magnaporthe grisea host-species specificity (Pw11) gene, complete cds.
5416	GM_102_B2_D08_T7	g4038056	BLASTX	397	4e-35	51	(AC005897) putative transposon [Arabidopsis thaliana]
5417	GM_102_B2_D09_MR	g245310	BLASTX	221	2e-17	67	reverse transcriptase [Solanum tuberosum=potatoes, cv. Pentland Squire, Peptide Transposon Partial, 78 aa]
5418	GM_102_B2_D10_T7	g3845197	BLASTN	437	1e-12	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
5419	GM_102_B2_D12_MR	g421955	BLASTX	208	2e-28	38	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387)
5420	GM_102_B2_D12_T7	g2970556	BLASTX	204	2e-14	83	ORF4 [Solanum tuberosum]
5421	GM_102_B2_F03_T7	g2947070	BLASTX	156	7e-10	47	(AF049708) aspartokinase-homoserine dehydrogenase [Glycine max]
5422	GM_102_B2_F05_T7	g3645899	BLASTX	196	1e-15	50	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]
5423	GM_102_B2_F06_MR	g3599418	BLASTN	774	4e-28	73	(U68408) 5' end not determined experimentally [Zea mays] Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5424	GM_102_B2_F06_T7	g629693	BLASTX	560	2e-53	55	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
5425	GM_102_B2_F07_T7	g507910	BLASTN	401	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5426	GM_102_B2_F09_T7	g3461846	BLASTX	323	6e-27	42	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
5427	GM_102_B2_F12_MR	g3367750	BLASTX	171	3e-11	61	(AL031155) putative amidase [Streptomyces coelicolor]
5428	GM_102_B2_F12_T7	g18559	BLASTN	403	3e-11	67	G.max gene for catalase
5429	GM_102_B2_F01_MR	g507910	BLASTN	585	8e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5430	GM_102_B2_F03_MR	g1666236	BLASTX	112	2e-13	30	(U76261) unknown [Hordeum vulgare]
5431	GM_102_B2_F04_T7	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5432	GM_102_B2_F06_MR	g507910	BLASTN	399	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5433	GM_102_B2_F06_T7	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5434	GM_102_B2_F07_MR	g3645899	BLASTX	146	3e-12	58	(U68408) 5' end not determined experimentally [Zea mays]
5435	GM_102_B2_F07_T7	g507910	BLASTN	438	4e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5436	GM_102_B2_F08_MR	g584825	BLASTX	171	3e-16	44	B2 PROTEIN gi 322726 pir S32124 B2 protein - carrot gi 297889 (X72385) B2 protein [Daucus carota]
5437	GM_102_B2_F08_T7	g3845068	BLASTN	418	7e-12	63	Plasmodium falciparum chromosome 2, section 1 of 73 of the complete sequence

Seq No.	ClonID	NCBI gi	Method	Score	P-value	% Ident	Description
5438	GM_102_B2_F10_T7	g3319362	BLASTX	270	2e-21	41	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
5439	GM_102_B2_G04_MR	g3810596	BLASTX	162	6e-10	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5440	GM_102_B2_G06_MR	g2213540	BLASTX	228	2e-21	59	(X98744) chloroplast DNA-binding protein PD3 [Pisum sativum]
5441	GM_102_B2_G06_T7	g2564048	BLASTN	378	5e-10	80	Arabidopsis thaliana genomic DNA: chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]
5442	GM_102_B2_G10_MR	g1173055	BLASTX	316	1e-27	85	60S RIBOSOMAL PROTEIN L11 (L5) gi 541961 pir S42497 ribosomal protein L11.e - alfalfa gi 1076504 pir S51819 RL5 ribosomal protein - alfalfa gi 463252 (X78284) RL5 ribosomal protein [Medicago sativa]
5443	GM_102_B2_G10_T7	g18768	BLASTN	351	2e-09	69	Soybean Tgm6 transposable element 3' end
5444	GM_102_B2_H01_MR	g2995405	BLASTX	303	4e-25	46	(Y12432) polypeptide [Ananas comosus]
5445	GM_102_B2_H01_T7	g3845197	BLASTN	546	1e-17	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
5446	GM_102_B2_H02_T7	g3377834	BLASTX	161	5e-10	27	(AF075598) No definition line found [Arabidopsis thaliana]
5447	GM_102_B2_H03_MR	g1666236	BLASTX	279	1e-23	34	(U76261) unknown [Hordeum vulgare]
5448	GM_102_B2_H04_T7	g2996647	BLASTN	519	2e-16	62	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL); complete sequence [Homo sapiens]
5449	GM_102_B2_H05_T7	g3779026	BLASTX	167	7e-24	50	(AC005171) putative retrotransposon [Arabidopsis thaliana]
5450	GM_102_B2_H06_MR	g507910	BLASTN	520	7e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
5451	GM_102_B2_H06_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5452	GM_102_B2_H09_MR	g3645899	BLASTX	180	2e-26	38	(U68408) 5' end not determined experimentally [Zea mays]
5453	GM_102_B2_H09_T7	g3449317	BLASTN	351	8e-09	64	Arabidopsis thaliana genomic DNA: chromosome 5, P1 clone: MKM21, complete sequence [Arabidopsis thaliana]
5454	GM_102_B2_H11_MR	g100484	BLASTX	433	2e-43	55	hypothetical protein - garden snapdragon
5455	GM_102_B2_H11_T7	g905361	BLASTX	167	9e-11	30	(U22103) gag-protease polypeptide [Glycine max]
5456	GM_103_A1_A04_MR	g507910	BLASTN	367	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5457	GM_103_A1_A04_T7	g905361	BLASTX	300	4e-25	78	(U22103) gag-protease polypeptide [Glycine max]
5458	GM_103_A1_B06_T7	g905361	BLASTX	321	2e-27	88	(U22103) gag-protease polypeptide [Glycine max]
5459	GM_103_A1_D02_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5460	GM_103_A1_D08_T7	g507910	BLASTN	495	9e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
5461	GM_103_A1_E02_T7	g4063760	BLASTX	182	6e-12	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5462	GM_103_A1_E05_T7	g507910	BLASTN	394	3e-11	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5463	GM_103_A1_F01_T7	g3097320	BLASTN	683	1e-39	82	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5464	GM_103_A1_F03_MR	g544018	BLASTX	192	2e-13	35	NITRATE/CHLORATE TRANSPORTER gi 1076359 pir A45772 nitrate-inducible nitrate transporter - Arabidopsis thaliana gi 166668 (L10357) CHL1 [Arabidopsis thaliana] gi 3157921 (AC002131) Identical to nitrate/chlorate transporter cDNA gb L10357 from A. thaliana. ESTs gb H37533 and gb R29790. gb T46117. gb T46068. gb T75688. gb R29817. gb R29862. gb Z34634 and gb Z34258 come from this gene. [Arabidopsis thaliana]
5465	GM_103_A1_F03_T7	g860800	BLASTN	355	4e-09	61	B.juncea Xle7-2EB gene
5466	GM_103_A1_G01_T7	g3004480	BLASTX	161	4e-11	52	(AJ228333) reverse transcriptase [Pinus elliottii]
5467	GM_103_A1_G05_MR	g2586082	BLASTX	150	4e-09	41	(U72725) retrofit [Oryza longistaminata]
5468	GM_103_A1_G08_T7	g100484	BLASTX	272	6e-22	57	hypothetical protein - garden snapdragon
5469	GM_103_B1_A02_T7	g18559	BLASTN	523	1e-16	68	G.max gene for catalase
5470	GM_103_B1_A04_T7	g507910	BLASTN	401	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5471	GM_103_B1_A06_MR	g3777527	BLASTX	183	5e-17	42	(AF053008) gag-pol polypeptide [Glycine max]
5472	GM_103_B1_A06_T7	g1256945	BLASTN	345	4e-10	65	Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.
5473	GM_103_B1_A07_MR	g505129	BLASTN	360	3e-09	68	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
5474	GM_103_B1_A10_MR	g2864608	BLASTX	128	3e-10	45	(AL021811) ferredoxin--NADP+ reductase - like protein [Arabidopsis thaliana]
5475	GM_103_B1_B01_T7	g3779030	BLASTX	146	7e-15	35	(AC005171) putative gag-protease polypeptide [Arabidopsis thaliana]
5476	GM_103_B1_B03_T7	g3142328	BLASTN	2483	6e-107	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
5477	GM_103_B1_B06_T7	g3845197	BLASTN	428	3e-12	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
5478	GM_103_B1_B08_MR	g3645899	BLASTX	277	3e-26	45	(U68408) 5' end not determined experimentally [Zea mays]
5479	GM_103_B1_B10_MR	g3645899	BLASTX	156	3e-09	40	(U68408) 5' end not determined experimentally [Zea mays]
5480	GM_103_B1_B12_MR	g3928090	BLASTX	150	5e-28	50	(AC005770) putative MTN3 protein [Arabidopsis thaliana]
5481	GM_103_B1_C01_MR	g508826	BLASTN	464	7e-20	65	Drosophila melanogaster Oregon-R mitochondrial A+T region.
5482	GM_103_B1_C07_T7	g2522230	BLASTX	335	1e-29	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5483	GM_103_B1_C10_MR	g4063770	BLASTX	221	2e-16	37	(AB004906) transposase [Ipomoea purpurea]
5484	GM_103_B1_C10_T7	g4063760	BLASTX	508	9e-47	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5485	GM_103_B1_C11_MR	g3097320	BLASTN	493	3e-15	69	Glycine max gene for Bd 30K. complete cds
5486	GM_103_B1_C12_T7	g2245104	BLASTX	305	3e-37	55	(Z97343) LTR retrotransposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5487	GM_103_B1_D01_MR	g522302	BLASTX	183	6e-16	49	(L35053) endonuclease [Magnaporthe grisea]
5488	GM_103_B1_D02_T7	g3645899	BLASTX	239	4e-18	51	(U68408) 5' end not determined experimentally [Zea mays]
5489	GM_103_B1_D05_MR	g4138343	BLASTX	223	1e-16	69	(AJ011979) RNA-directed RNA polymerase [Petunia x hybrida]
5490	GM_103_B1_D08_T7	g4063760	BLASTX	633	1e-63	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5491	GM_103_B1_E01_MR	g342965	BLASTN	434	3e-13	64	paramecium species 7.227 mt dna dimer: replication init. region.
5492	GM_103_B1_E05_T7	g2864613	BLASTX	192	2e-18	54	(AL021811) S-receptor kinase-like protein [Arabidopsis thaliana]
5493	GM_103_B1_E08_T7	g1769898	BLASTX	498	7e-47	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5494	GM_103_B1_E10_T7	g2244916	BLASTX	186	1e-19	44	(Z97339) hypothetical protein [Arabidopsis thaliana]
5495	GM_103_B1_F04_T7	g3892061	BLASTX	163	7e-14	28	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
5496	GM_103_B1_F06_T7	g3142328	BLASTN	955	3e-36	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds., and long terminal repeat, complete sequence (AF077409) similar to maize transposon MuDR mudrA protein (GB:AL021710) [Arabidopsis thaliana]
5497	GM_103_B1_F09_MR	g3319368	BLASTX	152	3e-09	32	G.max gene for catalase
5498	GM_103_B1_F10_T7	g18559	BLASTN	420	5e-12	66	(AF053008) gag-pol polyprotein [Glycine max]
5499	GM_103_B1_F12_MR	g3777527	BLASTX	433	2e-38	86	(U22103) gag-protease polyprotein [Glycine max]
5500	GM_103_B1_G01_T7	g905361	BLASTX	225	6e-17	33	(AF053008) gag-pol polyprotein [Glycine max]
5501	GM_103_B1_G03_MR	g3777527	BLASTX	922	7e-91	95	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
5502	GM_103_B1_G08_MR	g3777526	BLASTN	715	3e-25	66	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5503	GM_103_B1_G09_MR	g3599418	BLASTN	649	2e-22	84	(U76261) unknown [Hordeum vulgare]
5504	GM_103_B1_G09_T7	g1666236	BLASTX	172	7e-12	30	(AF053008) gag-pol polyprotein [Glycine max]
5505	GM_103_B1_G12_T7	g3777527	BLASTX	775	4e-75	94	Glycine max BSR-101 satellite SB92 genomic sequence.
5506	GM_103_B1_H02_T7	g507910	BLASTN	606	9e-21	82	Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I
5507	GM_103_B1_H04_MR	g13584	BLASTN	426	1e-12	60	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5508	GM_103_B1_H04_T7	g3695395	BLASTX	221	2e-16	44	(AC002561) putative squamosa-promoter binding protein [Arabidopsis thaliana]
5509	GM_103_B1_H05_MR	g2673911	BLASTX	160	1e-13	40	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
5510	GM_103_B1_H07_T7	g3377848	BLASTX	142	8e-20	52	Glycine max BSR-101 satellite SB92 genomic sequence.
5511	GM_103_B1_H08_MR	g507910	BLASTN	343	7e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5512	GM_103_B1_H08_T7	g507910	BLASTN	368	5e-10	73	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5513	GM_104_A1_A07_T7	g3510336	BLASTN	381	4e-10	67	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1817, complete sequence [Arabidopsis thaliana]
5514	GM_104_A1_A08_T7	g3810596	BLASTX	282	9e-23	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5515	GM_104_A1_A10_T7	g629693	BLASTX	332	3e-29	54	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
5516	GM_104_A1_B03_T7	g3810596	BLASTX	109	4e-11	40	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5517	GM_104_A1_B05_T7	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5518	GM_104_A1_B09_MR	g4063756	BLASTN	408	2e-11	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5519	GM_104_A1_B12_T7	g3097320	BLASTN	711	4e-25	84	Glycine max gene for Bd 30K, complete cds
5520	GM_104_A1_C03_T7	g1142702	BLASTN	385	7e-11	79	Glycine max satellite STR120-A.4.
5521	GM_104_A1_C11_T7	g4038056	BLASTX	230	6e-20	51	(AC005897) putative transposon [Arabidopsis thaliana]
5522	GM_104_A1_D03_MR	g4038056	BLASTX	262	3e-23	43	(AC005897) putative transposon [Arabidopsis thaliana]
5523	GM_104_A1_D08_T7	g2924777	BLASTX	158	2e-09	42	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]
5524	GM_104_A1_D11_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
5525	GM_104_A1_D11_T7	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5526	GM_104_A1_D12_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5527	GM_104_A1_E02_T7	g905361	BLASTX	207	5e-15	32	(U22103) gag-protease polypeptide [Glycine max]
5528	GM_104_A1_E07_T7	g4063760	BLASTX	145	5e-18	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5529	GM_104_A1_E10_T7	g2522228	BLASTX	519	4e-49	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
5530	GM_104_A1_E12_MR	g3645899	BLASTX	345	2e-29	49	(U68408) 5' end not determined experimentally [Zea mays]
5531	GM_104_A1_F02_T7	g3097320	BLASTN	506	7e-16	82	Glycine max gene for Bd 30K, complete cds
5532	GM_104_A1_F03_T7	g3142328	BLASTN	804	2e-29	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5533	GM_104_A1_F06_T7	g1431738	BLASTN	392	8e-11	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhspl7.5-M).
5534	GM_104_A1_F08_MR	g3097320	BLASTN	700	1e-24	82	Glycine max gene for Bd 30K, complete cds
5535	GM_104_A1_G02_T7	g507910	BLASTN	360	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5536	GM_104_A1_G04_T7	g840618	BLASTN	347	7e-09	58	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
5537	GM_104_A1_G05_MR	g2583130	BLASTX	169	2e-10	36	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
5538	GM_104_A1_G06_T7	g100484	BLASTX	212	7e-25	49	hypothetical protein - garden snapdragon
5539	GM_104_A1_G09_MR	g1040936	BLASTN	352	9e-10	63	Anopheles koneri NADH dehydrogenase subunit 2 gene.
5540	GM_104_A1_H08_MR	g2522228	BLASTX	328	7e-29	66	mitochondrial gene encoding mitochondrial product, partial cds.
5541	GM_104_A1_H10_MR	g320569	BLASTX	138	2e-11	38	(AB007466) reverse transcriptase-like protein [Vicia faba]
							transposon TNT1 - Arabidopsis thaliana (fragment)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5542	GM_104_A1_H11_T7	g905361	BLASTX	216	5e-16	63	(U22103) gag-protease polyprotein [Glycine max]
5543	GM_104_A2_A02_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5544	GM_104_A2_A02_T7	g905361	BLASTX	429	2e-39	95	(U22103) gag-protease polyprotein [Glycine max]
5545	GM_104_A2_A04_MR	g3892061	BLASTX	138	3e-11	28	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
5546	GM_104_A2_A07_T7	g1345977	BLASTX	163	1e-10	88	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 2 gi 904154 (L43921) microsomal omega-6 desaturase [Glycine max]
5547	GM_104_A2_A08_T7	g3097320	BLASTN	483	8e-15	70	Glycine max gene for Bd 30K, complete cds
5548	GM_104_A2_A09_T7	g1370204	BLASTN	375	1e-10	86	L-japonicus mRNA for small GTP-binding protein, RAN1B
5549	GM_104_A2_A10_T7	g3777527	BLASTX	768	3e-74	95	(AF053008) gag-pol polyprotein [Glycine max]
5550	GM_104_A2_A11_MR	g3241925	BLASTN	426	3e-12	61	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]
5551	GM_104_A2_B01_MR	g2264320	BLASTN	551	7e-18	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
5552	GM_104_A2_B03_T7	g1085922	BLASTX	201	2e-20	82	hypothetical protein 224 - evening primrose mitochondrion >gi 459533 (X78038) orf224; homology to ribosomal protein S1 of E. coli [Oenothera berteriana]
5553	GM_104_A2_B06_MR	g2522230	BLASTX	245	4e-20	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5554	GM_104_A2_B06_T7	g454847	BLASTN	405	2e-11	70	Glycine max ribosomal protein S11 gene, complete cds
5555	GM_104_A2_B07_T7	g2245104	BLASTX	241	4e-18	42	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
5556	GM_104_A2_B10_T7	g18559	BLASTN	993	5e-38	80	G.max gene for catalase
5557	GM_104_A2_C01_MR	g3738114	BLASTN	419	2e-14	67	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
5558	GM_104_A2_C02_T7	g2688657	BLASTX	158	5e-10	73	(AE001172) pyrophosphate-fructose 6-phosphate 1-phosphotransferase (pfk) [Borrelia burgdorferi]
5559	GM_104_A2_C04_T7	g18559	BLASTN	681	8e-24	75	G.max gene for catalase
5560	GM_104_A2_C08_T7	g507910	BLASTN	477	6e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
5561	GM_104_A2_C09_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5562	GM_104_A2_C09_T7	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5563	GM_104_A2_D02_MR	g18559	BLASTN	1195	3e-47	87	G.max gene for catalase
5564	GM_104_A2_D02_T7	g3820976	BLASTN	406	3e-11	60	Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complet...

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5565	GM_104_A2_D04_T7	g3319362	BLASTX	229	4e-17	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm. score 19.29) [Arabidopsis thaliana]
5566	GM_104_A2_D08_MR	g18559	BLASTN	682	7e-24	75	G.max gene for catalase
5567	GM_104_A2_D11_T7	g2522230	BLASTX	187	6e-14	46	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5568	GM_104_A2_E07_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5569	GM_104_A2_E07_T7	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5570	GM_104_A2_E08_MR	g4063760	BLASTX	439	2e-39	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5571	GM_104_A2_E09_T7	g2501460	BLASTX	159	9e-20	67	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOL-ESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gnl PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]
5572	GM_104_A2_E10_T7	g1345644	BLASTX	254	2e-20	54	CYTOCHROME P450 LXXXVI gi 9404446 (X90458) cytochrome p450 [Arabidopsis thaliana]
5573	GM_104_A2_F08_MR	g507910	BLASTN	351	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5574	GM_104_A2_F09_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5575	GM_104_A2_F11_MR	g2982320	BLASTX	221	2e-17	43	(AF051245) hypothetical protein [Picea mariana]
5576	GM_104_A2_G04_MR	g507910	BLASTN	352	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
5577	GM_104_A2_G04_T7	g507910	BLASTN	378	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5578	GM_104_A2_G08_MR	g4063760	BLASTX	286	5e-23	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5579	GM_104_A2_H01_T7	g3004545	BLASTX	190	1e-12	34	(AC003673) putative reverse transcriptase [Arabidopsis thaliana]
5580	GM_104_A2_H06_T7	g507910	BLASTN	598	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5581	GM_104_A2_H09_T7	g1165321	BLASTN	484	7e-15	79	Glycine max extensin (SHHRGP3) gene, complete cds
5582	GM_104_A2_H10_MR	g4063760	BLASTX	273	1e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5583	GM_104_B1_A09_T7	g3097320	BLASTN	542	2e-17	73	Glycine max gene for Bd 30K, complete cds
5584	GM_104_B1_A11_T7	g3386604	BLASTX	232	5e-19	56	(AC004665) putative protein kinase [Arabidopsis thaliana]
5585	GM_104_B1_C03_T7	g2493908	BLASTX	297	7e-25	55	CULLIN HOMOLOG 3 (CUL-3) gi 1381146 (U58089) Hs-CUL-3 [Homo sapiens]
5586	GM_104_B1_C04_T7	g100226	BLASTX	210	2e-15	43	hypothetical protein - tomato gi 19275 (Z12127) protein of unknown function [Lycopersicon esculentum] gi 445619 prf 1909366A Leu zipper protein [Lycopersicon esculentum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
5587	GM_104_B1_C05_T7	g2129618	BLASTX	235	1e-17	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5588	GM_104_B1_C07_T7	g4160362	BLASTN	402	4e-11	63	Saccharomyces cerevisiae complete mitochondrial genome (U22103) gag-protease polypeptide [Glycine max]
5589	GM_104_B1_C08_T7	g905361	BLASTX	216	5e-16	35	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae] (AC005561) putative POL3 protein [Arabidopsis thaliana]
5591	GM_104_B1_D02_T7	g4063760	BLASTX	279	3e-22	54	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana]
5592	GM_104_B1_D08_T7	g3142328	BLASTN	592	8e-20	76	G-max gene for catalase
5593	GM_104_B1_D11_T7	g3021276	BLASTX	159	2e-18	64	Glycine max BSR-101 satellite SB92 genomic sequence.
5594	GM_104_B1_E02_T7	g18559	BLASTN	1060	5e-41	78	Glycine max gene for Bd 30K, complete cds
5595	GM_104_B1_E04_T7	g507910	BLASTN	402	1e-11	75	Hordeum vulgare cultivar Bomi starch branching enzyme IIb (sbeIIb) gene, nuclear gene encoding plastid protein, partial cds
5596	GM_104_B1_E06_T7	g3097320	BLASTN	443	5e-13	74	Human Chromosome 16 BAC clone C1T987SK-A-598D4, complete sequence [Homo sapiens]
5597	GM_104_B1_E09_T7	g3851527	BLASTN	414	9e-12	65	(AC005561) putative POL3 protein [Arabidopsis thaliana] (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
5598	GM_104_B1_F02_T7	g2896804	BLASTN	393	1e-10	63	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5599	GM_104_B1_F05_T7	g4063760	BLASTX	195	1e-14	39	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]
5600	GM_104_B1_G01_T7	g3319362	BLASTX	228	9e-22	56	Glycine max BSR-101 satellite SB92 genomic sequence.
5601	GM_104_B1_G04_T7	g2129618	BLASTX	171	7e-11	36	(AL035064) putative ubiquitinone biosynthesis protein [Schizosaccharomyces pombe]
5602	GM_104_B1_G05_T7	g2961390	BLASTX	138	1e-15	78	(AC005314) putative peroxidase [Arabidopsis thaliana]
5603	GM_104_B1_G09_T7	g507910	BLASTN	369	4e-10	73	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
5604	GM_104_B1_G11_T7	g4106666	BLASTX	180	3e-13	44	AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPHOSPHATE: AMIDOTRANSFERASE) (ATASE) (GPAT) gi 439105 (L23834) glutamine phosphoribosylpyrophosphate amidotransferase [Vigna aconitifolia]
5605	GM_104_B1_H02_T7	g3608150	BLASTX	345	1e-30	60	
5606	GM_104_B1_H06_T7	g3250687	BLASTX	199	3e-15	36	
5607	GM_104_B2_A02_MR	g1709919	BLASTX	378	3e-34	72	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5608	GM_104_B2_A03_T7	g2979574	BLASTN	366	2e-09	66	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10. complete sequence [Homo sapiens]
5609	GM_104_B2_A04_MR	g2522228	BLASTX	335	1e-29	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
5610	GM_104_B2_A08_T7	g226407	BLASTX	110	5e-09	44	retrotransposon del1-46 [Lilium henryi]
5611	GM_104_B2_A11_T7	g3645899	BLASTX	279	2e-22	50	(U68408) 5' end not determined experimentally [Zea mays]
5612	GM_104_B2_A12_MR	g1769897	BLASTX	153	2e-09	32	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5613	GM_104_B2_B06_T7	g166884	BLASTN	457	2e-14	76	A.thaliana telomeric DNA. >gi 589934 gb I07744 Sequence 1 from Patent EP 0338266
5614	GM_104_B2_B07_T7	g4063760	BLASTX	140	2e-10	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5615	GM_104_B2_B08_MR	g1568538	BLASTN	370	1e-09	65	Human DNA sequence from PAC 253J14 on chromosome X contains polymorphic CA repeat
5616	GM_104_B2_C01_MR	g4038056	BLASTX	187	1e-12	42	(AC005897) putative transposon [Arabidopsis thaliana]
5617	GM_104_B2_C05_T7	g3947733	BLASTX	217	1e-20	73	(AJ009719) NL25 [Solanum tuberosum]
5618	GM_104_B2_D01_MR	g3097320	BLASTN	380	4e-10	62	Glycine max gene for Bd 30K, complete cds
5619	GM_104_B2_D02_MR	g2735017	BLASTX	272	9e-22	72	(U82481) KI domain interacting kinase 1 [Zea mays]
5620	GM_104_B2_D03_MR	g3777527	BLASTX	536	2e-49	97	(AF053008) gag-pol polypeptide [Glycine max]
5621	GM_104_B2_D06_T7	g4063760	BLASTX	345	3e-29	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5622	GM_104_B2_D07_MR	g4063756	BLASTN	422	5e-12	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5623	GM_104_B2_D07_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5624	GM_104_B2_D11_MR	g3142328	BLASTN	691	3e-24	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
5625	GM_104_B2_D11_T7	g4063760	BLASTX	177	2e-11	30	Glycine max gene for Bd 30K, complete cds
5626	GM_104_B2_E06_T7	g3097320	BLASTN	577	4e-19	71	(AJ000387) protease [Drosophila melanogaster]
5627	GM_104_B2_E08_T7	g2791289	BLASTX	143	5e-15	40	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
5628	GM_104_B2_E09_MR	g2316016	BLASTX	296	6e-24	58	(AB004906) transposase [Ipomoea purpurea]
5629	GM_104_B2_E12_T7	g4063770	BLASTX	193	2e-13	37	(U22103) gag-protease polypeptide [Glycine max]
5630	GM_104_B2_F01_MR	g905361	BLASTX	422	1e-38	95	Glycine max BSR-101 satellite SB92 genomic sequence.
5631	GM_104_B2_F09_MR	g507910	BLASTN	569	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5632	GM_104_B2_F09_T7	g507910	BLASTN	591	4e-20	81	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]
5633	GM_104_B2_F12_MR	g3869069	BLASTN	365	2e-09	65	G-max gene for catalase
5634	GM_104_B2_G01_T7	g18559	BLASTN	841	4e-31	76	G-max gene for catalase
5635	GM_104_B2_G03_MR	g18559	BLASTN	466	4e-14	67	(AC005897) putative transposon [Arabidopsis thaliana]
5636	GM_104_B2_G04_MR	g4038056	BLASTX	266	4e-21	52	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5637	GM_104_B2_G05_T7	g2098709	BLASTX	202	1e-14	67	(U82975) pectinesterase [Citrus sinensis]
5638	GM_104_B2_G08_MR	g18559	BLASTN	698	1e-24	75	G.max gene for catalase
5639	GM_104_B2_G09_MR	g1769899	BLASTX	230	2e-20	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5640	GM_104_B2_G11_MR	g2522228	BLASTX	187	3e-13	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
5641	GM_104_B2_H01_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5642	GM_104_B2_H01_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5643	GM_104_B2_H04_MR	g1588265	BLASTX	186	1e-12	84	100RNP protein [Spinacia oleracea]
5644	GM_104_B2_H05_MR	g3695395	BLASTX	183	5e-14	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5645	GM_104_B2_H06_MR	g3695395	BLASTX	185	3e-14	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5646	GM_104_B2_H08_MR	g3599418	BLASTN	396	6e-11	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5647	GM_104_B2_H10_T7	g2565011	BLASTX	194	2e-13	50	(AC002983) putative mudrA-like retrotransposon-associated protein [Arabidopsis thaliana]
5648	GM_105_A1_A01_MR	g3337395	BLASTN	442	6e-13	65	Homo sapiens Chromosome 16 BAC clone C1T987SK-A-24817, complete sequence [Homo sapiens]
5649	GM_105_A1_A04_MR	g322662	BLASTX	134	6e-18	69	S-receptor kinase-related protein - Chinese kale gi 17915 (Z18883)
5650	GM_105_A1_A09_MR	g507910	BLASTN	519	8e-17	78	S-receptor kinase related protein [Brassica oleracea]
5651	GM_105_A1_C04_MR	g3894210	BLASTN	352	7e-09	63	Glycine max BSR-101 satellite SB92 genomic sequence.
5652	GM_105_A1_C07_MR	g1142701	BLASTN	1188	2e-47	82	Homo sapiens PAC clone DJ0953B05 from 7p12-p14, complete sequence [Homo sapiens]
5653	GM_105_A1_C11_MR	g3142328	BLASTN	1709	1e-70	95	Glycine max satellite S1TR120-A.3.
5654	GM_105_A1_D05_MR	g2522230	BLASTX	293	4e-25	44	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5655	GM_105_A1_D10_MR	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
5656	GM_105_A1_E04_MR	g2160694	BLASTX	261	5e-21	67	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
5657	GM_105_A1_E07_MR	g2522227	BLASTX	181	4e-13	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5658	GM_105_A1_F09_MR	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5659	GM_105_A1_F03_MR	g4063760	BLASTX	225	1e-16	50	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
5660	GM_105_A1_F04_MR	g18559	BLASTN	794	1e-34	78	G.max gene for catalase
5661	GM_105_A1_G03_MR	g3097320	BLASTN	916	2e-34	77	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
5662	GM_105_A1_G04_MR	g3930515	BLASTX	109	2e-09	43	(AF059674) putative gag protein [Nicotiana tabacum]
5663	GM_105_A1_G10_MR	g100484	BLASTX	394	4e-35	54	hypothetical protein - garden snapdragon
5664	GM_105_A1_H05_MR	g421953	BLASTX	174	4e-12	40	hypothetical protein 2 - potato transposon Tst1 gi 21432 (X52387)
5665	GM_105_A1_H09_MR	g1167523	BLASTX	279	3e-22	36	ORF2 [Solanum tuberosum]
5666	GM_105_A1_H12_MR	g421954	BLASTX	211	5e-27	47	(D83003) ORF1AA 1-1338 [Nicotiana tabacum]
5667	GM_105_A2_A03_T7	g2995405	BLASTX	392	1e-34	54	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387)
5668	GM_105_A2_A07_MR	g4063756	BLASTN	473	3e-14	63	ORF3 [Solanum tuberosum]
5669	GM_105_A2_A07_T7	g3142379	BLASTX	213	5e-16	55	(Y12432) polyprotein [Ananas comosus]
5670	GM_105_A2_A09_MR	g3645899	BLASTX	190	8e-17	58	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence.
5671	GM_105_A2_A12_T7	g3142328	BLASTN	1179	2e-46	81	complete sequence [Arabidopsis thaliana]
5672	GM_105_A2_B04_MR	g1204057	BLASTN	416	9e-12	62	(AF053008) envelope-like [Glycine max]
5673	GM_105_A2_B04_T7	g2462936	BLASTX	389	3e-35	56	(U68408) 5' end not determined experimentally [Zea mays]
5674	GM_105_A2_B09_T7	g1142699	BLASTN	1360	4e-55	88	Glycine max partial SIRE-1 sequence ribonuclease II and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5675	GM_105_A2_B10_MR	g2244942	BLASTX	118	1e-09	44	Caenorhabditis elegans cosmid C04B4, complete sequence
5676	GM_105_A2_B11_T7	g507910	BLASTN	459	4e-14	77	[Caenorhabditis elegans]
5677	GM_105_A2_C04_MR	g1769897	BLASTX	166	8e-11	27	(Y12321) open reading frame 2 [Brassica oleracea]
5678	GM_105_A2_C06_MR	g3777527	BLASTX	570	1e-54	89	Glycine max satellite STR120-A.1.
5679	GM_105_A2_C06_T7	g4159703	BLASTN	350	9e-09	72	(Z97339) similarity to hypothetical protein [Arabidopsis thaliana]
5680	GM_105_A2_C07_MR	g4063760	BLASTX	240	2e-19	46	Glycine max BSR-101 satellite SB92 genomic sequence.
5681	GM_105_A2_C07_T7	g2995405	BLASTX	398	3e-35	52	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5682	GM_105_A2_C08_MR	g3600043	BLASTX	173	2e-21	49	(AF053008) gag-pol polyprotein [Glycine max]
5683	GM_105_A2_C09_T7	g100484	BLASTX	337	6e-29	56	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
5684	GM_105_A2_C10_MR	g507910	BLASTN	567	5e-19	80	K5F14, complete sequence [Arabidopsis thaliana]
5685	GM_105_A2_C12_MR	g13773	BLASTN	404	6e-12	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5686	GM_105_A2_C12_T7	g2827709	BLASTX	198	1e-13	53	(Y12432) polyprotein [Ananas comosus]
5687	GM_105_A2_D03_T7	g2160694	BLASTX	271	3e-22	83	(AF080119) No definition line found [Arabidopsis thaliana]
							hypothetical protein - garden snapdragon
							Glycine max BSR-101 satellite SB92 genomic sequence.
							Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb
							M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
							(AL021684) predicted protein [Arabidopsis thaliana]
							(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5688	GM_105_A2_D04_T7	g3142328	BLASTN	735	3e-26	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5689	GM_105_A2_E02_T7	g3037017	BLASTN	374	8e-11	66	Bodo saltans NADH dehydrogenase subunit 5 (ND5) mRNA, kinetoplast gene encoding kinetoplast protein, partial cds (AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5690	GM_105_A2_E04_T7	g2522227	BLASTX	223	9e-18	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5691	GM_105_A2_F04_MR	g4063760	BLASTX	299	2e-24	58	Glycine max gene for Bd 30K, complete cds
5692	GM_105_A2_F05_MR	g3097320	BLASTN	1040	4e-40	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5693	GM_105_A2_F06_T7	g3142328	BLASTN	673	2e-23	79	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5694	GM_105_A2_F08_MR	g4063756	BLASTN	459	1e-13	63	(Y12432) polyprotein [Ananas comosus]
5695	GM_105_A2_G06_T7	g2995405	BLASTX	368	4e-32	62	Glycine max BSR-101 satellite SB92 genomic sequence.
5696	GM_105_A2_G07_MR	g507910	BLASTN	393	4e-11	73	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
5697	GM_105_A2_G10_T7	g3461840	BLASTX	190	1e-12	34	(AC005679) Strong similarity to T16B12.3 gi 3746060 unknown protein from Arabidopsis thaliana BAC gb AC005311. [Arabidopsis thaliana]
5698	GM_105_A2_H03_MR	g3834313	BLASTX	327	7e-39	72	Glycine max BSR-101 satellite SB92 genomic sequence. (AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]
5699	GM_105_A2_H06_MR	g507910	BLASTN	410	6e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5700	GM_105_A2_H07_MR	g3860246	BLASTX	113	3e-09	47	(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]
5701	GM_105_A2_H12_MR	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
5702	GM_106_A1_A06_MR	g2459431	BLASTX	215	4e-16	44	(AC002332) unknown protein [Arabidopsis thaliana]
5703	GM_106_A1_B02_T7	g2995405	BLASTX	346	1e-29	48	(Y12432) polyprotein [Ananas comosus]
5704	GM_106_A1_B07_T7	g3777527	BLASTX	189	2e-12	33	(AF053008) gag-pol polyprotein [Glycine max]
5705	GM_106_A1_B09_T7	g3033389	BLASTX	200	5e-14	42	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
5706	GM_106_A1_C01_T7	g2129618	BLASTX	163	6e-16	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] (AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5707	GM_106_A1_C03_MR	g2522230	BLASTX	244	6e-20	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
5708	GM_106_A1_C04_T7	g130582	BLASTX	241	1e-20	40	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5709	GM_106_A1_C06_MR	g2894587	BLASTN	378	4e-10	65	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-112, complete sequence [Plasmodium falciparum]
5710	GM_106_A1_C10_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5711	GM_106_A1_D04_T7	g840618	BLASTN	346	8e-09	58	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
5712	GM_106_A1_D05_MR	g178858	BLASTN	383	9e-11	62	Human restriction fragment length polymorphism 3' to the apolipoprotein B gene.
5713	GM_106_A1_D08_T7	g2129618	BLASTX	218	6e-16	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5714	GM_106_A1_D09_T7	g2121303	BLASTN	477	2e-14	66	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
5715	GM_106_A1_E01_T7	g421954	BLASTX	326	8e-28	50	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
5716	GM_106_A1_E04_T7	g342954	BLASTN	389	2e-11	60	paramecium species 4.5 kb dna dimer: replication init. region, clone-1.
5717	GM_106_A1_E06_T7	g3645899	BLASTX	201	2e-15	50	(U68408) 5' end not determined experimentally [Zea mays]
5718	GM_106_A1_E07_T7	g3777527	BLASTX	154	9e-21	45	(AF053008) gag-pol polyprotein [Glycine max]
5719	GM_106_A1_E09_T7	g4038056	BLASTX	267	2e-27	46	(AC005897) putative transposon [Arabidopsis thaliana]
5720	GM_106_A1_E12_MR	g387902	BLASTX	154	2e-16	51	(L23524) ORF [Hordeum vulgare]
5721	GM_106_A1_F02_T7	g505129	BLASTN	375	5e-10	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5722	GM_106_A1_F03_T7	g4063760	BLASTX	654	2e-62	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5723	GM_106_A1_F05_T7	g3785991	BLASTX	234	4e-18	82	(AC005560) putative MAP kinase [Arabidopsis thaliana]
5724	GM_106_A1_F11_T7	g2996647	BLASTN	407	2e-11	59	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
5725	GM_106_A1_F12_T7	g3097320	BLASTN	414	1e-11	73	Glycine max gene for Bd 30K, complete cds
5726	GM_106_A1_G01_T7	g905361	BLASTX	122	4e-12	33	(U22103) gag-protease polyprotein [Glycine max]
5727	GM_106_A1_G02_MR	g3097320	BLASTN	1048	2e-40	75	Glycine max gene for Bd 30K, complete cds
5728	GM_106_A1_G04_MR	g905361	BLASTX	197	6e-14	31	(U22103) gag-protease polyprotein [Glycine max]
5729	GM_106_A1_G09_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5730	GM_106_A1_G11_T7	g18575	BLASTN	826	1e-30	89	Soybean ENOD2A gene for Ngm-75
5731	GM_106_A1_G12_MR	g1431738	BLASTN	696	1e-24	77	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
5732	GM_106_A1_G12_T7	g505129	BLASTN	410	1e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5733	GM_106_A1_H01_T7	g3777527	BLASTX	667	2e-63	84	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
5734	GM_106_A1_H02_MR	g3695387	BLASTX	239	4e-18	58	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
5735	GM_106_A1_H05_T7	g3097320	BLASTN	1205	2e-47	77	Glycine max gene for Bd 30K, complete cds
5736	GM_106_A1_H07_T7	g3777527	BLASTX	461	2e-41	57	(AF053008) gag-pol polyprotein [Glycine max]
5737	GM_106_A1_H10_T7	g3687234	BLASTX	211	4e-15	39	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
5738	GM_106_A1_H11_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5739	GM_106_A1_H12_MR	g3142328	BLASTN	682	7e-24	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5740	GM_106_B1_A01_MR	g1480927	BLASTN	718	1e-25	97	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
5741	GM_106_B1_A08_T7	g2522227	BLASTX	202	2e-15	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5742	GM_106_B1_A09_T7	g3249105	BLASTX	230	6e-18	61	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
5743	GM_106_B1_B04_T7	g541951	BLASTX	441	7e-41	84	SPC2 protein - soybean gi 310578 (L12258) nodulin-26 [Glycine max]
5744	GM_106_B1_B06_T7	g3695395	BLASTX	197	6e-14	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5745	GM_106_B1_B07_T7	g3097320	BLASTN	564	2e-18	75	Glycine max gene for Bd 30K, complete cds
5746	GM_106_B1_B11_MR	g1730557	BLASTX	238	4e-18	69	ALPHA-GLUCAN PHOSPHORYLASE, L. ISOZYME 2 PRECURSOR (STARCH PHOSPHORYLASE L-2) gi 421957 pir S34189 starch phosphorylase (EC 2.4.1.1) - potato gi 1084437 pir S53489 starch phosphorylase (EC 2.4.1.1) - potato gi 313349 (X73684) starch phosphorylase [Solanum tuberosum]
5747	GM_106_B1_B11_T7	g18559	BLASTN	428	2e-12	78	G.max gene for catalase
5748	GM_106_B1_B12_MR	g507910	BLASTN	398	2e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5749	GM_106_B1_B12_T7	g507910	BLASTN	381	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5750	GM_106_B1_C01_MR	g2982452	BLASTX	218	7e-16	45	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
5751	GM_106_B1_C01_T7	g541978	BLASTX	134	4e-17	96	guanine nucleotide regulatory protein - fava bean gi 303734 gnl PID d1002608 (D12550) GTP-binding protein [Pisum sativum] gi 452359 (Z29590) guanine nucleotide regulatory protein [Vicia faba] gi 738942 prf 2001457K GTP-binding protein [Pisum sativum] gi 1098293 prf 2115367A small GTP-binding protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5752	GM_106_B1_C04_T7	g2586083	BLASTX	193	3e-13	38	(U72725) receptor kinase-like protein [Oryza longistaminata]
5753	GM_106_B1_C09_MR	g1769898	BLASTX	195	1e-13	70	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5754	GM_106_B1_C12_MR	g507910	BLASTN	435	5e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
5755	GM_106_B1_D01_T7	g4038056	BLASTX	194	6e-21	56	(AC005897) putative transposon [Arabidopsis thaliana]
5756	GM_106_B1_D02_T7	g531389	BLASTX	124	2e-14	44	(U12626) copia-like retrotransposon Hopscotch polypeptide [Zea mays]
5757	GM_106_B1_D04_T7	g3250687	BLASTX	203	1e-15	54	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
5758	GM_106_B1_E02_T7	g4106408	BLASTN	674	4e-24	76	Oryza sativa subsp. indica dispersed centromeric repeat family RCS1
5759	GM_106_B1_E05_MR	g1769897	BLASTX	333	6e-29	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5760	GM_106_B1_E11_T7	g531389	BLASTX	111	4e-13	48	(U12626) copia-like retrotransposon Hopscotch polypeptide [Zea mays]
5761	GM_106_B1_E12_T7	g1769898	BLASTX	350	1e-30	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5762	GM_106_B1_F03_T7	g2129618	BLASTX	183	4e-12	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5763	GM_106_B1_F04_T7	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5764	GM_106_B1_G04_MR	g4056613	BLASTX	177	2e-12	41	(AF067400) Sc11 protein [Zea mays]
5765	GM_106_B1_G05_MR	g507910	BLASTN	514	1e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
5766	GM_106_B1_G11_T7	g2522227	BLASTX	202	1e-15	52	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5767	GM_106_B1_H05_MR	g4159707	BLASTN	515	3e-16	66	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence [Arabidopsis thaliana]
5768	GM_106_B1_H05_T7	g1708314	BLASTX	204	1e-14	69	HEAT SHOCK PROTEIN 83 gi 169296 (M99431) heat shock protein 83 [Pharbitis nil] gi 445625 prf 1909372A heat shock protein 83 [Ipomoea nil]
5769	GM_106_B1_H10_MR	g3777527	BLASTX	168	1e-14	52	(AF053008) gag-pol polypeptide [Glycine max]
5770	GM_106_B1_H12_T7	g2642431	BLASTX	284	1e-22	59	(AC002391) putative retrotransposon polypeptide [Arabidopsis thaliana]
5771	GM_107_A1_A02_MR	g1840106	BLASTN	385	5e-11	65	Human fragile site locus (FRA16B) minisatellite repeat
5772	GM_107_A1_A05_T7	g4063760	BLASTX	168	2e-10	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5773	GM_107_A1_A06_T7	g304040	BLASTN	1515	1e-62	85	Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene.
5774	GM_107_A1_A09_MR	g1171591	BLASTN	352	7e-09	62	P.falciapum complete gene map of plastid-like DNA (IR-B)
5775	GM_107_A1_A11_MR	g1813979	BLASTX	173	5e-35	71	(Y10860) hypothetical protein [Musa acuminata]
5776	GM_107_A1_B03_MR	g2443881	BLASTX	157	3e-09	51	(AC002294) contains beta-transducin motif [Arabidopsis thaliana]
5777	GM_107_A1_B06_MR	g4115373	BLASTX	156	3e-09	33	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
5778	GM_107_A1_B10_MR	g3142328	BLASTN	661	6e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Y10860) hypothetical protein [Musa acuminata]
5779	GM_107_A1_B11_MR	g1813979	BLASTX	170	8e-29	71	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5780	GM_107_A1_C02_T7	g3695395	BLASTX	187	7e-13	45	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
5781	GM_107_A1_C03_MR	g3319345	BLASTX	119	2e-10	32	(AF076274) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
5782	GM_107_A1_C06_MR	g3377855	BLASTX	209	7e-23	71	(Y13368) reverse transcriptase [Beta vulgaris]
5783	GM_107_A1_C06_T7	g2462134	BLASTX	92	1e-09	43	MITOGEN-ACTIVATED PROTEIN KINASE. HOMOLOG NTF6 (P43) gi 1076639 pir S51320 mitogen-activated protein kinase 6 (E:C 2.7.1.-) - common tobacco gi 2129967 pir S68189 serine/threonine protein kinase p43 - common tobacco gi 634068 (X83879) p43Nif6 serine/threonine protein kinase [Nicotiana tabacum]
5784	GM_107_A1_C09_MR	g2499616	BLASTX	267	2e-30	84	(U68408) 5' end not determined experimentally [Zea mays]
5785	GM_107_A1_D08_T7	g3645899	BLASTX	341	5e-29	50	Lupinus luteus leghemoglobin (LbI) gene, complete cds
5786	GM_107_A1_D10_T7	g2921625	BLASTN	524	1e-16	72	patatin A gene, patatin B gene [Solanum tuberosum=potatoes, HH578, tetraploid, Genomic, 4116 nt]
5787	GM_107_A1_E04_MR	g261221	BLASTN	352	6e-09	64	Glycine max BSR-101 satellite SB92 genomic sequence.
5788	GM_107_A1_E07_MR	g507910	BLASTN	340	9e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5789	GM_107_A1_E08_MR	g507910	BLASTN	647	1e-22	86	Glycine max BSR-101 satellite SB92 genomic sequence.
5790	GM_107_A1_E08_T7	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5791	GM_107_A1_E10_MR	g1142701	BLASTN	1367	2e-55	86	Glycine max satellite STR120-A.3.
5792	GM_107_A1_E12_T7	g2073447	BLASTN	365	2e-09	64	L.japonicus gln1, pge1 & krm genes
5793	GM_107_A1_F01_T7	g3779030	BLASTX	113	2e-09	38	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
5794	GM_107_A1_F04_MR	g507910	BLASTN	407	9e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5795	GM_107_A1_F04_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5796	GM_107_A1_F07_MR	g4038056	BLASTX	330	4e-33	51	(AC005897) putative transposon [Arabidopsis thaliana]
5797	GM_107_A1_F08_T7	g1769898	BLASTX	280	6e-23	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5798	GM_107_A1_F11_T7	g2979574	BLASTN	352	7e-09	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
5799	GM_107_A1_G03_MR	g1747310	BLASTX	213	2e-15	91	(D58424) Myb-like DNA binding protein [Arabidopsis thaliana]
5800	GM_107_A1_G04_T7	g507910	BLASTN	414	4e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5801	GM_107_A1_G08_T7	g3075398	BLASTX	136	1e-16	66	(AC004484) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5802	GM_107_A1_H02_T7	g3142328	BLASTN	668	3e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U76261) unknown [Hordeum vulgare]
5803	GM_107_A1_H03_MR	g1666236	BLASTX	220	2e-17	30	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5804	GM_107_A1_H07_T7	g3810596	BLASTX	185	2e-12	32	Glycine max BSR-101 satellite SB92 genomic sequence.
5805	GM_107_A1_H09_MR	g507910	BLASTN	461	3e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
5806	GM_107_A1_H09_T7	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5807	GM_107_A1_H12_MR	g507910	BLASTN	596	3e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
5808	GM_107_A1_H12_T7	g507910	BLASTN	545	5e-18	81	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
5809	GM_107_B1_A06_T7	g3426334	BLASTN	374	7e-10	66	(AC004786) putative chloroplast envelope Ca2+-ATPase
5810	GM_107_B1_A11_T7	g3445212	BLASTX	218	6e-16	51	[Arabidopsis thaliana]
5811	GM_107_B1_B10_T7	g3645899	BLASTX	265	7e-21	49	(U68408) 5' end not determined experimentally [Zea mays]
5812	GM_107_B1_C02_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5813	GM_107_B1_C07_T7	g2642431	BLASTX	286	7e-23	57	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
5814	GM_107_B1_D01_T7	g3810596	BLASTX	188	8e-13	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5815	GM_107_B1_E01_T7	g905361	BLASTX	163	3e-10	39	(U22103) gag-protease polyprotein [Glycine max]
5816	GM_107_B1_E03_T7	g2462134	BLASTX	182	2e-12	46	(Y13368) reverse transcriptase [Beta vulgaris]
5817	GM_107_B1_E08_T7	g507910	BLASTN	378	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5818	GM_107_B1_E09_T7	g1872521	BLASTX	149	7e-10	71	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]
5819	GM_107_B1_E12_T7	g4063760	BLASTX	294	6e-24	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5820	GM_107_B1_F07_T7	g2129618	BLASTX	96	1e-09	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5821	GM_107_B1_F09_T7	g170080	BLASTN	495	2e-15	74	Soybean seed lectin gene transposable element tgm1.
5822	GM_107_B1_G03_T7	g507910	BLASTN	610	6e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5823	GM_107_B1_G07_T7	g18559	BLASTN	822	3e-30	76	G.max gene for catalase
5824	GM_107_B1_G12_T7	g4063760	BLASTX	253	1e-19	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5825	GM_107_B1_H03_T7	g1769897	BLASTX	268	2e-25	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5826	GM_107_B1_H05_T7	g507910	BLASTN	369	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5827	GM_107_B1_H07_T7	g2244839	BLASTX	141	2e-12	48	(Z97337) hypothetical protein [Arabidopsis thaliana]
5828	GM_107_B1_H08_T7	g1066859	BLASTX	185	9e-14	65	(L49020) acetyl-CoA carboxylase [Glycine max]
5829	GM_108_A1_A02_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5830	GM_108_A1_A03_MR	g3810596	BLASTX	311	7e-26	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
5831	GM_108_A1_A03_T7	g3421038	BLASTN	377	5e-10	69	Human DNA sequence from clone 35C21 on chromosome 1q23-24. Contains STSs, complete sequence [Homo sapiens]
5832	GM_108_A1_A04_MR	g3334663	BLASTX	508	6e-48	67	(Y10491) putative cytochrome P450 [Glycine max]
5833	GM_108_A1_A05_T7	g507910	BLASTN	387	7e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5834	GM_108_A1_A06_T7	g507910	BLASTN	370	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5835	GM_108_A1_A08_MR	g1684913	BLASTX	480	8e-44	60	(U77888) receptor-like protein kinase [Ipomoea nil]
5836	GM_108_A1_A08_T7	g3779020	BLASTN	491	4e-15	63	Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence [Arabidopsis thaliana]
5837	GM_108_A1_A11_MR	g130582	BLASTX	237	3e-19	40	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
5838	GM_108_A1_B03_MR	g18559	BLASTN	1150	4e-45	75	G.max gene for catalase
5839	GM_108_A1_B08_T7	g507910	BLASTN	380	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
5840	GM_108_A1_B10_MR	g4150933	BLASTN	393	1e-10	63	Homo sapiens BAC clone NH0520M18 from 7q31.1-q31.2, complete sequence [Homo sapiens]
5841	GM_108_A1_C04_MR	g3810596	BLASTX	345	2e-29	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5842	GM_108_A1_C07_MR	g3777527	BLASTX	778	2e-75	97	(AF053008) gag-pol polyprotein [Glycine max]
5843	GM_108_A1_C10_MR	g3935187	BLASTX	498	7e-47	64	(AC004557) F17L21.30 [Arabidopsis thaliana]
5844	GM_108_A1_D03_MR	g3142328	BLASTN	1139	1e-44	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U68408) 5' end not determined experimentally [Zea mays]
5845	GM_108_A1_D08_MR	g3645899	BLASTX	176	2e-16	42	(AJ228325) reverse transcriptase [Ginkgo biloba]
5846	GM_108_A1_D08_T7	g3688328	BLASTX	304	2e-26	57	(AJ009720) NL27 [Solanum tuberosum]
5847	GM_108_A1_D12_MR	g3947735	BLASTX	89	6e-09	41	(AJ009719) NL25 [Solanum tuberosum]
5848	GM_108_A1_D12_T7	g3947733	BLASTX	202	1e-14	46	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF022157) CYP71A10 [Glycine max]
5849	GM_108_A1_E01_T7	g3142328	BLASTN	635	9e-22	72	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) gi 868003 gnl PID d1006662 (D29629) aconitase [Cucurbita sp.]
5850	GM_108_A1_E02_MR	g2738982	BLASTX	311	1e-26	71	(U76261) unknown [Hordeum vulgare]
5851	GM_108_A1_E04_MR	g1351856	BLASTX	631	7e-61	89	(AL021687) putative protein [Arabidopsis thaliana]
5852	GM_108_A1_E09_T7	g1666236	BLASTX	164	6e-11	35	Glycine max BSR-101 satellite SB92 genomic sequence.
5853	GM_108_A1_E10_MR	g2828294	BLASTX	178	2e-24	40	
5854	GM_108_A1_F01_MR	g507910	BLASTN	369	4e-10	73	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5855	GM_108_A1_F01_T7	g507910	BLASTN	359	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5856	GM_108_A1_F02_T7	g3142328	BLASTN	1018	4e-39	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U76261) unknown [Hordeum vulgare]
5857	GM_108_A1_F03_MR	g1666236	BLASTX	144	9e-09	28	Glycine max gene for Bd 30K, complete cds
5858	GM_108_A1_F03_T7	g3097320	BLASTN	813	9e-30	75	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300
5859	GM_108_A1_F06_T7	g2501353	BLASTX	496	9e-47	84	transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
5860	GM_108_A1_F09_T7	g3687234	BLASTX	154	4e-10	31	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
5861	GM_108_A1_G01_T7	g3913420	BLASTX	450	8e-42	77	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi 1421752 (U60592) S-adenosylmethionine decarboxylase [Pisum sativum]
5862	GM_108_A1_G04_MR	g421955	BLASTX	444	3e-41	58	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
5863	GM_108_A1_G05_MR	g1929056	BLASTX	171	3e-11	64	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]
5864	GM_108_A1_G07_MR	g3845197	BLASTN	366	2e-09	59	Plasmidium falciparum chromosome 2, section 35 of 73 of the complete sequence
5865	GM_108_A1_G09_T7	g1946279	BLASTX	159	5e-17	46	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
5866	GM_108_A1_H02_MR	g2129618	BLASTX	105	3e-12	46	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5867	GM_108_A1_H03_T7	g2522228	BLASTX	116	1e-12	54	(AB007466) reverse transcriptase-like protein [Vicia faba]
5868	GM_108_A1_H07_T7	g2522227	BLASTX	221	2e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5869	GM_108_A1_H08_T7	g2708743	BLASTX	180	1e-11	35	(AC003952) putative Tat-1-like reverse transcriptase [Arabidopsis thaliana]
5870	GM_108_A1_H10_MR	g3142328	BLASTN	901	7e-34	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
5871	GM_108_A1_H11_MR	g4063760	BLASTX	340	7e-29	52	(Y12432) polyprotein [Ananas comosus]
5872	GM_108_A1_H12_MR	g2995405	BLASTX	337	1e-28	48	Glycine max satellite STR120-A.1.
5873	GM_109_A1_A03_MR	g1142699	BLASTN	264	8e-09	68	hypothetical protein - garden snapdragon
5874	GM_109_A1_B02_T7	g100484	BLASTX	359	3e-31	52	(Y13389) reverse transcriptase [Antirrhinum majus]
5875	GM_109_A1_B03_MR	g2462058	BLASTX	396	4e-36	54	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5876	GM_109_A1_B06_T7	g3097320	BLASTN	723	1e-25	74	Glycine max gene for Bd 30K, complete cds
5877	GM_109_A1_B09_MR	g3142328	BLASTN	983	1e-37	87	Glycine max partial SIRE-I sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5878	GM_109_A1_C05_T7	g507910	BLASTN	396	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5879	GM_109_A1_C12_MR	g2042431	BLASTX	214	3e-15	53	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
5880	GM_109_A1_D03_MR	g100484	BLASTX	270	1e-21	52	hypothetical protein - garden snapdragon
5881	GM_109_A1_E02_T7	g3810596	BLASTX	231	3e-17	61	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5882	GM_109_A1_E03_MR	g1142703	BLASTN	839	2e-31	85	Glycine max satellite STR120-B.1.
5883	GM_109_A1_E09_T7	g2522228	BLASTX	232	3e-18	44	(AB007466) reverse transcriptase-like protein [Vicia faba]
5884	GM_109_A1_E10_MR	g2462134	BLASTX	164	1e-10	30	(Y13368) reverse transcriptase [Beta vulgaris]
5885	GM_109_A1_F09_MR	g2160189	BLASTX	270	2e-21	50	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475.gb ATTS4362 come from this gene. [Arabidopsis thaliana]
5886	GM_109_A1_G04_MR	g3097320	BLASTN	675	2e-23	80	Glycine max gene for Bd 30K, complete cds
5887	GM_109_A1_H01_MR	g4160362	BLASTN	357	4e-09	63	Saccharomyces cerevisiae complete mitochondrial genome
5888	GM_109_A1_H10_T7	g1431738	BLASTN	672	1e-23	83	Soybean (Glycine max) low MW heat shock protein gene (Gmhspl7.5-M).
5889	GM_109_A1_H11_MR	g1890152	BLASTX	207	3e-15	74	(X92510) allene oxide synthase [Arabidopsis thaliana]
5890	GM_109_A2_A01_T7	g3097320	BLASTN	709	5e-25	69	Glycine max gene for Bd 30K, complete cds
5891	GM_109_A2_A02_MR	g1142703	BLASTN	264	7e-14	74	Glycine max satellite STR120-B.1.
5892	GM_109_A2_A02_T7	g505129	BLASTN	362	2e-09	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5893	GM_109_A2_A04_T7	g3377834	BLASTX	207	5e-15	35	(AF075598) No definition line found [Arabidopsis thaliana]
5894	GM_109_A2_A10_MR	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5895	GM_109_A2_B03_MR	g3435286	BLASTX	148	3e-15	93	(AF082597) cytosolic glyceraldehyde-3-phosphate dehydrogenase [Leavenworthia crassa]
5896	GM_109_A2_B06_T7	g2351065	BLASTN	349	1e-08	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15
5897	GM_109_A2_B10_MR	g3097320	BLASTN	859	7e-32	78	Glycine max gene for Bd 30K, complete cds
5898	GM_109_A2_B12_T7	g3924609	BLASTX	380	6e-33	48	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
5899	GM_109_A2_C01_MR	g2828293	BLASTX	200	6e-14	76	(AL021687) putative protein [Arabidopsis thaliana]
5900	GM_109_A2_C01_T7	g2569938	BLASTX	147	9e-09	35	(Y15193) GAI [Arabidopsis thaliana]
5901	GM_109_A2_C02_T7	g1814401	BLASTX	189	4e-13	69	(U84888) phosphoglucosyltransferase [Mesembryanthemum crystallinum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
5902	GM_109_A2_C03_T7	g2443320	BLASTX	201	3e-18	33	(D85597) polyprotein [Oryza australiensis]
5903	GM_109_A2_C07_MR	g1769898	BLASTX	158	5e-16	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5904	GM_109_A2_C09_T7	g3033389	BLASTX	213	6e-20	40	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
5905	GM_109_A2_D04_MR	g469153	BLASTN	355	5e-09	72	P.sativum (Birte) Lox1:Ps:2 gene.
5906	GM_109_A2_D06_MR	g3097320	BLASTN	1339	1e-53	78	Glycine max gene for Bd 30K, complete cds
5907	GM_109_A2_D06_T7	g3645899	BLASTX	341	1e-33	51	(U68408) 5' end not determined experimentally [Zea mays]
5908	GM_109_A2_E01_T7	g3249073	BLASTX	146	9e-09	33	(AC004473) Contains similarity to reverse transcriptase-like protein gb 2244803 from A. thaliana chromosome 4 contig gb Z97336.
5909	GM_109_A2_E03_T7	g58340	BLASTN	444	3e-13	62	[Arabidopsis thaliana]
5910	GM_109_A2_E06_MR	g507910	BLASTN	383	1e-10	75	D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val
5911	GM_109_A2_E07_MR	g3097320	BLASTN	390	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5912	GM_109_A2_E07_T7	g22447	BLASTN	367	1e-09	63	Glycine max gene for Bd 30K, complete cds
5913	GM_109_A2_E09_T7	g4049647	BLASTN	352	7e-09	60	Zea mays ZMPMS2 gene for 19 kDa zein protein.
5914	GM_109_A2_E12_T7	g3033393	BLASTX	264	4e-22	71	Melanoplus sanguinipes entomopoxvirus, complete genome (AC004238) putative phosphatidylinositol-glycan-class C (PIGC) [Arabidopsis thaliana]
5915	GM_109_A2_F04_MR	g3142328	BLASTN	599	4e-20	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
5916	GM_109_A2_F05_MR	g4063760	BLASTX	420	2e-37	62	(AF053008) gag-pol polyprotein [Glycine max]
5917	GM_109_A2_F07_T7	g3777527	BLASTX	769	2e-74	94	FK506-binding protein - Arabidopsis thaliana gi 1354207 (U49453)
5918	GM_109_A2_G01_MR	g2146731	BLASTX	161	2e-24	74	rofl [Arabidopsis thaliana]
5919	GM_109_A2_G01_T7	g541817	BLASTX	168	6e-12	72	protein kinase - common ice plant
5920	GM_109_A2_G02_T7	g3777527	BLASTX	199	1e-13	36	(AF053008) gag-pol polyprotein [Glycine max]
5921	GM_109_A2_G08_T7	g99922	BLASTX	581	1e-55	74	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
5922	GM_109_A2_G09_MR	g2129618	BLASTX	157	8e-17	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5923	GM_109_A2_G12_T7	g3645899	BLASTX	161	9e-10	57	(U68408) 5' end not determined experimentally [Zea mays]
5924	GM_109_A2_H02_T7	g3273387	BLASTN	477	2e-14	63	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
5925	GM_109_A2_H08_MR	g18559	BLASTN	610	1e-20	75	G.max gene for catalase
5926	GM_109_A2_H09_MR	g4063760	BLASTX	362	3e-31	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5927	GM_109_A2_H09_T7	g4063760	BLASTX	218	8e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
5928	GM_109_A2_H10_T7	g3645899	BLASTX	396	7e-35	58	(U68408) 5' end not determined experimentally [Zea mays]
5929	GM_109_B1_A09_MR	g3097320	BLASTN	492	3e-15	70	Glycine max gene for Bd 30K, complete cds
5930	GM_109_B1_A12_MR	g3777527	BLASTX	715	1e-68	94	(AF053008) gag-pol polyprotein [Glycine max]
5931	GM_109_B1_B09_MR	g3777527	BLASTX	231	8e-20	42	(AF053008) gag-pol polyprotein [Glycine max]
5932	GM_109_B1_B10_MR	g2522228	BLASTX	392	1e-35	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
5933	GM_109_B1_D08_MR	g2443320	BLASTX	209	9e-15	50	(D85597) polyprotein [Oryza australiensis]
5934	GM_109_B1_D12_MR	g421948	BLASTX	336	9e-30	56	UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase - garden petunia
5935	GM_109_B1_E02_T7	g3122638	BLASTX	101	4e-11	76	PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1 gi 1076381 pir S49820 PRL1 protein - Arabidopsis thaliana gi 577733 (X82824) PRL1 gene product [Arabidopsis thaliana] gi 577735 (X82825) PRL1 gene product [Arabidopsis thaliana] gi 2244947 gnl PID e326958 (Z97339) PRL1 protein - Arabidopsis thaliana [Arabidopsis thaliana]
5936	GM_109_B1_E05_T7	g18559	BLASTN	1067	2e-41	75	G.max gene for catalase
5937	GM_109_B1_E07_MR	g4038056	BLASTX	261	7e-23	43	(AC005897) putative transposon [Arabidopsis thaliana]
5938	GM_109_B1_E09_T7	g3894172	BLASTX	169	1e-11	32	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]
5939	GM_109_B1_F11_T7	g905361	BLASTX	377	2e-33	98	(U22103) gag-protease polyprotein [Glycine max]
5940	GM_109_B1_F01_MR	g3142328	BLASTN	553	5e-18	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5941	GM_109_B1_F04_MR	g507910	BLASTN	356	2e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5942	GM_109_B1_F10_MR	g507910	BLASTN	495	9e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
5943	GM_109_B1_G02_MR	g4102839	BLASTX	294	1e-24	49	(AF016713) LeOPT1 [Lycopersicon esculentum]
5944	GM_109_B1_G02_T7	g2323254	BLASTN	360	3e-09	65	Human Chromosome X, complete sequence [Homo sapiens]
5945	GM_109_B1_G04_T7	g18559	BLASTN	869	2e-32	72	G.max gene for catalase
5946	GM_109_B1_G07_MR	g1769899	BLASTX	167	8e-12	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5947	GM_109_B1_G10_MR	g4063760	BLASTX	514	2e-47	67	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
5948	GM_109_B1_G10_T7	g18559	BLASTN	801	3e-29	72	G.max gene for catalase
5949	GM_109_B1_G11_T7	g2522228	BLASTX	305	2e-26	53	(AB007466) reverse transcriptase-like protein [Vicia faba]
5950	GM_109_B1_H05_MR	g559278	BLASTN	274	1e-11	70	Saccharomyces cerevisiae mitochondrion origin of replication (ori3 and ori4).
5951	GM_109_B1_H10_MR	g585565	BLASTX	165	1e-11	75	RIBOSOME RECYCLING FACTOR HOMOLOG (NUCLEAR LOCATED PROTEIN D2) gi 629661 pir S32716 nuclear protein - carrot gi 297891 (X72384) nuclear located protein [Daucus carota]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5952	GM_109_B1_H10_T7	g3004480	BLASTX	211	2e-16	55	(AJ228333) reverse transcriptase [Pinus eliottii]
5953	GM_109_B2_A01_T7	g2522227	BLASTX	220	2e-17	56	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5954	GM_109_B2_A08_T7	g2443320	BLASTX	189	1e-12	31	(D85597) polyprotein [Oryza australiensis]
5955	GM_109_B2_B02_T7	g1480927	BLASTN	617	4e-21	75	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
5956	GM_109_B2_B03_T7	g3142328	BLASTN	1323	5e-53	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Z97178) elongation factor 2 [Beta vulgaris]
5957	GM_109_B2_B04_T7	g2369714	BLASTX	668	7e-65	83	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5958	GM_109_B2_B07_T7	g1769898	BLASTX	287	1e-23	49	Arabidopsis thaliana chromosome II BAC T9F-8 genomic sequence, complete sequence [Arabidopsis thaliana]
5959	GM_109_B2_B12_T7	g4063756	BLASTN	446	4e-13	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5960	GM_109_B2_C03_T7	g505129	BLASTN	424	3e-12	62	Glycine max gene for Bd 30K, complete cds
5961	GM_109_B2_C04_T7	g3097320	BLASTN	707	6e-25	74	Glycine max gene for Bd 30K, complete cds
5962	GM_109_B2_C08_T7	g3097320	BLASTN	355	5e-09	67	(Y12321) open reading frame 1 [Brassica oleracea]
5963	GM_109_B2_C12_T7	g2462935	BLASTX	144	6e-12	43	(AC004483) reverse-transcriptase-like protein [Arabidopsis thaliana]
5964	GM_109_B2_D01_T7	g3327392	BLASTX	166	2e-18	58	Glycine max BSR-101 satellite SB92 genomic sequence.
5965	GM_109_B2_D03_T7	g507910	BLASTN	601	1e-20	84	Glycine max gene for Bd 30K, complete cds
5966	GM_109_B2_D04_T7	g3097320	BLASTN	798	4e-29	78	(U13940) cysteine proteinase [Alnus glutinosa]
5967	GM_109_B2_D10_T7	g535454	BLASTX	215	8e-17	69	(AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]
5968	GM_109_B2_E05_T7	g4140691	BLASTX	152	2e-12	50	HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION gi 626631 pir S46811 hypothetical protein YHR074w - yeast (Saccharomyces cerevisiae) gi 500832 (U10556)
5969	GM_109_B2_E09_T7	g731675	BLASTX	149	7e-14	67	Yhr074wp [Saccharomyces cerevisiae]
5970	GM_109_B2_E10_T7	g2828293	BLASTX	162	7e-10	72	(AL021687) putative protein [Arabidopsis thaliana]
5971	GM_109_B2_F07_T7	g1272349	BLASTX	278	3e-23	49	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
5972	GM_109_B2_F12_T7	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5973	GM_109_B2_G02_T7	g19205	BLASTN	541	2e-17	69	L.esculentum enolase gene.
5974	GM_109_B2_G03_T7	g3097320	BLASTN	1042	4e-40	79	Glycine max gene for Bd 30K, complete cds
5975	GM_109_B2_G05_T7	g100484	BLASTX	358	4e-31	51	hypothetical protein - garden snapdragon
5976	GM_109_B2_G06_T7	g3142328	BLASTN	415	9e-12	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5977	GM_109_B2_G09_T7	g421955	BLASTX	283	4e-24	44	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum] (AF022157) CYP71A10 [Glycine max] (AC002396) Hypothetical protein [Arabidopsis thaliana] (AF080118) contains similarity to reverse transcriptases (Pfam); rvt.hmm, score: 11.19 [Arabidopsis thaliana] M.fusca microsatellite DNA, MFGT27 region Glycine max BSR-101 satellite SB92 genomic sequence. Broad bean (V faba) BamHI repetitive element, 990 bp family. Pisum sativum repeated element highly similar to the BamHI repeated sequence families of Vicia faba Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECOR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens] (Y12432) polyprotein [Ananas comosus] Glycine max satellite STR120-A.3. (U96400) MRP-like ABC transporter [Arabidopsis thaliana] G.max gene for catalase Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. (AB007466) reverse transcriptase-like protein [Vicia faba] pol polyprotein homolog - fungus (Cladosporium fulvum) transposon CTT-1 (fragment) gi 2564 (Z11866) Reverse Transcriptase [Cladosporium fulvum] GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) gi 169965 (L11632) glutathione reductase [Glycine max] (AC005398) putative reverse-transcriptase [Arabidopsis thaliana] Glycine max gene for Bd 30K, complete cds Homo sapiens chromosome 17, clone HRP41C23, complete sequence [Homo sapiens] (AC005561) putative POL3 protein [Arabidopsis thaliana] Glycine max gene for Bd 30K, complete cds Cajanus cajan copia-like retrotransposon.Panzee
5978	GM_109_B2_H08_T7	g2738982	BLASTX	372	2e-33	79	
5979	GM_110_A2_A09_T7	g2829870	BLASTX	144	1e-16	60	
5980	GM_110_A2_D01_T7	g3513747	BLASTX	279	4e-22	53	
5981	GM_110_A2_D04_T7	g4138188	BLASTN	383	4e-11	68	
5982	GM_110_A2_E05_T7	g507910	BLASTN	350	3e-09	77	
5983	GM_110_A2_F03_T7	g170603	BLASTN	346	5e-09	71	
5984	GM_110_A2_F04_T7	g3821288	BLASTN	424	1e-12	65	
5985	GM_110_A2_F06_T7	g4126312	BLASTN	370	1e-09	74	
5986	GM_110_B2_A02_T7	g2995405	BLASTX	265	1e-38	53	
5987	GM_110_B2_A03_MR	g1142701	BLASTN	1394	1e-56	88	
5988	GM_110_B2_A03_T7	g2316024	BLASTX	154	2e-15	56	
5989	GM_110_B2_A04_T7	g18559	BLASTN	956	3e-36	77	
5990	GM_110_B2_A05_MR	g507910	BLASTN	581	1e-19	81	
5991	GM_110_B2_A05_T7	g507910	BLASTN	532	2e-17	80	
5992	GM_110_B2_A09_T7	g2522228	BLASTX	253	1e-20	45	
5993	GM_110_B2_B04_MR	g280492	BLASTX	171	7e-11	42	
5994	GM_110_B2_B07_T7	g1346192	BLASTX	189	2e-13	97	
5995	GM_110_B2_B11_T7	g3810595	BLASTX	112	5e-09	48	
5996	GM_110_B2_C04_T7	g3097320	BLASTN	1186	1e-46	83	
5997	GM_110_B2_C07_T7	g3184508	BLASTN	459	1e-13	65	
5998	GM_110_B2_C08_MR	g4063760	BLASTX	193	4e-13	41	
5999	GM_110_B2_C09_T7	g3097320	BLASTN	568	1e-18	73	
6000	GM_110_B2_C11_T7	g2832901	BLASTN	1114	2e-43	78	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6001	GM_110_B2_D04_T7	g629693	BLASTX	233	2e-18	46	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6002	GM_110_B2_D07_MR	g2618683	BLASTN	525	1e-16	67	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]
6003	GM_110_B2_D08_MR	g3142328	BLASTN	1086	3e-42	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB007466) reverse transcriptase-like protein [Vicia faba]
6004	GM_110_B2_D09_T7	g2522228	BLASTX	392	1e-35	76	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6005	GM_110_B2_D10_MR	g4063760	BLASTX	325	2e-31	58	(AL021710) putative protein [Arabidopsis thaliana]
6006	GM_110_B2_E01_T7	g2832657	BLASTX	250	8e-20	52	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana
6007	GM_110_B2_E03_MR	g99755	BLASTX	244	4e-19	49	retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
6008	GM_110_B2_E04_MR	g2244802	BLASTX	127	2e-13	57	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
6009	GM_110_B2_E08_T7	g3522943	BLASTX	113	1e-09	69	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
6010	GM_110_B2_E10_T7	g3142328	BLASTN	1189	6e-47	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6011	GM_110_B2_E11_T7	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence
6012	GM_110_B2_E12_T7	g1352460	BLASTX	117	2e-16	71	IN2-1 PROTEIN gi 100896 pir S17743 In2-1 protein - maize gi 22347 (X58573) In2-1 gene product [Zea mays]
6013	GM_110_B2_F01_T7	g3645899	BLASTX	224	5e-26	46	(U68408) 5' end not determined experimentally [Zea mays]
6014	GM_110_B2_F04_MR	g1142701	BLASTN	240	9e-21	74	Glycine max satellite STR120-A.3.
6015	GM_110_B2_F08_T7	g905361	BLASTX	203	1e-14	31	(U22103) gag-protease polyprotein [Glycine max]
6016	GM_110_B2_F10_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence
6017	GM_110_B2_F10_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence
6018	GM_110_B2_G08_MR	g4063756	BLASTN	404	3e-11	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
6019	GM_110_B2_G09_T7	g1431738	BLASTN	618	4e-21	80	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
6020	GM_110_B2_G10_T7	g3319362	BLASTX	464	3e-42	62	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6021	GM_110_B2_H01_MR	g3036807	BLASTX	460	8e-43	69	(AL022373) putative protein [Arabidopsis thaliana]
6022	GM_110_B2_H02_MR	g905361	BLASTX	530	6e-56	95	(U22103) gag-protease polyprotein [Glycine max]
6023	GM_110_B2_H08_T7	g2911280	BLASTX	162	5e-34	86	(U73937) PK12 protein kinase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
6024	GM_111_A1_A03_MR	g2996647	BLASTN	631	2e-21	66	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
6025	GM_111_A1_A03_T7	g1769898	BLASTX	303	2e-25	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6026	GM_111_A1_A06_MR	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6027	GM_111_A1_A06_T7	g4063760	BLASTX	202	4e-14	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6028	GM_111_A1_A07_T7	g3142328	BLASTN	441	6e-13	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6029	GM_111_A1_A12_T7	g3142328	BLASTN	1055	7e-41	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6030	GM_111_A1_B01_MR	g905361	BLASTX	817	1e-80	98	(U22103) gag-protease polyprotein [Glycine max]
6031	GM_111_A1_B02_MR	g905361	BLASTX	420	3e-38	98	(U22103) gag-protease polyprotein [Glycine max]
6032	GM_111_A1_B02_T7	g507910	BLASTN	432	6e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6033	GM_111_A1_B07_T7	g1669599	BLASTX	223	3e-26	63	(D88746) AR791 [Arabidopsis thaliana]
6034	GM_111_A1_B08_T7	g2522230	BLASTX	233	9e-19	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6035	GM_111_A1_B10_T7	g3334661	BLASTX	504	2e-47	72	(Y10490) putative cytochrome P450 [Glycine max]
6036	GM_111_A1_C02_MR	g3738312	BLASTX	183	8e-13	64	(AC005309) hypothetical protein [Arabidopsis thaliana]
6037	GM_111_A1_C02_T7	g3193284	BLASTX	569	2e-54	74	(AF069298) No definition line found [Arabidopsis thaliana]
6038	GM_111_A1_C03_MR	g2443320	BLASTX	167	3e-10	35	(D85597) polyprotein [Oryza australiensis]
6039	GM_111_A1_C03_T7	g4033838	BLASTX	293	1e-24	50	(Y18550) sigma-like factor [Arabidopsis thaliana]
6040	GM_111_A1_C04_MR	g975703	BLASTN	406	2e-11	84	P.sativum GR gene
6041	GM_111_A1_C08_T7	g3021268	BLASTX	92	7e-12	45	(AL022347) putative protein [Arabidopsis thaliana]
6042	GM_111_A1_C09_T7	g2702277	BLASTX	173	2e-11	33	(AC003033) putative cyclin g-associated kinase [Arabidopsis thaliana] gi 2914689 (AC003974) putative cyclin g-associated kinase [Arabidopsis thaliana]
6043	GM_111_A1_C10_MR	g3097320	BLASTN	479	1e-14	68	Glycine max gene for Bd 30K, complete cds
6044	GM_111_A1_C10_T7	g4006831	BLASTX	101	1e-09	33	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
6045	GM_111_A1_C12_MR	g4038056	BLASTX	384	9e-34	51	(AC005897) putative transposon [Arabidopsis thaliana]
6046	GM_111_A1_C12_T7	g4038056	BLASTX	356	9e-31	53	(AC005897) putative transposon [Arabidopsis thaliana]
6047	GM_111_A1_D02_T7	g3510264	BLASTX	379	3e-34	56	(AC005310) hypothetical protein, 5' partial [Arabidopsis thaliana]
6048	GM_111_A1_D03_MR	g2281085	BLASTX	211	2e-16	77	(AC002333) CTR1 protein kinase isolog [Arabidopsis thaliana]
6049	GM_111_A1_D05_MR	g507910	BLASTN	641	2e-22	87	Glycine max BSR-101 satellite SB92 genomic sequence.
6050	GM_111_A1_D05_T7	g3550435	BLASTN	480	1e-14	63	Hordeum vulgare Hotr1 gene
6051	GM_111_A1_D07_MR	g3645899	BLASTX	256	7e-20	47	(U06408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6052	GM_111_A1_D10_MR	g3319362	BLASTX	218	4e-17	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6053	GM_111_A1_D11_MR	g2665890	BLASTX	237	2e-18	75	(AF035944) calcium-dependent protein kinase [Fragaria x ananassa]
6054	GM_111_A1_D12_T7	g18768	BLASTN	374	1e-10	72	Soybean Tgm6 transposable element 3' end
6055	GM_111_A1_E03_MR	g1236920	BLASTN	262	7e-10	63	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
6056	GM_111_A1_E04_MR	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6057	GM_111_A1_E04_T7	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6058	GM_111_A1_E07_MR	g3746069	BLASTX	128	7e-17	41	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
6059	GM_111_A1_E08_T7	g507910	BLASTN	634	5e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
6060	GM_111_A1_E12_MR	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6061	GM_111_A1_E12_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6062	GM_111_A1_F01_MR	g99755	BLASTX	403	9e-37	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
6063	GM_111_A1_F03_MR	g3777527	BLASTX	134	7e-13	28	(AF053008) gag-pol polyprotein [Glycine max]
6064	GM_111_A1_F03_T7	g3097320	BLASTN	476	2e-14	67	Glycine max gene for Bd 30K, complete cds
6065	GM_111_A1_F07_MR	g2213598	BLASTX	191	9e-13	35	(AC000348) T7N9 18 [Arabidopsis thaliana]
6066	GM_111_A1_F09_MR	g1514643	BLASTX	178	2e-11	71	(Z70524) PDR5-like ABC transporter [Spiridella polytricha]
6067	GM_111_A1_F10_T7	g3599418	BLASTN	587	1e-19	79	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
6068	GM_111_A1_F11_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6069	GM_111_A1_G03_MR	g2842490	BLASTX	211	3e-16	78	(AL021749) heat-shock protein [Arabidopsis thaliana]
6070	GM_111_A1_G04_MR	g1946265	BLASTX	204	9e-16	82	(Y11414) myb [Oryza sativa]
6071	GM_111_A1_G04_T7	g3063469	BLASTX	179	2e-13	43	(AC003981) F22O13.31 [Arabidopsis thaliana]
6072	GM_111_A1_G06_MR	g18695	BLASTN	582	1e-19	87	Soybean nodulin 22 gene
6073	GM_111_A1_G06_T7	g3790188	BLASTX	228	5e-18	95	(Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana tabacum]
6074	GM_111_A1_G08_MR	g905361	BLASTX	215	7e-16	34	(U22103) gag-protease polyprotein [Glycine max]
6075	GM_111_A1_G09_MR	g2522228	BLASTX	266	4e-22	73	(AB007466) reverse transcriptase-like protein [Vicia faba]
6076	GM_111_A1_G09_T7	g3687234	BLASTX	191	6e-13	52	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
6077	GM_111_A1_G11_MR	g505129	BLASTN	380	3e-10	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6078	GM_111_A1_H01_MR	g3171159	BLASTN	358	4e-09	63	Homo sapiens chromosome 21q22.3 PAC 211.13, complete sequence [Homo sapiens]
6079	GM_111_A1_H02_MR	g18559	BLASTN	442	5e-13	64	G.max gene for catalase
6080	GM_111_A1_H04_MR	g3695395	BLASTX	186	2e-19	55	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6081	GM_111_A1_H04_T7	g3176788	BLASTN	422	7e-13	63	Homo sapiens allele 8 fragile site locus (FRA10B) minisatellite sequence
6082	GM_111_A1_H07_T7	g2582971	BLASTX	244	4e-28	77	(D83711) TKRP125 [Nicotiana tabacum]
6083	GM_111_A1_H11_T7	g3142328	BLASTN	697	1e-24	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6084	GM_111_A1_H12_MR	g4038056	BLASTX	186	8e-15	52	(AC005897) putative transposon [Arabidopsis thaliana]
6085	GM_111_A1_H12_T7	g2443320	BLASTX	327	2e-27	48	(D85597) polyprotein [Oryza australiensis]
6086	GM_111_A2_A04_T7	g3319366	BLASTX	166	1e-11	69	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
6087	GM_111_A2_A08_MR	g2791896	BLASTX	266	7e-21	57	(Y08997) 146kDa nuclear protein [Xenopus laevis]
6088	GM_111_A2_A11_MR	g3242785	BLASTX	219	2e-26	56	(AF055355) respiratory burst oxidase protein C [Arabidopsis thaliana]
6089	GM_111_A2_B04_MR	g4038056	BLASTX	207	3e-18	34	(AC005897) putative transposon [Arabidopsis thaliana]
6090	GM_111_A2_B04_T7	g3142328	BLASTN	1895	3e-79	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6091	GM_111_A2_B10_MR	g58340	BLASTN	376	4e-10	59	D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val
6092	GM_111_A2_B11_MR	g905361	BLASTX	266	2e-21	42	(U22103) gag-protease polyprotein [Glycine max]
6093	GM_111_A2_C02_T7	g100484	BLASTX	452	2e-41	54	hypothetical protein - garden snapdragon
6094	GM_111_A2_C03_T7	g4038056	BLASTX	283	6e-23	43	(AC005897) putative transposon [Arabidopsis thaliana]
6095	GM_111_A2_C04_T7	g2708743	BLASTX	187	2e-13	38	(AC003952) putative Tal-I-like reverse transcriptase [Arabidopsis thaliana]
6096	GM_111_A2_C09_MR	g2129618	BLASTX	311	7e-26	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6097	GM_111_A2_C12_T7	g4156188	BLASTN	385	2e-10	59	Homo sapiens clone DJ0784G16, complete sequence [Homo sapiens]
6098	GM_111_A2_D03_T7	g3687222	BLASTX	197	5e-15	37	(AC005169) hypothetical protein [Arabidopsis thaliana]
6099	GM_111_A2_D04_T7	g3097320	BLASTN	459	9e-14	71	Glycine max gene for Bd 30K, complete cds
6100	GM_111_A2_D07_T7	g3046704	BLASTX	147	8e-09	50	(AL022223) putative protein [Arabidopsis thaliana]
6101	GM_111_A2_D12_MR	g3142328	BLASTN	1590	3e-65	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
6102	GM_111_A2_E04_T7	g140292	BLASTX	131	1e-10	42	HYPOTHETICAL 21.5 KD PROTEIN (ORF 184) gi 82208 pir A05197 hypothetical protein 184 - common tobacco chloroplast gi 11843 (Z00044) hypothetical protein [Nicotiana tabacum] gi 225211 prf 1211235AR ORF 184 [Nicotiana tabacum] (AF053008) gag-pol polyprotein [Glycine max] (Z35598) Phosphoribosylformylglycinamide synthase; cDNA EST EMBL:D35229 comes from this gene; cDNA EST EMBL:D32558 comes from this gene; cDNA EST EMBL:D35376 comes from this gene; cDNA EST EMBL:D34213 comes from this gene;... (AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana] (AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana] (U96295) envelope-like [Glycine max] Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; MEB13, complete sequence [Arabidopsis thaliana] (AC005561) putative POL3 protein [Arabidopsis thaliana] (AF053008) gag-pol polyprotein [Glycine max] Human BAC clone GS200K05 from 7q21-q22, complete sequence [Homo sapiens] (D12839) reverse transcriptase [Glycine max] (AC002354) No definition line found [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana] Glycine max gene for Bd 30K, complete cds (Z94180) branched chain alpha-keto acid dehydrogenase E1-alpha subunit [Lycopersicon esculentum] Glycine max gene for Bd 30K, complete cds (AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana] Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence (Y08010) lectin receptor kinase [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. (Y08010) lectin receptor kinase [Arabidopsis thaliana]
6103	GM_111_A2_E07_T7	g3777527	BLASTX	784	5e-76	96	
6104	GM_111_A2_E11_T7	g3875706	BLASTX	101	5e-14	50	
6105	GM_111_A2_F01_T7	g2262107	BLASTX	156	8e-18	96	
6106	GM_111_A2_F03_T7	g3033400	BLASTX	147	2e-12	31	
6107	GM_111_A2_F09_T7	g3142330	BLASTX	149	2e-10	79	
6108	GM_111_A2_F11_T7	g2760169	BLASTN	824	3e-30	67	
6109	GM_111_A2_G02_MR	g4063760	BLASTX	153	7e-09	50	
6110	GM_111_A2_G02_T7	g3777527	BLASTX	736	7e-71	96	
6111	GM_111_A2_G04_T7	g2335067	BLASTN	375	7e-10	61	
6112	GM_111_A2_G08_T7	g218269	BLASTX	373	1e-33	86	
6113	GM_111_A2_G09_MR	g2558657	BLASTX	195	2e-13	39	
6114	GM_111_A2_G10_MR	g507910	BLASTN	620	2e-21	84	
6115	GM_111_A2_G11_MR	g3513745	BLASTX	205	3e-14	33	
6116	GM_111_A2_H02_T7	g3097320	BLASTN	1934	1e-80	84	
6117	GM_111_A2_H06_T7	g1945277	BLASTX	140	5e-16	77	
6118	GM_111_A2_H12_MR	g3097320	BLASTN	622	4e-21	80	
6119	GM_111_B1_A02_MR	g3650039	BLASTX	204	1e-14	35	
6120	GM_111_B1_A02_T7	g3142328	BLASTN	1281	4e-51	85	
6121	GM_111_B1_A06_MR	g1769899	BLASTX	163	2e-11	48	
6122	GM_111_B1_A08_MR	g507910	BLASTN	466	2e-14	77	
6123	GM_111_B1_A09_MR	g507910	BLASTN	610	6e-21	84	
6124	GM_111_B1_A10_T7	g1769898	BLASTX	365	3e-32	66	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6125	GM_111_B1_A12_T7	g1769898	BLASTX	355	4e-31	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6126	GM_111_B1_B01_T7	g2522228	BLASTX	176	4e-12	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
6127	GM_111_B1_B02_T7	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
6128	GM_111_B1_B03_MR	g1142701	BLASTN	1171	1e-46	81	Glycine max satellite STR120-A.3.
6129	GM_111_B1_B06_MR	g3128172	BLASTX	336	4e-29	48	(AC004521) hypothetical protein [Arabidopsis thaliana]
6130	GM_111_B1_B07_MR	g3777527	BLASTX	736	7e-71	95	(AF053008) gag-pol polyprotein [Glycine max]
6131	GM_111_B1_B12_T7	g4038056	BLASTX	209	5e-15	42	(AC005897) putative transposon [Arabidopsis thaliana]
6132	GM_111_B1_C01_MR	g2245104	BLASTX	427	6e-38	57	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
6133	GM_111_B1_C03_MR	g905361	BLASTX	614	4e-59	95	(U22103) gag-protease polyprotein [Glycine max]
6134	GM_111_B1_C03_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6135	GM_111_B1_C04_MR	g1666236	BLASTX	224	8e-18	29	(U76261) unknown [Hordeum vulgare]
6136	GM_111_B1_C05_MR	g1431738	BLASTN	412	1e-11	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
6137	GM_111_B1_D03_MR	g3142328	BLASTN	1181	1e-46	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6138	GM_111_B1_D04_T7	g3510344	BLASTN	447	4e-13	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]
6139	GM_111_B1_D06_MR	g905361	BLASTX	706	6e-69	93	(U22103) gag-protease polyprotein [Glycine max]
6140	GM_111_B1_D10_MR	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6141	GM_111_B1_D11_MR	g4063760	BLASTX	359	8e-31	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6142	GM_111_B1_E01_MR	g2129618	BLASTX	169	5e-12	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6143	GM_111_B1_E02_MR	g100484	BLASTX	404	3e-36	54	hypothetical protein - garden snapdragon
6144	GM_111_B1_E04_T7	g3930515	BLASTX	126	1e-11	40	(AF059674) putative gag protein [Nicotiana tabacum]
6145	GM_111_B1_E05_T7	g2642157	BLASTX	319	5e-27	91	(AC003000) ankyrin-like protein [Arabidopsis thaliana]
6146	GM_111_B1_E06_T7	g1769897	BLASTX	433	5e-40	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6147	GM_111_B1_E10_MR	g2522228	BLASTX	190	1e-13	78	(AB007466) reverse transcriptase-like protein [Vicia faba]
6148	GM_111_B1_F06_T7	g1769899	BLASTX	247	3e-20	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6149	GM_111_B1_F07_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6150	GM_111_B1_F08_MR	g3242789	BLASTX	251	2e-19	57	(AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]
6151	GM_111_B1_F12_MR	g3097320	BLASTN	369	1e-09	74	Glycine max gene for Bd 30K, complete cds
6152	GM_111_B1_G01_MR	g99922	BLASTX	660	5e-64	82	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
6153	GM_111_B1_G04_MR	g4063760	BLASTX	571	2e-53	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
6154	GM_111_B1_G10_MR	g629693	BLASTX	263	6e-22	48	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6155	GM_111_B1_H04_MR	g507910	BLASTN	362	9e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6156	GM_111_B1_H07_T7	g3482933	BLASTX	475	2e-43	83	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]
6157	GM_111_B1_H09_T7	g3810596	BLASTX	218	6e-16	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
6158	GM_111_B1_H11_T7	g3193221	BLASTN	468	4e-14	68	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6159	GM_111_B1_H12_T7	g4063760	BLASTX	299	2e-24	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6160	GM_111_B2_A02_T7	g3777527	BLASTX	458	3e-41	93	(AF053008) gag-pol polyprotein [Glycine max]
6161	GM_111_B2_A03_T7	g4063760	BLASTX	446	4e-40	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6162	GM_111_B2_A06_MR	g3777527	BLASTX	242	3e-18	38	(AF053008) gag-pol polyprotein [Glycine max]
6163	GM_111_B2_A07_T7	g3510505	BLASTX	193	3e-22	46	(AF030881) pol polyprotein [Fugu rubripes]
6164	GM_111_B2_A08_MR	g2673917	BLASTX	507	3e-46	84	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
6165	GM_111_B2_A09_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6166	GM_111_B2_A09_T7	g4063760	BLASTX	357	1e-30	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6167	GM_111_B2_A10_T7	g2244994	BLASTX	652	3e-63	81	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]
6168	GM_111_B2_A11_MR	g3097320	BLASTN	575	5e-19	79	Glycine max gene for Bd 30K, complete cds
6169	GM_111_B2_A11_T7	g2911040	BLASTX	176	2e-11	45	(AL021961) receptor protein kinase - like protein [Arabidopsis thaliana]
6170	GM_111_B2_B01_T7	g2982518	BLASTN	351	7e-09	63	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-07, complete sequence [Plasmodium falciparum]
6171	GM_111_B2_B07_MR	g905361	BLASTX	209	3e-15	36	(U22103) gag-protease polyprotein [Glycine max]
6172	GM_111_B2_B07_T7	g13610	BLASTN	359	2e-09	60	Yeast mitochondrial var1 gene (allele 40.0) a ribosomal protein >gi 343948 gb J01525 YSCMTVAR1 Yeast (S.cerevisiae) mitochondrial var1 gene, 40.0 allele.
6173	GM_111_B2_B09_T7	g2244994	BLASTX	215	8e-16	48	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]
6174	GM_111_B2_B11_MR	g629693	BLASTX	202	5e-15	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6175	GM_111_B2_C01_T7	g2995405	BLASTX	370	3e-32	50	(Y12432) polyprotein [Ananas comosus]
6176	GM_111_B2_C05_MR	g3695294	BLASTN	879	7e-33	92	Glycine max module-specific glutamine synthetase gene, complete cds
6177	GM_111_B2_C07_MR	g169984	BLASTN	418	4e-12	67	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.6-L).

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6178	GM_111_B2_C11_T7	g3171875	BLASTN	413	1e-11	65	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylamine Monooxygenase (N-Oxide 3, EC1.14.1... P-falcaparum 3.8 gene for putative serine kinase (partial) and GBP130 gene for glycoprotein binding protein (partial) (Z973336) retrovirus-related polypeptide homolog [Arabidopsis thaliana]
6179	GM_111_B2_D01_T7	g9837	BLASTN	349	9e-09	62	
6180	GM_111_B2_D02_MR	g2244802	BLASTX	353	4e-30	53	
6181	GM_111_B2_D06_MR	g3645899	BLASTX	212	3e-15	36	(U68408) 5' end not determined experimentally [Zea mays]
6182	GM_111_B2_D07_MR	g2995405	BLASTX	453	3e-41	59	(Y12432) polypeptide [Ananas comosus]
6183	GM_111_B2_E03_T7	g531389	BLASTX	351	8e-30	51	(U12626) copia-like retrotransposon Hopscotch polypeptide [Zea mays]
6184	GM_111_B2_E05_MR	g2708743	BLASTX	192	7e-14	40	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
6185	GM_111_B2_E09_MR	g13774	BLASTN	342	4e-12	62	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T. glabrata) mitochondrial gene for ribosomal protein VAR1.
6186	GM_111_B2_F10_T7	g1707007	BLASTX	180	5e-12	36	(U78721) hypothetical protein [Arabidopsis thaliana]
6187	GM_111_B2_F01_T7	g3097320	BLASTN	448	3e-13	72	Glycine max gene for Bd 30K, complete cds
6188	GM_111_B2_F12_MR	g3142328	BLASTN	823	3e-30	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase [Brassica napus]
6189	GM_111_B2_G05_T7	g1149595	BLASTX	180	7e-13	79	
6190	GM_111_B2_G10_MR	g4063760	BLASTX	424	9e-38	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6191	GM_111_B2_H02_MR	g4160362	BLASTN	313	2e-11	68	Saccharomyces cerevisiae complete mitochondrial genome
6192	GM_111_B2_H06_T7	g3142328	BLASTN	1131	3e-44	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6193	GM_112_A1_A03_MR	g1944341	BLASTN	350	8e-09	71	Soybean DNA for cysteine proteinase inhibitor, complete cds
6194	GM_112_A1_A03_T7	g2316016	BLASTX	200	9e-14	51	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
6195	GM_112_A1_A04_MR	g2129473	BLASTX	174	1e-12	39	arabinogalactan-like protein - loblolly pine gi 607774 (U095556) arabinogalactan-like protein [Pinus taeda]
6196	GM_112_A1_A05_MR	g2244803	BLASTX	226	4e-18	46	(Z973336) reverse transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6197	GM_112_A1_A06_T7	g130405	BLASTX	183	4e-12	37	RETROVIRUS-RELATED POL POLYPYRPTIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster] (AF053008) gag-pol polyprotein [Glycine max] (Y10099) P-glycoprotein homologue [Hordeum vulgare] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence Mus musculus phosphoenolpyruvate carboxykinase (PEPCK) gene, complete cds (Y12321) open reading frame 2 [Brassica oleracea] G.max N-20t gene G.max gene for catalase (U11034) ent-kaurene synthetase A [Arabidopsis thaliana] hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] (AB004906) transposase [Ipomoea purpurea] Glycine max cv. Dare nodulin 26 gene fragment. (AC003000) ankyrin-like protein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (Y08010) lectin receptor kinase [Arabidopsis thaliana] (AF060941) extra-large G-protein [Arabidopsis thaliana] (Y12432) polyprotein [Ananas comosus] Glycine max gene for Bd 30K, complete cds Human DNA sequence from cosmid U223G7, between markers DXS6791 and DXS8038 on chromosome X (AB007466) reverse transcriptase-like protein [Vicia faba] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB004906) transposase [Ipomoea purpurea] (Y08010) lectin receptor kinase [Arabidopsis thaliana]
6198	GM_112_A1_A09_T7	g3777527	BLASTX	651	8e-62	94	
6199	GM_112_A1_A10_MR	g2292907	BLASTX	235	1e-17	35	
6200	GM_112_A1_A11_T7	g3142328	BLASTN	600	4e-20	87	
6201	GM_112_A1_B06_MR	g4102181	BLASTN	350	9e-09	66	
6202	GM_112_A1_B11_T7	g2462936	BLASTX	316	1e-27	53	
6203	GM_112_A1_B12_T7	g18683	BLASTN	640	4e-22	72	
6204	GM_112_A1_C04_MR	g18559	BLASTN	398	5e-11	62	
6205	GM_112_A1_C12_MR	g571330	BLASTX	184	2e-12	56	
6206	GM_112_A1_D01_T7	g2129618	BLASTX	230	3e-17	43	
6207	GM_112_A1_D02_MR	g4063770	BLASTX	280	3e-30	51	
6208	GM_112_A1_D02_T7	g170029	BLASTN	371	9e-10	78	
6209	GM_112_A1_D03_T7	g2642157	BLASTX	212	2e-15	39	
6210	GM_112_A1_E01_T7	g507910	BLASTN	663	2e-23	86	
6211	GM_112_A1_E02_MR	g1769899	BLASTX	246	3e-20	68	
6212	GM_112_A1_E05_T7	g3201680	BLASTX	197	6e-31	59	
6213	GM_112_A1_E10_T7	g2995405	BLASTX	305	2e-27	57	
6214	GM_112_A1_F04_MR	g3097320	BLASTN	647	3e-22	77	
6215	GM_112_A1_F06_MR	g1524103	BLASTN	405	1e-12	61	
6216	GM_112_A1_G01_T7	g2522228	BLASTX	485	2e-45	63	
6217	GM_112_A1_G03_T7	g3142328	BLASTN	865	3e-32	74	
6218	GM_112_A1_G05_MR	g4063770	BLASTX	160	8e-10	43	
6219	GM_112_A1_G10_T7	g1769898	BLASTX	484	2e-45	69	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6220	GM_112_A1_G12_T7	g1346389	BLASTX	83	7e-09	75	KNOTTED-LIKE HOMEBOX PROTEIN 5 >gi 1045046 (X92394) KNAT5 homeobox protein [Arabidopsis thaliana]
6221	GM_112_A1_H03_T7	g4063760	BLASTX	283	2e-25	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6222	GM_112_A1_H11_T7	g3695395	BLASTX	181	3e-12	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6223	GM_112_B1_A01_MR	g2388577	BLASTX	212	3e-15	39	(AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb AC002329). [Arabidopsis thaliana]
6224	GM_112_B1_A02_MR	g3746069	BLASTX	204	3e-17	40	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
6225	GM_112_B1_A05_MR	g1488267	BLASTX	142	3e-13	70	(U57412) low affinity calcium antiporter CAX2 [Arabidopsis thaliana]
6226	GM_112_B1_A11_T7	g4038056	BLASTX	304	4e-25	47	(AC005897) putative transposon [Arabidopsis thaliana]
6227	GM_112_B1_A12_T7	g3599418	BLASTN	351	7e-09	86	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds (AF013294) No definition line found [Arabidopsis thaliana]
6228	GM_112_B1_B01_T7	g2252856	BLASTX	122	2e-11	53	G.max gene for catalase
6229	GM_112_B1_B02_MR	g18559	BLASTN	560	2e-18	70	(AB007467) retrotransposon-like gene, the first amino acid was determined to be leucine [Vicia faba]
6230	GM_112_B1_B02_T7	g2522230	BLASTX	297	1e-25	42	Glycine max gene for Bd 30K, complete cds (U22103) gag-protease polypeptide [Glycine max]
6231	GM_112_B1_B04_MR	g3097320	BLASTN	425	3e-12	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6232	GM_112_B1_B05_MR	g905361	BLASTX	351	1e-30	79	Glycine max gene for Bd 30K, complete cds (U22103) gag-protease polypeptide [Glycine max]
6233	GM_112_B1_B05_T7	g507910	BLASTN	398	2e-11	75	Glycine max gene for Bd 30K, complete cds (U22103) gag-protease polypeptide [Glycine max]
6234	GM_112_B1_B08_MR	g3097320	BLASTN	467	4e-14	71	Homo sapiens allele 7 fragile site locus (FRA10B) minisatellite sequence
6235	GM_112_B1_B10_T7	g905361	BLASTX	192	2e-13	35	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
6236	GM_112_B1_C01_T7	g3176784	BLASTN	383	5e-11	65	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
6237	GM_112_B1_C03_MR	g3810596	BLASTX	331	5e-28	42	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6238	GM_112_B1_C05_MR	g1431738	BLASTN	684	4e-24	83	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana]
6239	GM_112_B1_C06_MR	g629693	BLASTX	360	7e-38	54	Soybean (G.max) proline-rich cell wall protein (SbPRP3) gene, complete cds.
6240	GM_112_B1_C11_MR	g3142303	BLASTX	452	1e-40	62	Glycine max satellite STR120-B.1.
6241	GM_112_B1_C11_T7	g170067	BLASTN	367	1e-09	66	
6242	GM_112_B1_D02_MR	g1142703	BLASTN	277	2e-15	75	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
6243	GM_112_B1_D03_T7	g507910	BLASTN	350	3e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
6244	GM_112_B1_D06_MR	g905361	BLASTX	241	1e-18	39	(U22103) gag-protease polyprotein [Glycine max]
6245	GM_112_B1_D06_T7	g2522230	BLASTX	245	5e-20	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6246	GM_112_B1_D08_MR	g3985952	BLASTN	404	3e-11	77	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]
6247	GM_112_B1_D08_T7	g4038056	BLASTX	235	8e-18	38	(AC005897) putative transposon [Arabidopsis thaliana]
6248	GM_112_B1_E01_T7	g1335862	BLASTX	355	3e-30	71	(U42608) clathrin heavy chain [Glycine max]
6249	GM_112_B1_E02_MR	g4063760	BLASTX	251	3e-19	50	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6250	GM_112_B1_E05_T7	g3738294	BLASTX	315	2e-26	63	(AC005309) hypothetical protein [Arabidopsis thaliana]
6251	GM_112_B1_E07_MR	g1666236	BLASTX	169	1e-11	29	(U76261) unknown [Hordeum vulgare]
6252	GM_112_B1_E12_MR	g3810595	BLASTX	329	1e-29	52	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
6253	GM_112_B1_E12_T7	g2245109	BLASTX	202	6e-15	68	(Z97343) carboxyl-terminal proteinase homolog [Arabidopsis thaliana]
6254	GM_112_B1_F02_MR	g1480927	BLASTN	624	2e-21	85	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
6255	GM_112_B1_F02_T7	g3334667	BLASTX	295	7e-25	43	(Y10493) putative cytochrome P450 [Glycine max]
6256	GM_112_B1_F04_MR	g4138290	BLASTX	122	1e-14	82	(AJ005841) thioredoxin M [Oryza sativa]
6257	GM_112_B1_F05_MR	g3142328	BLASTN	1273	9e-51	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6258	GM_112_B1_F05_T7	g3510343	BLASTN	802	3e-29	78	like genes, partial cds, and long terminal repeat, complete sequence
6259	GM_112_B1_F06_T7	g2522230	BLASTX	200	3e-15	37	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]
6260	GM_112_B1_F11_MR	g99719	BLASTX	157	1e-17	50	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6261	GM_112_B1_F11_T7	g2979574	BLASTN	424	4e-12	66	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Tal-2 (strain Landsberg) (fragment) gi 16384 (X53976) orf 2 [Arabidopsis thaliana]
6262	GM_112_B1_G01_MR	g3738208	BLASTX	178	6e-20	55	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
6263	GM_112_B1_G03_T7	g3097320	BLASTN	576	5e-19	74	(AL031853) strong similarity to human Rev interacting protein Rip-1 [Schizosaccharomyces pombe]
6264	GM_112_B1_G04_MR	g3513747	BLASTX	163	9e-10	45	Glycine max gene for Bd 30K, complete cds (AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6265	GM_112_B1_G09_T7	g1703200	BLASTX	278	2e-32	88	PROTEIN KINASE AFC2 gi 601789 (U16177) protein kinase [Arabidopsis thaliana] gi 642130 gnl PID d1008809 (D45353) protein kinase [Arabidopsis thaliana] (Z97343) LTR retrotransposon [Arabidopsis thaliana]
6266	GM_112_B1_H05_MR	g2245104	BLASTX	218	8e-19	37	Glycine max BSR-101 satellite SB92 genomic sequence. (AC005171) putative gag-protease polyprotein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (AC003028) putative diphenol oxidase [Arabidopsis thaliana] (U68408) 5' end not determined experimentally [Zea mays] (AF000657) unknown protein [Arabidopsis thaliana] probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum] (AF053008) gag-pol polyprotein [Glycine max] probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum] Glycine max BSR-101 satellite SB92 genomic sequence. Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region TUBULIN BETA-1 CHAIN gi 16122 (X54852) beta-tubulin [Avena sativa] hypothetical protein - garden snapdragon (D83003) ORF(AA 1-1338) [Nicotiana tabacum] (AF053008) envelope-like [Glycine max] hypothetical protein - garden snapdragon hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA): pid.e150225 [Glycine max] (Z97337) hypothetical protein [Arabidopsis thaliana] Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana] G.max gene for catalase (U75248) reverse transcriptase [Gossypium barbadense]
6267	GM_112_B1_H06_T7	g507910	BLASTN	581	1e-19	81	
6268	GM_112_B1_H07_MR	g3779030	BLASTX	201	2e-15	36	
6269	GM_112_B1_H09_MR	g507910	BLASTN	393	4e-11	72	
6270	GM_112_B1_H10_T7	g3335357	BLASTX	308	4e-26	48	
6271	GM_113_A1_A09_T7	g3645899	BLASTX	290	2e-23	54	
6272	GM_113_A1_A10_T7	g2462826	BLASTX	198	1e-13	51	
6273	GM_113_A1_B10_T7	g629693	BLASTX	148	4e-09	41	
6274	GM_113_A1_C01_MR	g3777527	BLASTX	211	6e-15	72	
6275	GM_113_A1_C02_MR	g629693	BLASTX	90	6e-10	63	
6276	GM_113_A1_C04_MR	g507910	BLASTN	534	2e-17	78	
6277	GM_113_A1_C05_T7	g505129	BLASTN	353	5e-09	66	
6278	GM_113_A1_C12_T7	g135444	BLASTX	282	5e-24	86	
6279	GM_113_A1_D06_T7	g100484	BLASTX	252	9e-20	43	
6280	GM_113_A1_D12_MR	g1167523	BLASTX	297	4e-24	52	
6281	GM_113_A1_E10_MR	g3142379	BLASTX	208	2e-15	68	
6282	GM_113_A1_E11_T7	g100484	BLASTX	352	1e-30	57	
6283	GM_113_A1_F06_T7	g99922	BLASTX	348	4e-41	66	
6284	GM_113_A1_F09_MR	g2244859	BLASTX	166	1e-10	40	
6285	GM_113_A1_F10_T7	g2264312	BLASTN	413	1e-11	68	
6286	GM_113_A1_G09_T7	g18559	BLASTN	527	7e-17	71	
6287	GM_113_A1_H02_T7	g1658457	BLASTX	329	6e-29	70	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6288	GM_113_A1_H09_MR	g1465818	BLASTX	91	8e-10	94	(U64855) coded for by <i>C. elegans</i> cDNA CEES516F; coded for by <i>C. elegans</i> cDNA yk76b10.3; coded for by <i>C. elegans</i> cDNA yk14d4.3; coded for by <i>C. elegans</i> cDNA CEES516F; coded for by <i>C. elegans</i> cDNA yk49a11.5; coded for by <i>C. elegans</i> cDNA yk48c6...
6289	GM_113_A1_H10_T7	g2462936	BLASTX	160	5e-11	56	(Y12321) open reading frame 2 [Brassica oleracea]
6290	GM_113_A1_H12_T7	g3777527	BLASTX	533	3e-49	90	(AF053008) gag-pol polyprotein [Glycine max]
6291	GM_113_B1_A04_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6292	GM_113_B1_A04_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6293	GM_113_B1_A05_T7	g18559	BLASTN	991	6e-38	74	G.max gene for catalase
6294	GM_113_B1_A09_MR	g1000971	BLASTN	472	3e-14	65	Hansenula wingei mitochondrial DNA. complete sequence
6295	GM_113_B1_A10_T7	g2522226	BLASTN	544	1e-17	65	Vicia faba mRNA for reverse transcriptase-like protein. complete cds
6296	GM_113_B1_B03_T7	g2462058	BLASTX	209	8e-20	60	(Y13389) reverse transcriptase [Antirrhinum majus]
6297	GM_113_B1_B08_MR	g1480927	BLASTN	493	2e-15	78	Glycine max cdc2 protein kinase (cdc2(1)) nonprocessed pseudogene
6298	GM_113_B1_B11_MR	g100484	BLASTX	378	2e-33	53	hypothetical protein - garden snapdragon
6299	GM_113_B1_B12_T7	g4156188	BLASTN	357	4e-09	64	Homo sapiens clone D0784G16. complete sequence [Homo sapiens]
6300	GM_113_B1_C01_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6301	GM_113_B1_C03_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence
6302	GM_113_B1_C03_T7	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6303	GM_113_B1_C05_T7	g507910	BLASTN	593	3e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6304	GM_113_B1_C07_MR	g1170878	BLASTX	188	4e-13	80	MALATE SYNTHASE. GLYOXYSOMAL (MS) gi 170026 (L01629) malate synthase [Glycine max]
6305	GM_113_B1_C09_T7	g507910	BLASTN	378	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6306	GM_113_B1_D01_T7	g1142702	BLASTN	249	2e-12	71	Glycine max satellite STR120-A.4.
6307	GM_113_B1_D03_T7	g3777527	BLASTX	187	2e-12	36	(AF053008) gag-pol polyprotein [Glycine max]
6308	GM_113_B1_D04_MR	g3097320	BLASTN	476	2e-14	68	Glycine max gene for Bd 30K. complete cds
6309	GM_113_B1_E02_T7	g505129	BLASTN	423	4e-12	63	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
6310	GM_113_B1_E04_MR	g2642431	BLASTX	187	3e-13	52	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
6311	GM_113_B1_F04_T7	g1710587	BLASTX	121	4e-12	58	60S ACIDIC RIBOSOMAL PROTEIN P0 gi 1196897 (L46848) acidic ribosomal protein P0 [Glycine max]
6312	GM_113_B1_F01_MR	g3395938	BLASTX	134	4e-13	65	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6313	GM_113_B1_F02_T7	g3097320	BLASTN	431	2e-12	73	Glycine max gene for Bd 30K, complete cds
6314	GM_113_B1_F03_T7	g4115363	BLASTX	237	6e-18	45	(AC005957) putative disease resistance protein [Arabidopsis thaliana]
6315	GM_113_B1_F06_T7	g4063760	BLASTX	422	1e-37	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6316	GM_113_B1_G04_MR	g1769556	BLASTX	160	1e-10	62	(U81158) Forsythia x intermedia (+)-pinoselinol/(+)-laricresinol reductase (PLR) protein, complete sequence [Forsythia x intermedia]
6317	GM_113_B1_G07_T7	g3142328	BLASTN	1065	3e-41	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6318	GM_113_B1_G08_T7	g313723	BLASTN	353	2e-15	74	P.sativum hemC mRNA for hydroxymethylbilane synthase
6319	GM_113_B1_G11_T7	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6320	GM_113_B1_H08_MR	g1840106	BLASTN	415	2e-12	68	Human fragile site locus (FRA16B) minisatellite repeat
6321	GM_113_B1_H08_T7	g2462058	BLASTX	332	3e-29	52	(Y13389) reverse transcriptase [Antirrhinum majus]
6322	GM_113_B1_H09_MR	g1769898	BLASTX	235	4e-18	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6323	GM_113_B1_H10_T7	g226407	BLASTX	204	3e-14	39	retrotransposon dell-46 [Lilium henryi]
6324	GM_113_B2_A01_MR	g100484	BLASTX	405	3e-36	53	hypothetical protein - garden snapdragon
6325	GM_113_B2_A01_T7	g3097320	BLASTN	465	5e-14	69	Glycine max gene for Bd 30K, complete cds
6326	GM_113_B2_A03_T7	g629693	BLASTX	150	3e-09	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6327	GM_113_B2_A06_T7	g3097320	BLASTN	645	4e-22	79	Glycine max gene for Bd 30K, complete cds
6328	GM_113_B2_A07_T7	g18559	BLASTN	851	2e-31	72	G.max gene for catalase
6329	GM_113_B2_A12_MR	g507910	BLASTN	519	8e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
6330	GM_113_B2_B02_T7	g342952	BLASTN	331	7e-09	59	Glycine max BSR-101 satellite SB92 genomic sequence.
6331	GM_113_B2_B03_MR	g3746069	BLASTX	220	1e-17	40	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
6332	GM_113_B2_B08_MR	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6333	GM_113_B2_B09_T7	g100484	BLASTX	241	1e-18	52	hypothetical protein - garden snapdragon
6334	GM_113_B2_B11_T7	g4063760	BLASTX	243	2e-18	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6335	GM_113_B2_C03_MR	g2979597	BLASTN	438	9e-13	66	Homo sapiens PAC clone DJ1100F2.3 from 7q31, complete sequence [Homo sapiens]
6336	GM_113_B2_C07_MR	g454847	BLASTN	948	5e-36	74	Glycine max ribosomal protein S11 gene, complete cds
6337	GM_113_B2_C10_MR	g3650039	BLASTX	171	4e-11	35	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
6338	GM_113_B2_D01_MR	g2462936	BLASTX	288	2e-30	45	(Y12321) open reading frame 2 [Brassica oleracea]
6339	GM_113_B2_D09_MR	g3142379	BLASTX	266	6e-22	59	(AF053008) envelope-like [Glycine max]
6340	GM_113_B2_D11_MR	g2462134	BLASTX	333	4e-29	48	(Y13368) reverse transcriptase [Beta vulgaris]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6341	GM_113_B2_E02_MR	g4092471	BLASTN	492	3e-15	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
6342	GM_113_B2_E03_MR	g3319362	BLASTX	188	4e-25	59	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6343	GM_113_B2_F01_MR	g4063760	BLASTX	267	5e-21	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6344	GM_113_B2_F05_T7	g2495365	BLASTX	173	3e-11	49	HEAT SHOCK PROTEIN 81-2 (HSP81-2) gi 445127 prf 1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]
6345	GM_113_B2_F06_T7	g3449315	BLASTN	481	1e-14	73	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]
6346	GM_113_B2_F07_MR	g1666236	BLASTX	238	2e-19	33	(U76261) unknown [Hordeum vulgare]
6347	GM_113_B2_F09_MR	g2832611	BLASTN	391	1e-10	66	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)
6348	GM_113_B2_F10_MR	g2129648	BLASTX	369	3e-33	72	MYB-related protein 33.3K - Arabidopsis thaliana gi 1263095 gnl PID e197888 (Z54136) MYB-related protein [Arabidopsis thaliana]
6349	GM_113_B2_G07_T7	g18559	BLASTN	769	8e-28	72	G.max gene for catalase
6350	GM_113_B2_G08_MR	g1769897	BLASTX	257	1e-20	37	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6351	GM_113_B2_G09_MR	g1769898	BLASTX	201	4e-28	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6352	GM_113_B2_G11_MR	g3645899	BLASTX	114	5e-19	56	(U08408) 5' end not determined experimentally [Zea mays]
6353	GM_113_B2_H02_MR	g2522228	BLASTX	277	2e-23	48	(AB007466) reverse transcriptase-like protein [Vicia faba]
6354	GM_113_B2_H03_MR	g2443320	BLASTX	383	3e-33	48	(D85597) polyprotein [Oryza australiensis]
6355	GM_113_B2_H04_T7	g2398853	BLASTX	176	9e-12	58	(AB004822) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana]
6356	GM_113_B2_H06_MR	g2129618	BLASTX	233	2e-17	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6357	GM_113_B2_H08_MR	g2801423	BLASTN	358	4e-09	64	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
6358	GM_113_B2_H11_MR	g2465923	BLASTX	189	8e-13	52	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
6359	GM_113_B2_H12_MR	g2522227	BLASTX	278	1e-23	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
6360	GM_114_A1_A03_MR	g2213582	BLASTX	177	2e-24	45	(AC000348) T7N9.2 [Arabidopsis thaliana]
6361	GM_114_A1_A04_MR	g3176965	BLASTX	121	7e-15	82	(AF067967) pyrroline-5-carboxylate synthetase [Mesembryanthemum crystallinum]
6362	GM_114_A1_A11_MR	g2995405	BLASTX	367	6e-32	59	(Y12432) polyprotein [Ananas comosus]
6363	GM_114_A1_A12_T7	g3097320	BLASTN	438	9e-13	74	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6364	GM_114_A1_B03_MR	g3930515	BLASTX	117	6e-14	47	(AF059674) putative gag protein [Nicotiana tabacum]
6365	GM_114_A1_B03_T7	g3645899	BLASTX	226	6e-24	51	(U68408) 5' end not determined experimentally [Zea mays]
6366	GM_114_A1_B04_T7	g2129618	BLASTX	211	4e-15	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6367	GM_114_A1_B05_T7	g505129	BLASTN	397	5e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
6368	GM_114_A1_B09_T7	g3264544	BLASTN	378	5e-10	65	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
6369	GM_114_A1_C02_MR	g4006831	BLASTX	174	3e-15	34	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
6370	GM_114_A1_C03_MR	g2244802	BLASTX	219	2e-28	43	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
6371	GM_114_A1_C03_T7	g2522228	BLASTX	453	4e-42	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
6372	GM_114_A1_C07_MR	g4160362	BLASTN	421	6e-12	62	Saccharomyces cerevisiae complete mitochondrial genome
6373	GM_114_A1_C08_MR	g507910	BLASTN	462	3e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6374	GM_114_A1_C09_T7	g2655926	BLASTX	94	6e-11	60	(Y09057) sf21 [Helianthus annuus]
6375	GM_114_A1_C11_T7	g507910	BLASTN	529	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
6376	GM_114_A1_D10_MR	g508826	BLASTN	359	3e-09	63	Drosophila melanogaster Oregon-R mitochondrial A+T region.
6377	GM_114_A1_E01_T7	g507910	BLASTN	368	5e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6378	GM_114_A1_E03_T7	g3097320	BLASTN	1190	7e-47	80	Glycine max gene for Bd 30K, complete cds
6379	GM_114_A1_E04_MR	g2579858	BLASTN	392	1e-11	62	Homo sapiens genomic DNA, 21q region, clone: S39BG29
6380	GM_114_A1_E04_T7	g2213602	BLASTX	205	8e-15	56	(AC000348) T7N9.22 [Arabidopsis thaliana]
6381	GM_114_A1_E05_MR	g4063760	BLASTX	315	4e-26	58	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6382	GM_114_A1_E07_MR	g4050011	BLASTN	719	2e-25	66	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
6383	GM_114_A1_E09_T7	g2462936	BLASTX	201	4e-29	49	(Y12321) open reading frame 2 [Brassica oleracea]
6384	GM_114_A1_F01_MR	g4049647	BLASTN	351	8e-09	62	Melanoplus sanguinipes entomopoxvirus, complete genome
6385	GM_114_A1_F03_MR	g507910	BLASTN	445	2e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6386	GM_114_A1_F03_T7	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6387	GM_114_A1_F04_MR	g2191194	BLASTX	190	3e-14	56	(AF007271) contains weak to the SAPB protein (TR:E236624) [Arabidopsis thaliana]
6388	GM_114_A1_F07_MR	g100484	BLASTX	310	5e-26	46	hypothetical protein - garden snapdragon
6389	GM_114_A1_G05_MR	g478148	BLASTX	379	3e-34	83	reverse transcriptase (copia-like retrotransposon) - soybean (fragment) >gi 169949 (M94493) reverse transcriptase [Glycine max]
6390	GM_114_A1_G07_T7	g2462058	BLASTX	285	2e-24	55	(Y13389) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
6391	GM_114_A1_G09_MR	g421954	BLASTX	191	3e-13	44	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
6392	GM_114_A1_G11_MR	g18559	BLASTN	823	3e-30	74	G.max gene for catalase
6393	GM_114_A1_G12_MR	g2914700	BLASTX	289	7e-46	84	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]
6394	GM_114_A1_H01_MR	g18559	BLASTN	1009	1e-38	75	G.max gene for catalase
6395	GM_114_A1_H07_MR	g3377848	BLASTX	200	1e-14	44	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
6396	GM_114_A1_H10_MR	g478148	BLASTX	416	3e-38	87	reverse transcriptase (copa-like retrotransposon) - soybean (fragment) >gi 169949 (M94493) reverse transcriptase [Glycine max]
6397	GM_114_A1_H12_T7	g547683	BLASTX	135	5e-15	64	HEAT SHOCK COGNATE PROTEIN 80 gi 170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] gi 445601 prf1909348A heat shock protein hsp80 [Lycopersicon esculentum] (Y12432) polyprotein [Ananas comosus]
6398	GM_114_B1_A01_T7	g2995405	BLASTX	191	1e-24	56	Glycine max BSR-101 satellite SB92 genomic sequence.
6399	GM_114_B1_A04_T7	g507910	BLASTN	420	2e-12	74	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
6400	GM_114_B1_A05_T7	g505129	BLASTN	371	1e-12	71	(U76261) unknown [Hordeum vulgare]
6401	GM_114_B1_A08_T7	g1666236	BLASTX	196	1e-14	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6402	GM_114_B1_A12_MR	g4063760	BLASTX	478	1e-43	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6403	GM_114_B1_B01_T7	g1769898	BLASTX	310	3e-26	48	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1
6404	GM_114_B1_B02_T7	g136636	BLASTX	189	4e-14	88	(UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER (UBIQUITIN 1) gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana Ubiquitin Conjugation. Ligase Mol_id: 1; Molecule: Ubiquitin Conjugating Enzyme; Chain: Null; Synonym: Ubc1; Ec: 6.3.2.19; Engineered: Yes gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] gi 431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]
6405	GM_114_B1_B10_T7	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6406	GM_114_B1_C03_MR	g3097320	BLASTN	724	9e-26	75	Glycine max gene for Bd 30K. complete cds
6407	GM_114_B1_C04_MR	g18559	BLASTN	982	2e-37	73	G.max gene for catalase
6408	GM_114_B1_C05_T7	g2995405	BLASTX	293	5e-24	44	(Y12432) polyprotein [Ananas comosus]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	% Ident	Description
6409	GM_114_B1_C11_MR	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6410	GM_114_B1_D10_T7	g4038056	BLASTX	392	1e-34	54	(AC005897) putative transposon [Arabidopsis thaliana]
6411	GM_114_B1_D12_T7	g387902	BLASTX	145	1e-12	51	(L23524) ORF [Hordeum vulgare]
6412	GM_114_B1_E01_MR	g13619	BLASTN	489	4e-16	66	Saccharomyces douglasi mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
6413	GM_114_B1_E02_MR	g629693	BLASTX	154	1e-09	48	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6414	GM_114_B1_E03_MR	g2443320	BLASTX	492	6e-45	63	(D85597) polyprotein [Oryza australiensis]
6415	GM_114_B1_E04_MR	g4006831	BLASTX	245	1e-18	34	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
6416	GM_114_B1_E09_T7	g4038056	BLASTX	335	2e-28	48	(AC005897) putative transposon [Arabidopsis thaliana]
6417	GM_114_B1_E10_MR	g3777527	BLASTX	713	2e-68	95	(AF053008) gag-pol polyprotein [Glycine max]
6418	GM_114_B1_F01_T7	g2623307	BLASTX	151	8e-09	65	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]
6419	GM_114_B1_F07_MR	g4063760	BLASTX	467	2e-42	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6420	GM_114_B1_F08_MR	g4063760	BLASTX	556	7e-52	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6421	GM_114_B1_F08_T7	g2244915	BLASTX	260	2e-20	48	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
6422	GM_114_B1_F10_MR	g507910	BLASTN	567	5e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6423	GM_114_B1_G01_T7	g1769898	BLASTX	247	1e-25	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6424	GM_114_B1_G03_MR	g3892061	BLASTX	130	3e-09	34	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
6425	GM_114_B1_G12_MR	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6426	GM_116_B2_A05_T7	g100484	BLASTX	245	5e-19	53	hypothetical protein - garden snapdragon
6427	GM_116_B2_B02_MR	g2864621	BLASTX	129	2e-16	52	hypothetical protein [Arabidopsis thaliana]
6428	GM_116_B2_B12_T7	g130582	BLASTX	293	7e-28	56	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
6429	GM_116_B2_C02_T7	g3845197	BLASTN	363	2e-09	66	(TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
6430	GM_116_B2_C04_T7	g2828293	BLASTX	220	4e-16	72	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
6431	GM_116_B2_C08_T7	g3142328	BLASTN	573	6e-19	71	(AL021687) putative protein [Arabidopsis thaliana]
6432	GM_116_B2_D04_T7	g4115920	BLASTX	321	4e-27	44	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF118222) similar to the subtilase family of serine proteases (Pfam: PF00082, score; 45.8, E=1.1e-11, n=2) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6433	GM_116_B2_D08_T7	g14293	BLASTN	342	3e-09	63	Yeast R0.54 mutant mitochondrial DNA lacking ori1 sequence recombination junction with tRNA-Pro and 15S rRNA genes
6434	GM_116_B2_D10_MR	g2384672	BLASTN	363	1e-09	73	Arabidopsis thaliana putative potassium transporter AtKT3p (AtKT3) mRNA, partial cds.
6435	GM_116_B2_E01_T7	g2462134	BLASTX	167	7e-11	29	(Y13368) reverse transcriptase [Beta vulgaris]
6436	GM_116_B2_E02_MR	g3142328	BLASTN	1011	7e-39	78	Glycine max partial SIRE-1 sequence ribonuclease II and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6437	GM_116_B2_E03_T7	g2764526	BLASTN	429	2e-12	62	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
6438	GM_116_B2_E05_T7	g3777527	BLASTX	420	3e-58	93	(AF053008) gag-pol polyprotein [Glycine max]
6439	GM_116_B2_E06_MR	g1326016	BLASTX	154	5e-09	41	TY3-2 orfB
6440	GM_116_B2_E08_MR	g1086625	BLASTX	106	2e-12	48	(U41012) Similar to aminoacylase-1, [Caenorhabditis elegans]
6441	GM_116_B2_E08_T7	g2121303	BLASTN	447	4e-13	67	Homo sapiens cosmid Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
6442	GM_116_B2_E11_MR	g18559	BLASTN	961	2e-36	78	G.max gene for catalase
6443	GM_116_B2_E11_T7	g1769897	BLASTX	170	4e-11	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6444	GM_116_B2_F02_MR	g3282170	BLASTN	730	6e-26	71	Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana]
6445	GM_116_B2_F05_MR	g527618	BLASTN	370	2e-21	84	Glycine max 3-methylcrotonyl-CoA carboxylase mRNA, biotin-carrier domain, partial cds.
6446	GM_116_B2_F07_T7	g13583	BLASTN	286	2e-09	68	Yeast mitochondrial ori(o) repeat unit of petite mutant 5 (petite strain s-10/7/2)
6447	GM_116_B2_G01_MR	g2369714	BLASTX	467	4e-47	70	(Z97178) elongation factor 2 [Beta vulgaris]
6448	GM_116_B2_G04_T7	g3273111	BLASTN	382	3e-10	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-09, complete sequence [Plasmodium falciparum] (U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
6449	GM_116_B2_H03_MR	g1184075	BLASTX	209	7e-15	48	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans])
6450	GM_116_B2_H03_T7	g2429543	BLASTX	150	4e-14	54	G.max gene for catalase
6451	GM_116_B2_H09_T7	g18559	BLASTN	1055	8e-41	78	(AJ007366) calcium-dependent protein kinase [Zea mays]
6452	GM_116_B2_H12_T7	g3320104	BLASTX	179	5e-12	77	Soybean DNA for nodulin 35, partial cds
6453	GM_117_B1_A01_T7	g1944188	BLASTN	568	4e-19	74	Arabidopsis thaliana chromosome IV map near 2.1 cM, complete sequence [Arabidopsis thaliana]
6454	GM_117_B1_A07_MR	g4092471	BLASTN	482	1e-14	66	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6455	GM_117_B1_B02_MR	g1402878	BLASTX	370	2e-33	65	(X98130) unknown [Arabidopsis thaliana]
6456	GM_117_B1_B04_T7	g3319362	BLASTX	275	5e-22	47	(AF077408) contains similarity to reverse transcriptase (PFam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6457	GM_117_B1_B08_T7	g4063770	BLASTX	222	2e-16	39	(AB004906) transposase [Ipomoea purpurea]
6458	GM_117_B1_B09_MR	g1666236	BLASTX	194	2e-14	28	(U76261) unknown [Hordeum vulgare]
6459	GM_117_B1_B09_T7	g2995405	BLASTX	196	1e-13	38	(Y12432) polyprotein [Ananas comosus]
6460	GM_117_B1_C02_T7	g100484	BLASTX	228	1e-30	55	hypothetical protein - garden snapdragon
6461	GM_117_B1_C03_T7	g507910	BLASTN	657	4e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
6462	GM_117_B1_C05_T7	g4063760	BLASTX	261	2e-20	50	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6463	GM_117_B1_C06_MR	g507910	BLASTN	623	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
6464	GM_117_B1_C06_T7	g4063760	BLASTX	280	2e-22	55	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6465	GM_117_B1_C07_T7	g226407	BLASTX	518	1e-47	64	retrotransposon del1-46 [Lilium henryi]
6466	GM_117_B1_C09_MR	g4063760	BLASTX	459	2e-41	59	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6467	GM_117_B1_C09_T7	g905361	BLASTX	176	1e-11	30	(U22103) gag-protease polyprotein [Glycine max]
6468	GM_117_B1_D01_MR	g507910	BLASTN	429	9e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
6469	GM_117_B1_D01_T7	g507910	BLASTX	390	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6470	GM_117_B1_D03_MR	g4063760	BLASTX	295	5e-24	53	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6471	GM_117_B1_D03_T7	g507910	BLASTN	678	5e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
6472	GM_117_B1_D09_MR	g1619300	BLASTX	119	9e-09	40	(X95269) LRR protein [Lycopersicon esculentum]
6473	GM_117_B1_D11_T7	g3695294	BLASTN	447	3e-13	78	Glycine max nodule-specific glutamine synthetase gene, complete cds
6474	GM_117_B1_E02_T7	g3319351	BLASTX	338	2e-28	47	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
6475	GM_117_B1_E04_T7	g629693	BLASTX	372	1e-33	51	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6476	GM_117_B1_E10_MR	g507910	BLASTN	388	6e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6477	GM_117_B1_E10_T7	g507910	BLASTN	407	9e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6478	GM_117_B1_E12_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6479	GM_117_B1_E12_T7	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6480	GM_117_B1_F01_MR	g4115365	BLASTX	173	6e-11	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
6481	GM_117_B1_F01_T7	g3810596	BLASTX	322	4e-28	53	(AC005398) reverse transcriptase-like protein [Arabidopsis thaliana]
6482	GM_117_B1_F02_T7	g1352316	BLASTX	150	5e-10	76	DR1 PROTEIN HOMOLOG gi 633026 gnl PID d1007866 (D38110)
6483	GM_117_B1_F08_T7	g3142379	BLASTX	175	6e-12	64	Dr1 [Arabidopsis thaliana]
6484	GM_117_B1_F11_MR	g4063760	BLASTX	388	3e-35	60	(AF053008) envelope-like [Glycine max] (AC005561) putative POL.3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6485	GM_117_B1_G01_MR	g2288886	BLASTN	397	4e-11	80	Arabidopsis thaliana mRNA for mevalonate diphosphate decarboxylase.
6486	GM_117_B1_G05_T7	g421953	BLASTX	105	3e-10	40	hypothetical protein 2 - potato transposon Tst1 gi 21432 (X52387) ORF2 [Solanum tuberosum]
6487	GM_117_B1_G10_MR	g18695	BLASTN	347	9e-09	67	Soybean nodulin 22 gene
6488	GM_117_B1_H04_T7	g4140712	BLASTX	154	2e-10	38	(AF110183) putative integrase [Oryza sativa]
6489	GM_117_B1_H07_T7	g18559	BLASTN	896	1e-33	70	G.max gene for catalase
6490	GM_117_B1_H08_MR	g4115365	BLASTX	202	1e-23	41	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
6491	GM_117_B1_H09_MR	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
6492	GM_117_B1_H09_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6493	GM_117_B2_A02_MR	g3219937	BLASTX	159	2e-10	40	HYPOTHETICAL 35.1 KD PROTEIN C57A10.07 IN CHROMOSOME 1 gi 2058374 gnl PID e313998 (Z794864) unknown [Schizosaccharomyces pombe]
6494	GM_117_B2_A08_T7	g3979928	BLASTN	372	9e-10	64	Caenorhabditis elegans cosmid Y18D10A, complete sequence
6495	GM_117_B2_A12_MR	g3738114	BLASTN	365	2e-09	63	[Caenorhabditis elegans]
6496	GM_117_B2_B03_MR	g99755	BLASTX	356	2e-31	55	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
6497	GM_117_B2_B08_MR	g2244881	BLASTX	164	1e-15	40	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Tal-1 (fragment) gi 163556 (X53973) reverse transcriptase [Arabidopsis thaliana]
6498	GM_117_B2_C02_MR	g3426334	BLASTN	348	1e-08	62	(Z97338) PDR5-like ABC transporter [Arabidopsis thaliana]
6499	GM_117_B2_C04_T7	g3142328	BLASTN	461	7e-14	88	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
6500	GM_117_B2_C05_T7	g1142701	BLASTN	1292	5e-52	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6501	GM_117_B2_D01_MR	g100484	BLASTX	348	4e-30	59	Glycine max satellite STR120-A.3.
6502	GM_117_B2_D03_MR	g1666236	BLASTX	164	6e-11	34	hypothetical protein - garden snapdragon (U76261) unknown [Hordeum vulgare]
6503	GM_117_B2_D05_T7	g3810596	BLASTX	247	5e-19	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
6504	GM_117_B2_D06_MR	g507910	BLASTN	396	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6505	GM_117_B2_D07_T7	g3645899	BLASTX	316	3e-26	49	(U68408) 5' end not determined experimentally [Zea mays]
6506	GM_117_B2_D09_MR	g507910	BLASTX	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6507	GM_117_B2_D10_T7	g507910	BLASTN	411	6e-12	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6508	GM_117_B2_E01_MR	g3097320	BLASTN	573	3e-19	72	Glycine max gene for Bd 30K, complete cds
6509	GM_117_B2_E02_T7	g4063760	BLASTX	231	4e-17	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6510	GM_117_B2_E04_T7	g4063760	BLASTX	189	3e-24	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6511	GM_117_B2_E11_T7	g130582	BLASTX	160	1e-09	35	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF: [Nicotiana tabacum]
6512	GM_117_B2_F01_T7	g3695395	BLASTX	128	1e-15	55	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6513	GM_117_B2_F02_T7	g3953466	BLASTX	164	3e-10	58	(AC002328) F20N2.11 [Arabidopsis thaliana]
6514	GM_117_B2_F03_T7	g2443320	BLASTX	234	2e-17	47	(D85597) polyprotein [Oryza australiensis]
6515	GM_117_B2_F05_T7	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
6516	GM_117_B2_F07_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6517	GM_117_B2_F08_T7	g3777527	BLASTX	469	5e-43	96	(AF053008) gag-pol polyprotein [Glycine max]
6518	GM_117_B2_F09_MR	g4063770	BLASTX	166	2e-10	43	(AB004906) transposase [Ipomoea purpurea]
6519	GM_117_B2_F10_MR	g18559	BLASTN	787	1e-28	76	G.max gene for catalase
6520	GM_117_B2_F11_T7	g4063760	BLASTX	319	2e-26	63	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6521	GM_117_B2_F12_MR	g507910	BLASTN	433	6e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6522	GM_117_B2_G02_MR	g3033375	BLASTX	329	2e-31	49	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
6523	GM_117_B2_G02_T7	g3688209	BLASTX	157	9e-10	68	(AJ010093) MAP3K beta 1 protein kinase [Brassica napus]
6524	GM_117_B2_G03_MR	g3785991	BLASTX	242	5e-19	65	(AC005560) putative MAP kinase [Arabidopsis thaliana]
6525	GM_117_B2_G06_MR	g1769898	BLASTX	332	1e-28	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6526	GM_117_B2_G11_MR	g421955	BLASTX	350	3e-31	57	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
6527	GM_117_B2_G11_T7	g4063760	BLASTX	254	1e-19	48	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6528	GM_117_B2_G12_MR	g3548808	BLASTX	556	5e-53	81	(AC005313) unknown protein [Arabidopsis thaliana]
6529	GM_117_B2_H01_MR	g18559	BLASTN	629	2e-21	73	G.max gene for catalase
6530	GM_117_B2_H01_T7	g3142328	BLASTN	722	1e-25	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6531	GM_117_B2_H04_T7	g3738114	BLASTN	355	5e-09	64	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
6532	GM_117_B2_H06_T7	g4063760	BLASTX	259	4e-20	56	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6533	GM_117_B2_H07_MR	g3108025	BLASTN	407	2e-11	71	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]
6534	GM_117_B2_H08_MR	g3142328	BLASTN	1014	5e-39	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6535	GM_117_B2_H11_T7	g3341443	BLASTX	156	2e-10	90	(AJ223074) acid phosphatase [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6536	GM_118_A1_A03_MR	g3142328	BLASTN	998	3e-38	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana] (U94784) unconventional myosin [Helianthus annuus] (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza] Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-14, complete sequence [Plasmodium falciparum] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR gi 479738 pir S35270 hypothetical protein - Arabidopsis thaliana gi 166926 (L11367) [Arabidopsis thaliana] unidentified mRNA sequence, complete cds,], gene product [Arabidopsis thaliana]
6537	GM_118_A1_A04_T7	g3810596	BLASTX	291	9e-24	47	(AL021687) putative protein [Arabidopsis thaliana]
6538	GM_118_A1_A08_MR	g2444178	BLASTX	181	9e-12	70	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]
6539	GM_118_A1_A08_T7	g1514643	BLASTX	210	8e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6540	GM_118_A1_A09_T7	g2982521	BLASTN	378	5e-10	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
6541	GM_118_A1_B02_T7	g3142328	BLASTN	1576	1e-64	85	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
6542	GM_118_A1_B09_T7	g1169198	BLASTX	151	9e-10	77	hypothetical protein - garden snapdragon (U76261) unknown [Hordeum vulgare]
6543	GM_118_A1_B12_T7	g2828293	BLASTX	213	2e-15	70	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
6544	GM_118_A1_C07_T7	g3046855	BLASTN	379	4e-10	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
6545	GM_118_A1_C09_T7	g507910	BLASTN	595	3e-20	83	Glycine max gene for Bd 30K, complete cds (U22103) gag-protease polyprotein [Glycine max]
6546	GM_118_A1_C10_MR	g505129	BLASTN	359	3e-09	71	(Y15366) cycloartenol synthase [Medicago truncatula] (D12839) reverse transcriptase [Glycine max] probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6547	GM_118_A1_D02_T7	g99922	BLASTX	630	7e-61	76	Glycine max BSR-101 satellite SB92 genomic sequence.
6548	GM_118_A1_D06_T7	g100484	BLASTX	375	5e-33	60	Glycine max BSR-101 satellite SB92 genomic sequence.
6549	GM_118_A1_D07_MR	g1666236	BLASTX	180	9e-13	30	Glycine max BSR-101 satellite SB92 genomic sequence.
6550	GM_118_A1_D07_T7	g99922	BLASTX	232	1e-18	60	(AL020223) putative protein [Arabidopsis thaliana]
6551	GM_118_A1_D09_MR	g3097320	BLASTN	884	5e-33	76	
6552	GM_118_A1_E03_MR	g905361	BLASTX	239	2e-18	41	
6553	GM_118_A1_E08_T7	g2598587	BLASTX	123	4e-16	92	
6554	GM_118_A1_E09_T7	g218269	BLASTX	190	3e-14	71	
6555	GM_118_A1_E12_T7	g629693	BLASTX	343	2e-30	50	
6556	GM_118_A1_F11_MR	g507910	BLASTN	375	2e-10	78	
6557	GM_118_A1_F11_T7	g507910	BLASTN	568	5e-19	79	
6558	GM_118_A1_G04_MR	g2924523	BLASTX	221	4e-18	36	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6559	GM_118_A1_G08_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6560	GM_118_A1_G09_T7	g4063760	BLASTX	424	9e-38	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6561	GM_118_A1_G11_T7	g4063760	BLASTX	314	5e-26	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6562	GM_118_A1_G12_MR	g507910	BLASTN	425	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
6563	GM_118_A1_H12_T7	g99726	BLASTX	111	3e-13	56	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976)
6564	GM_118_A2_A02_MR	g3142328	BLASTN	723	9e-26	73	orf 3 [Arabidopsis thaliana]
6565	GM_118_A2_A05_T7	g950319	BLASTX	252	1e-19	37	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (M11240) unknown protein [Drosophila melanogaster]
6566	GM_118_A2_B01_MR	g507910	BLASTN	537	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6567	GM_118_A2_B03_T7	g3097320	BLASTN	466	5e-14	70	Glycine max gene for Bd 30K, complete cds
6568	GM_118_A2_B07_T7	g1346790	BLASTX	115	3e-09	68	PATHOGENESIS-RELATED HOMEODOMAIN PROTEIN (PRHA) gi 507220 (L21991) homeodomain protein [Arabidopsis thaliana] gi 2501810 (U48864) PRHA [Arabidopsis thaliana] (U68408) 5' end not determined experimentally [Zea mays] (AC005561) putative POL3 protein [Arabidopsis thaliana]
6569	GM_118_A2_B09_MR	g3645899	BLASTX	323	4e-27	48	Glycine max BSR-101 satellite SB92 genomic sequence
6570	GM_118_A2_B09_T7	g4063760	BLASTX	258	5e-20	53	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6571	GM_118_A2_B10_MR	g507910	BLASTN	511	2e-16	82	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
6572	GM_118_A2_B10_T7	g2522230	BLASTX	230	2e-18	38	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
6573	GM_118_A2_B11_T7	g2244802	BLASTX	98	8e-11	26	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
6574	GM_118_A2_C01_MR	g3142328	BLASTN	1498	5e-61	86	Glycine max gene for Bd 30K, complete cds
6575	GM_118_A2_C02_MR	g4063760	BLASTX	195	2e-13	35	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18C1, complete sequence.
6576	GM_118_A2_C07_MR	g3513747	BLASTX	141	6e-19	62	Glycine max BSR-101 satellite SB92 genomic sequence.
6577	GM_118_A2_C08_T7	g3097320	BLASTN	461	8e-14	69	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
6578	GM_118_A2_C09_MR	g3142328	BLASTN	747	7e-51	84	
6579	GM_118_A2_C10_T7	g3046848	BLASTN	485	7e-15	65	
6580	GM_118_A2_D01_T7	g507910	BLASTN	400	2e-11	72	
6581	GM_118_A2_D03_MR	g2316016	BLASTX	349	1e-29	64	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6582	GM_118_A2_D04_T7	g130582	BLASTX	208	1e-14	34	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum] (AC005561) putative POL3 protein [Arabidopsis thaliana] Glycine max gene for Bd 30K, complete cds retrotransposon del1-46 [Lilium henryi] (Y08501) orf145a [Arabidopsis thaliana] (AC005561) putative POL3 protein [Arabidopsis thaliana] Glycine max gene for Bd 30K, complete cds G-max gene for catalase Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence (AC000098) Similar to Sequence 10 from patent 5477002 (gb 1253956). [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (AC005561) putative POL3 protein [Arabidopsis thaliana] retrotransposon del1-46 [Lilium henryi] (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] gi 3559809 gnl PID e1319149 (AJ010713) fiddlehead protein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. A-egypti DNA, copia-like transposable element Zebedeell (U70076) Lemir [Lycopersicon esculentum] Bactrocera umbrosa strain Vanuatu mitochondrial D-loop region, complete sequence Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana] G-max gene for catalase (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185 and gb AA605362 come from this gene. [Arabidopsis thaliana] (Y12321) open reading frame 2 [Brassica oleracea]
6583	GM_118_A2_D09_T7	g4063760	BLASTX	138	1e-10	45	
6584	GM_118_A2_E01_T7	g3097320	BLASTN	494	2e-15	82	
6585	GM_118_A2_E03_T7	g226407	BLASTX	182	8e-12	32	
6586	GM_118_A2_E04_T7	g1785699	BLASTX	133	4e-12	36	
6587	GM_118_A2_E09_MR	g4063760	BLASTX	346	2e-29	61	
6588	GM_118_A2_F04_T7	g3097320	BLASTN	826	2e-30	73	
6589	GM_118_A2_F08_MR	g18559	BLASTN	488	4e-15	64	
6590	GM_118_A2_G01_MR	g3176798	BLASTN	422	7e-13	62	
6591	GM_118_A2_G02_MR	g2388580	BLASTX	180	2e-15	82	
6592	GM_118_A2_G03_MR	g507910	BLASTN	586	7e-20	83	
6593	GM_118_A2_G07_MR	g4063760	BLASTX	137	7e-17	67	
6594	GM_118_A2_G10_MR	g226407	BLASTX	185	4e-12	36	
6595	GM_118_A2_H03_T7	g3075394	BLASTX	287	8e-24	38	
6596	GM_118_B1_A06_MR	g507910	BLASTN	381	1e-10	73	
6597	GM_118_B1_A06_T7	g507910	BLASTN	363	8e-10	72	
6598	GM_118_B1_A08_MR	g1890143	BLASTN	371	8e-10	65	
6599	GM_118_B1_A09_MR	g2654440	BLASTX	188	5e-14	45	
6600	GM_118_B1_A09_T7	g2655313	BLASTN	261	5e-10	69	
6601	GM_118_B1_B02_MR	g4092470	BLASTN	393	1e-10	64	
6602	GM_118_B1_B06_MR	g18559	BLASTN	606	2e-20	80	
6603	GM_118_B1_B07_T7	g3157949	BLASTX	177	5e-12	43	
6604	GM_118_B1_B11_MR	g2462936	BLASTX	290	7e-25	38	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6605	GM_118_B1_C01_T7	g3097320	BLASTN	465	5e-14	72	Glycine max gene for Bd 30K, complete cds
6606	GM_118_B1_C09_T7	g3142328	BLASTN	455	1e-13	69	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Y08010) lectin receptor kinase [Arabidopsis thaliana]
6607	GM_118_B1_C11_MR	g1769898	BLASTX	265	2e-21	45	Glycine max BSR-101 satellite SB92 genomic sequence.
6608	GM_118_B1_C12_MR	g507910	BLASTN	371	4e-10	68	Arabidopsis thaliana chromosome 1 BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]
6609	GM_118_B1_D01_T7	g2182289	BLASTN	351	8e-09	66	(X98130) unknown [Arabidopsis thaliana] gi 1495263 gnl PID e242837 (X97487) orf09 [Arabidopsis thaliana]
6610	GM_118_B1_D02_MR	g1402883	BLASTX	130	2e-10	40	(Y13368) reverse transcriptase [Beta vulgaris]
6611	GM_118_B1_D03_T7	g2462134	BLASTX	209	2e-15	41	(AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
6612	GM_118_B1_D09_MR	g3421384	BLASTX	243	2e-19	63	Homo sapiens Chromosome 16 BAC clone CTT987SK-A-427H10, complete sequence [Homo sapiens]
6613	GM_118_B1_D09_T7	g3337396	BLASTN	380	4e-10	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]
6614	GM_118_B1_D12_MR	g2564048	BLASTN	386	2e-10	67	Figure 6. DNA sequence of three 3' apoB VNTR alleles. (L23524) ORF [Hordeum vulgare]
6615	GM_118_B1_E03_MR	g340796	BLASTN	384	3e-11	62	(AF098951) breast cancer resistance protein [Homo sapiens]
6616	GM_118_B1_E04_T7	g387902	BLASTX	163	1e-25	53	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
6617	GM_118_B1_E09_T7	g4038352	BLASTX	163	1e-16	37	Glycine max BSR-101 satellite SB92 genomic sequence.
6618	GM_118_B1_F05_T7	g4150930	BLASTN	425	4e-12	65	Glycine max BSR-101 satellite SB92 genomic sequence.
6619	GM_118_B1_F08_MR	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6620	GM_118_B1_F09_MR	g507910	BLASTN	578	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6621	GM_118_B1_G04_T7	g507910	BLASTN	416	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
6622	GM_118_B1_H02_MR	g3777527	BLASTX	283	3e-29	58	(AF053008) gag-pol polypeptide [Glycine max]
6623	GM_118_B1_H04_MR	g507910	BLASTN	366	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6624	GM_118_B1_H04_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6625	GM_118_B1_H06_T7	g2522226	BLASTN	444	4e-13	63	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
6626	GM_118_B1_H09_T7	g130582	BLASTX	240	4e-18	46	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
6627	GM_118_B2_A04_MR	g2522228	BLASTX	211	6e-16	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
6628	GM_118_B2_A05_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
6629	GM_118_B2_A08_T7	g2340108	BLASTX	161	7e-10	51	(U65948) starch branching enzyme IIa [Zea mays]
6630	GM_118_B2_A11_MR	g2995405	BLASTX	236	6e-18	47	(Y12432) polyprotein [Ananas comosus]
6631	GM_118_B2_C07_T7	g2970554	BLASTN	403	3e-11	66	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
6632	GM_118_B2_C12_MR	g4063760	BLASTX	243	2e-18	50	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6633	GM_118_B2_D04_MR	g3142328	BLASTN	380	3e-10	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6634	GM_118_B2_D05_T7	g2995405	BLASTX	280	1e-22	64	(Y12432) polyprotein [Ananas comosus]
6635	GM_118_B2_D06_T7	g4063760	BLASTX	329	1e-27	68	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6636	GM_118_B2_E08_T7	g1705678	BLASTX	317	1e-26	91	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) gi 862480 (U20213)
6637	GM_118_B2_E10_MR	g18768	BLASTN	407	5e-12	76	valosin-containing protein [Glycine max]
6638	GM_118_B2_E12_MR	g2995405	BLASTX	325	2e-27	60	Soybean Tgm6 transposable element 3' end
6639	GM_118_B2_G12_T7	g507910	BLASTN	386	8e-11	71	(Y12432) polyprotein [Ananas comosus]
6640	GM_118_B2_H02_T7	g132086	BLASTX	290	7e-25	100	Glycine max BSR-101 satellite SB92 genomic sequence.
6641	GM_118_B2_H03_T7	g1142699	BLASTN	226	1e-09	70	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR gi 68053 pir RKSYS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor SRS1 - soybean gi 18742 (V00458) rubpase [Glycine max]
6642	GM_119_B2_A05_MR	g2827514	BLASTX	193	1e-13	75	Glycine max satellite STR120-A.1.
6643	GM_119_B2_A06_MR	g1143381	BLASTX	175	3e-12	42	(AL021633) predicted protein [Arabidopsis thaliana]
6644	GM_119_B2_A11_MR	g507910	BLASTN	391	5e-11	72	(Z49063) polygalacturonase inhibitor [Actinidia deliciosa]
6645	GM_119_B2_B11_MR	g2443320	BLASTX	268	5e-21	54	Glycine max BSR-101 satellite SB92 genomic sequence.
6646	GM_119_B2_B12_MR	g507910	BLASTN	574	3e-19	82	(D85597) polyprotein [Oryza australiensis]
6647	GM_119_B2_C01_MR	g507910	BLASTN	611	5e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6648	GM_119_B2_C04_MR	g507910	BLASTN	611	5e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
6649	GM_119_B2_D02_MR	g18559	BLASTN	981	2e-37	76	G.max gene for catalase
6650	GM_119_B2_D05_MR	g18559	BLASTN	987	1e-37	77	G.max gene for catalase
6651	GM_119_B2_D08_MR	g2130082	BLASTX	373	2e-32	53	protein kinase Xa21 (EC 2.7.1.-) - rice gi 1122443 (U37133) receptor kinase-like protein [Oryza sativa] gi 2586085 (U72723) receptor kinase-like protein [Oryza longistaminata] gi 1586408 prf 2203451A receptor kinase-like protein [Oryza sativa]
6652	GM_119_B2_D09_MR	g3097320	BLASTN	664	5e-23	75	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6653	GM_119_B2_D10_MR	g130582	BLASTX	319	2e-26	52	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
6654	GM_119_B2_D12_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6655	GM_119_B2_E01_MR	g3283026	BLASTX	226	5e-17	34	putative transposase [Arabidopsis thaliana]
6656	GM_119_B2_E03_MR	g3645899	BLASTX	436	3e-39	62	(U68408) 5' end not determined experimentally [Zea mays]
6657	GM_119_B2_E08_MR	g4063760	BLASTX	256	7e-20	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6658	GM_119_B2_F01_MR	g507910	BLASTN	397	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6659	GM_119_B2_F03_MR	g3281870	BLASTX	184	9e-12	38	(AL031004) putative protein [Arabidopsis thaliana]
6660	GM_120_A1_A07_T7	g130582	BLASTX	400	4e-35	62	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
6661	GM_120_A1_A08_MR	g3786414	BLASTN	374	7e-10	71	Caenorhabditis elegans cosmid H28G03
6662	GM_120_A1_A09_T7	g507910	BLASTN	603	1e-20	85	Glycine max BSR-101 satellite SB92 genomic sequence.
6663	GM_120_A1_A10_MR	g2522228	BLASTX	560	2e-53	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
6664	GM_120_A1_A10_T7	g3377836	BLASTX	84	6e-09	32	(AF075598) contains similarity to reverse transcriptases [Arabidopsis thaliana]
6665	GM_120_A1_A11_MR	g3985957	BLASTN	365	2e-09	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]
6666	GM_120_A1_A11_T7	g4063760	BLASTX	371	4e-32	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6667	GM_120_A1_A12_T7	g1167523	BLASTX	365	2e-31	49	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
6668	GM_120_A1_B04_T7	g13619	BLASTN	334	1e-08	58	Saccharomyces douglasii mtDNA for tRNA(fMet) and put. tRNA synthesis locus (TSL)
6669	GM_120_A1_B05_T7	g3378134	BLASTX	240	8e-19	40	(AF071503) brahma associated protein 60 kDa [Drosophila melanogaster]
6670	GM_120_A1_B06_MR	g3135969	BLASTN	358	4e-09	64	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
6671	GM_120_A1_B08_MR	g4063760	BLASTX	396	9e-35	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6672	GM_120_A1_B09_T7	g2443320	BLASTX	373	4e-33	52	(D85597) polyprotein [Oryza australiensis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
6673	GM_120_A1_B12_T7	g4063760	BLASTX	403	2e-35	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6674	GM_120_A1_C02_MR	g4063760	BLASTX	353	3e-30	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6675	GM_120_A1_C03_MR	g4050011	BLASTN	488	5e-15	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
6676	GM_120_A1_C04_MR	g4063760	BLASTX	275	7e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6677	GM_120_A1_C05_MR	g2924653	BLASTN	327	7e-09	85	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]
6678	GM_120_A1_C06_MR	g4160362	BLASTN	351	8e-09	61	Saccharomyces cerevisiae complete mitochondrial genome (AF059674) putative gag protein [Nicotiana tabacum]
6679	GM_120_A1_C11_MR	g3930515	BLASTX	122	4e-12	38	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
6680	GM_120_A1_D03_MR	g2522227	BLASTX	226	4e-18	38	(U76261) unknown [Hordeum vulgare]
6681	GM_120_A1_D05_MR	g1666236	BLASTX	164	6e-11	26	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
6682	GM_120_A1_D07_MR	g4050011	BLASTN	474	2e-14	64	(AC004238) Cf-2, 1-like protein [Arabidopsis thaliana]
6683	GM_120_A1_D08_MR	g3033389	BLASTX	198	8e-14	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6684	GM_120_A1_D11_MR	g3695395	BLASTX	152	4e-09	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6685	GM_120_A1_D11_T7	g4063760	BLASTX	389	5e-34	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6686	GM_120_A1_D12_MR	g4063760	BLASTX	191	5e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6687	GM_120_A1_E07_MR	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6688	GM_120_A1_F07_T7	g507910	BLASTN	401	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6689	GM_120_A1_E09_T7	g3738114	BLASTN	374	7e-10	61	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
6690	GM_120_A1_F03_T7	g4050011	BLASTN	560	3e-18	66	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
6691	GM_120_A1_F04_MR	g547683	BLASTX	660	4e-64	94	HEAT SHOCK COGNATE PROTEIN 80 gi 170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] gi 445601 prf 1909348A heat shock protein hsp80 [Lycopersicon esculentum]
6692	GM_120_A1_F06_MR	g18559	BLASTN	875	1e-32	75	G.max gene for catalase
6693	GM_120_A1_F08_T7	g100484	BLASTX	379	2e-33	54	hypothetical protein - garden snapdragon
6694	GM_120_A1_F09_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6695	GM_120_A1_F09_T7	g507910	BLASTN	342	7e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6696	GM_120_A1_G01_T7	g1769898	BLASTX	316	7e-27	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6697	GM_120_A1_G03_T7	g3097320	BLASTN	619	5e-21	78	Glycine max gene for Bd 30K, complete cds
6698	GM_120_A1_G04_T7	g18559	BLASTN	1147	5e-45	76	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
6699	GM_120_A1_G05_MR	g226407	BLASTX	161	7e-15	44	retrotransposon dell-46 [Lilium henryi]
6700	GM_120_A1_G09_MR	g2832304	BLASTX	299	9e-26	46	(AF044489) receptor-like protein kinase [Oryza sativa]
6701	GM_120_A1_G10_T7	g1419129	BLASTX	171	3e-12	72	(Z75517) reverse transcriptase [Oryza sativa]
6702	GM_120_A1_G12_MR	g3645899	BLASTX	208	1e-16	48	(U68408) 5' end not determined experimentally [Zea mays]
6703	GM_120_A1_H01_T7	g2522228	BLASTX	460	8e-43	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
6704	GM_120_A1_H07_T7	g4063760	BLASTX	208	1e-14	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6705	GM_120_A1_H10_MR	g3810596	BLASTX	182	4e-12	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
6706	GM_120_A2_A02_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6707	GM_120_A2_A05_MR	g417073	BLASTX	607	8e-57	90	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH- GOGAT) gi 484529 pir JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa gi 166412 (L01660) NADH-glutamate synthase [Medicago sativa]
6708	GM_120_A2_B03_MR	g4115382	BLASTX	164	4e-11	35	(AC005967) hypothetical protein [Arabidopsis thaliana]
6709	GM_120_A2_B08_MR	g3426334	BLASTN	530	6e-17	63	Pisum sativum pectin methylesterase (repmel) gene, complete cds
6710	GM_120_A2_B12_MR	g3237327	BLASTX	356	7e-32	60	(AF030260) CYP94A1 [Vicia sativa]
6711	GM_120_A2_C07_MR	g18559	BLASTN	767	9e-28	72	G.max gene for catalase
6712	GM_120_A2_D12_MR	g1769897	BLASTX	237	2e-18	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6713	GM_120_A2_E03_MR	g18559	BLASTN	361	3e-09	65	G.max gene for catalase
6714	GM_120_A2_E05_MR	g3645899	BLASTX	372	2e-32	58	(U68408) 5' end not determined experimentally [Zea mays]
6715	GM_120_A2_E09_MR	g3810595	BLASTX	303	9e-25	46	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
6716	GM_120_A2_F04_MR	g3777527	BLASTX	691	3e-67	95	(AF053008) gag-pol polyprotein [Glycine max]
6717	GM_120_A2_G06_MR	g4092471	BLASTN	513	4e-16	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
6718	GM_120_A2_G08_MR	g4050011	BLASTN	535	4e-17	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
6719	GM_120_A2_G12_MR	g3047085	BLASTX	186	3e-13	55	(AF058914) No definition line found [Arabidopsis thaliana]
6720	GM_120_A2_H07_MR	g3930515	BLASTX	108	2e-11	47	(AF059674) putative gag protein [Nicotiana tabacum]
6721	GM_120_B2_A11_T7	g1142703	BLASTN	286	3e-16	76	Glycine max satellite STR120-B.1.
6722	GM_120_B2_C11_T7	g2244749	BLASTX	216	3e-16	76	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
6723	GM_120_B2_D02_T7	g4063760	BLASTX	251	3e-19	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6724	GM_120_B2_D12_T7	g3377855	BLASTX	305	2e-26	71	(AF076274) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf- CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
6725	GM_120_B2_E04_T7	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
6726	GM_120_B2_F12_T7	g3283435	BLASTX	155	5e-16	61	(AF069495) cytochrome P450 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6727	GM_120_B2_G08_T7	g18559	BLASTN	408	2e-11	72	G.max gene for catalase
6728	GM_120_B2_H04_T7	g531389	BLASTX	214	3e-15	54	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
6729	GM_121_A1_A06_MR	g4140712	BLASTX	160	4e-11	64	(AF110183) putative integrase [Oryza sativa]
6730	GM_121_A1_A06_T7	g3097320	BLASTN	464	6e-14	68	Glycine max gene for Bd 30K, complete cds
6731	GM_121_A1_A09_MR	g4063760	BLASTX	145	2e-16	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6732	GM_121_A1_A10_MR	g3777527	BLASTX	204	3e-14	86	(AF053008) gag-pol polyprotein [Glycine max]
6733	GM_121_A1_B03_T7	g2522227	BLASTX	218	3e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
6734	GM_121_A1_B09_T7	g3176791	BLASTN	342	3e-09	62	Homo sapiens allele 11 fragile site locus (FRA10B) minisatellite, 5' sequence
6735	GM_121_A1_C02_T7	g1769897	BLASTX	198	3e-14	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6736	GM_121_A1_C03_MR	g3128168	BLASTX	156	7e-10	61	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]
6737	GM_121_A1_C08_MR	g2995405	BLASTX	192	6e-21	47	(Y12432) polyprotein [Ananas comosus]
6738	GM_121_A1_D02_T7	g507910	BLASTN	491	1e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
6739	GM_121_A1_D07_T7	g4063760	BLASTX	311	1e-25	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6740	GM_121_A1_D08_MR	g18559	BLASTN	705	6e-25	71	G.max gene for catalase
6741	GM_121_A1_E06_MR	g3319362	BLASTX	199	7e-14	51	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6742	GM_121_A1_F02_T7	g1666236	BLASTX	202	3e-15	31	(U76261) unknown [Hordeum vulgare]
6743	GM_121_A1_F12_T7	g3097320	BLASTN	474	2e-14	69	Glycine max gene for Bd 30K, complete cds
6744	GM_121_A1_G01_T7	g3763850	BLASTN	395	7e-11	77	Glycine max GmENOD93 gene for early nodulin, complete cds
6745	GM_121_A1_G05_MR	g507910	BLASTN	468	1e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6746	GM_121_A1_G05_T7	g4063760	BLASTX	196	2e-13	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6747	GM_121_A1_G10_MR	g3142379	BLASTX	199	1e-14	77	(AF053008) envelope-like [Glycine max]
6748	GM_121_A1_H07_MR	g2407790	BLASTX	131	2e-13	50	(AF019910) grr1 [Glycine max]
6749	GM_121_A2_A01_T7	g1769897	BLASTX	101	2e-14	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6750	GM_121_A2_A05_MR	g531389	BLASTX	180	1e-11	34	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
6751	GM_121_A2_A08_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6752	GM_121_A2_A11_T7	g2494111	BLASTX	170	1e-10	80	(AC002376) Contains similarity to Glycine protein kinase 6 (gb M67449). [Arabidopsis thaliana]
6753	GM_121_A2_B01_MR	g2443320	BLASTX	315	5e-26	56	(D85597) polyprotein [Oryza australiensis]
6754	GM_121_A2_B02_T7	g18559	BLASTN	622	4e-21	71	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6755	GM_121_A2_B04_MR	g4063760	BLASTX	202	4e-14	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6756	GM_121_A2_B07_T7	g1769898	BLASTX	336	5e-29	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6757	GM_121_A2_B10_T7	g1769899	BLASTX	167	8e-12	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6758	GM_121_A2_C01_MR	g4165194	BLASTX	228	7e-17	41	(AJ009736) Pol protein [Drosophila melanogaster]
6759	GM_121_A2_C02_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6760	GM_121_A2_C02_T7	g507910	BLASTN	410	6e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6761	GM_121_A2_C03_MR	g2129618	BLASTX	208	7e-15	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6762	GM_121_A2_C05_MR	g538067	BLASTX	166	4e-10	34	(M77661) putative pol polyprotein [Magnaporthe grisea]
6763	GM_121_A2_C07_T7	g18559	BLASTN	523	1e-16	67	G.max gene for catalase
6764	GM_121_A2_C10_T7	g4063756	BLASTN	532	5e-17	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
6765	GM_121_A2_C11_MR	g3142328	BLASTN	581	3e-19	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6766	GM_121_A2_D04_MR	g3142328	BLASTN	833	9e-31	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6767	GM_121_A2_D05_T7	g508826	BLASTN	405	3e-11	64	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6768	GM_121_A2_D10_T7	g2130150	BLASTX	358	5e-34	62	Drosophila melanogaster Oregon-R mitochondrial A+T region, hypothetical protein 137 - maize chloroplast gi 902263 gnl PID e225682 (X86563) ORF137 [Zea mays] gi 902308 gnl PID e225686 (X86563) ORF137 [Zea mays]
6769	GM_121_A2_D12_T7	g18559	BLASTN	446	5e-26	65	G.max gene for catalase
6770	GM_121_A2_E02_T7	g2443320	BLASTX	395	1e-34	52	(D85597) polyprotein [Oryza australiensis]
6771	GM_121_A2_E05_T7	g2244802	BLASTX	292	2e-23	47	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
6772	GM_121_A2_E08_MR	g3695395	BLASTX	194	1e-13	45	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6773	GM_121_A2_E11_MR	g4063760	BLASTX	253	2e-19	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6774	GM_121_A2_E12_MR	g531389	BLASTX	161	2e-18	51	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
6775	GM_121_A2_F06_T7	g4063760	BLASTX	489	1e-44	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6776	GM_121_A2_G04_MR	g3142328	BLASTN	604	2e-20	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6777	GM_121_A2_G10_MR	g4105800	BLASTX	109	4e-10	47	(AF049931) PGP301 [Petunia x hybrida]
6778	GM_121_A2_G11_T7	g469153	BLASTN	381	3e-10	68	P.sativum (Birte) Lox1:Ps.2 gene.
6779	GM_121_A2_H01_MR	g3097320	BLASTN	503	1e-15	63	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
6780	GM_121_A2_H09_T7	g2129618	BLASTX	201	4e-14	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (AL022198) putative protein [Ananas comosus] (Y12432) polyprotein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max] (AF053008) gag-pol polyprotein [Glycine max] Glycine max BSR-101 satellite SB92 genomic sequence. (U22103) gag-protease polyprotein [Glycine max] Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence Glycine soja chloroplast omega-3 fatty acid desaturase (Fadd) mRNA, complete cds. (AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon] Glycine max BSR-101 satellite SB92 genomic sequence. hypothetical protein - garden snapdragon Glycine max BSR-101 satellite SB92 genomic sequence. (AC005897) putative transposon [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. (AF053008) envelope-like [Glycine max] (AJ006025) acyl-coA synthetase [Cicer arietinum] Homo sapiens allele 11 fragile site locus (FRA10B) minisatellite, 5' sequence Glycine max BSR-101 satellite SB92 genomic sequence. (AF053008) gag-pol polyprotein [Glycine max] (U68408) 5' end not determined experimentally [Zea mays] (AF053008) envelope-like [Glycine max] Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6781	GM_121_B2_B06_MR	g507910	BLASTN	485	3e-15	76	
6782	GM_121_B2_C09_MR	g2980777	BLASTX	189	7e-15	54	
6783	GM_121_B2_D03_MR	g2995405	BLASTX	272	9e-26	57	
6784	GM_121_B2_D07_MR	g507910	BLASTN	365	7e-10	73	
6785	GM_121_B2_E05_MR	g507910	BLASTN	620	2e-21	84	
6786	GM_121_B2_F09_MR	g99922	BLASTX	265	3e-22	60	
6787	GM_121_B2_F12_MR	g3777527	BLASTX	358	1e-30	89	
6788	GM_121_B2_G02_MR	g507910	BLASTN	635	4e-22	85	
6789	GM_121_B2_G03_MR	g905361	BLASTX	419	3e-38	93	
6790	GM_121_B2_G09_MR	g3395421	BLASTN	491	4e-15	68	
6791	GM_121_B2_H02_MR	g3142328	BLASTN	1323	5e-53	93	
6792	GM_121_B2_H05_MR	g408791	BLASTN	356	3e-09	83	
6793	GM_121_B2_H07_MR	g2997694	BLASTX	139	6e-11	35	
6794	GM_121_B2_H08_MR	g507910	BLASTN	350	3e-09	71	
6795	GM_122_A1_A03_MR	g100484	BLASTX	96	5e-12	39	
6796	GM_122_A1_A05_T7	g507910	BLASTN	527	3e-17	78	
6797	GM_122_A1_B05_T7	g4038056	BLASTX	244	9e-19	48	
6798	GM_122_A1_C03_MR	g507910	BLASTN	428	1e-12	77	
6799	GM_122_A1_C03_T7	g3142379	BLASTX	349	1e-42	77	
6800	GM_122_A1_C04_MR	g3127892	BLASTX	240	1e-19	74	
6801	GM_122_A1_C07_MR	g3176791	BLASTN	376	9e-11	65	
6802	GM_122_A1_D03_T7	g507910	BLASTN	510	2e-16	75	
6803	GM_122_A1_E04_MR	g3777527	BLASTX	196	2e-13	40	
6804	GM_122_A1_F07_T7	g3645899	BLASTX	141	2e-11	61	
6805	GM_122_A1_F01_MR	g3142379	BLASTX	208	1e-15	54	
6806	GM_122_A1_F03_T7	g3142328	BLASTN	875	1e-32	89	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
6807	GM_122_A1_G03_MR	g2429543	BLASTX	200	6e-19	41	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans])
6808	GM_122_A1_G04_T7	g2129618	BLASTX	148	3e-10	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6809	GM_122_A1_H01_T7	g3142328	BLASTN	605	2e-20	69	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6810	GM_122_A2_A02_MR	g3142328	BLASTN	463	6e-14	68	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6811	GM_122_A2_A03_MR	g3243214	BLASTN	359	3e-09	64	Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
6812	GM_122_A2_A03_T7	g4063760	BLASTX	199	9e-14	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6813	GM_122_A2_A04_MR	g336279	BLASTN	413	1e-11	69	Apis mellifera ligustica complete mitochondrial genome
6814	GM_122_A2_A08_T7	g507910	BLASTN	478	5e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
6815	GM_122_A2_A09_T7	g2462748	BLASTX	187	3e-13	84	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]
6816	GM_122_A2_B04_MR	g99729	BLASTX	273	5e-23	45	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Tal-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
6817	GM_122_A2_B12_MR	g507910	BLASTN	654	6e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
6818	GM_122_A2_C02_MR	g507910	BLASTN	449	1e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6819	GM_122_A2_C02_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6820	GM_122_A2_C04_T7	g507910	BLASTN	557	1e-18	82	Glycine max BSR-101 satellite SB92 genomic sequence
6821	GM_122_A2_C07_MR	g3097320	BLASTN	471	3e-14	68	Glycine max gene for Bd 30K, complete cds
6822	GM_122_A2_C08_MR	g1217971	BLASTN	368	1e-09	66	P.tetraulera gamma1-51D immobilisation antigen gene, 3' coding and non-coding region
6823	GM_122_A2_C09_MR	g3930515	BLASTX	149	5e-09	33	(AF059674) putative gag protein [Nicotiana tabacum]
6824	GM_122_A2_C12_MR	g507910	BLASTN	665	2e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
6825	GM_122_A2_C12_T7	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6826	GM_122_A2_D03_MR	g2815519	BLASTN	380	4e-10	67	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]
6827	GM_122_A2_D07_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6828	GM_122_A2_D10_MR	g3367517	BLASTX	233	5e-18	51	(AC004392) Similar to F411.26 putative beta-glucosidase gi 3128187 from A. thaliana BAC gb AC004521. ESTs gb N97083, gb F19868 and gb F15482 come from this gene. [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6829	GM_122_A2_E01_T7	g18559	BLASTN	487	5e-15	76	G-max gene for catalase
6830	GM_122_A2_E05_T7	g4063760	BLASTX	153	7e-09	54	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6831	GM_122_A2_E08_MR	g3287695	BLASTX	227	6e-17	52	(AC003979) Similar to hypothetical protein C34B7.2 gb 1729503 from <i>C. elegans</i> cosmid gb Z83220. [Arabidopsis thaliana]
6832	GM_122_A2_E09_T7	g1769897	BLASTX	288	6e-24	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6833	GM_122_A2_F01_T7	g2160694	BLASTX	375	8e-34	97	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
6834	GM_122_A2_F02_MR	g3142328	BLASTN	523	9e-34	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6835	GM_122_A2_F04_MR	g3777527	BLASTX	246	1e-18	43	(AF053008) gag-pol polyprotein [Glycine max]
6836	GM_122_A2_F08_MR	g4063760	BLASTX	178	2e-11	67	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6837	GM_122_A2_F08_T7	g507910	BLASTN	517	9e-17	84	Glycine max BSR-101 satellite SB92 genomic sequence.
6838	GM_122_A2_F09_MR	g1142614	BLASTX	223	1e-17	88	(U17250) ubiquitin conjugating enzyme, E2 [Brassica oleracea]
6839	GM_122_A2_F10_T7	g1813979	BLASTX	126	5e-12	74	(Y10860) hypothetical protein [Musa acuminata]
6840	GM_122_A2_F11_MR	g3402749	BLASTX	145	1e-09	47	(AI031187) putative protein [Arabidopsis thaliana]
6841	GM_122_A2_F12_MR	g3645899	BLASTX	237	1e-23	54	(U68408) 5' end not determined experimentally [Zea mays]
6842	GM_122_A2_G03_MR	g3421038	BLASTN	421	6e-12	64	Human DNA sequence from clone 35C21 on chromosome 1q23-24. Contains STSs, complete sequence [Homo sapiens]
6843	GM_122_A2_G05_MR	g4115365	BLASTX	169	2e-10	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
6844	GM_122_A2_G05_T7	g3777527	BLASTX	408	7e-36	94	(AF053008) gag-pol polyprotein [Glycine max]
6845	GM_122_A2_G10_T7	g4063760	BLASTX	188	3e-13	58	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6846	GM_122_A2_G11_MR	g2522228	BLASTX	280	9e-24	79	(AB007466) reverse transcriptase-like protein [Vicia faba]
6847	GM_122_A2_H03_T7	g3687234	BLASTX	166	3e-10	49	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
6848	GM_122_A2_H06_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6849	GM_122_A2_H06_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6850	GM_122_A2_H07_MR	g1769899	BLASTX	262	7e-22	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6851	GM_122_A2_H11_MR	g4063756	BLASTN	464	6e-14	72	Arabidopsis thaliana chromosome II BAC T9I:8 genomic sequence, complete sequence [Arabidopsis thaliana]
6852	GM_122_B2_A01_T7	g4063760	BLASTX	417	5e-37	62	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
6853	GM_122_B2_A04_MR	g1769898	BLASTX	419	3e-38	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6854	GM_122_B2_A05_T7	g4006867	BLASTX	363	2e-31	63	(Z99707) putative protein [Arabidopsis thaliana]
6855	GM_122_B2_B03_MR	g343595	BLASTN	343	7e-09	62	T-brucei kinetoplast cytochrome c oxidase III (COIII) gene, complete cds.
6856	GM_122_B2_B05_T7	g3777527	BLASTX	651	8e-62	96	(AF053008) gag-pol polyprotein [Glycine max]
6857	GM_122_B2_B09_MR	g4063760	BLASTX	488	1e-44	68	(AC005561) putative POL.3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6858	GM_122_B2_C04_MR	g4063760	BLASTX	411	2e-36	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6859	GM_122_B2_C04_T7	g4063760	BLASTX	478	2e-43	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6860	GM_122_B2_C08_MR	g4063760	BLASTX	257	6e-20	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6861	GM_122_B2_C08_T7	g507910	BLASTN	497	7e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
6862	GM_122_B2_C09_MR	g3869068	BLASTN	360	2e-16	71	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone; MDC16, complete sequence [Arabidopsis thaliana]
6863	GM_122_B2_C12_MR	g2865424	BLASTX	221	5e-16	53	(AF039371) polyprotein [Arabidopsis thaliana]
6864	GM_122_B2_D01_MR	g2443320	BLASTX	105	1e-11	42	(D85597) polyprotein [Oryza australiensis]
6865	GM_122_B2_D01_T7	g18559	BLASTN	354	4e-12	72	G max gene for catalase
6866	GM_122_B2_D06_MR	g226407	BLASTX	303	9e-25	44	retrotransposon dell-46 [Lilium henryi]
6867	GM_122_B2_D06_T7	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6868	GM_122_B2_D10_MR	g343344	BLASTN	464	4e-18	81	Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end), Ile-tRNA, and Ala-tRNA genes.
6869	GM_122_B2_E06_MR	g629693	BLASTX	277	1e-32	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6870	GM_122_B2_E08_T7	g507910	BLASTN	565	6e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6871	GM_122_B2_E10_MR	g3097320	BLASTN	374	7e-10	71	Glycine max gene for Bd 30K, complete cds
6872	GM_122_B2_E12_T7	g1022917	BLASTN	371	2e-10	63	Trypanosoma cruzi kinetoplast minicircle ATPase subunit 6 mRNA, complete cds.
6873	GM_122_B2_F01_MR	g507910	BLASTN	433	6e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6874	GM_122_B2_F03_MR	g4106408	BLASTN	733	6e-27	68	Oryza sativa subsp. indica dispersed centromeric repeat family RCS1 (U68408) 5' end not determined experimentally [Zea mays]
6875	GM_122_B2_F04_T7	g3645890	BLASTX	318	2e-26	49	Glycine max BSR-101 satellite SB92 genomic sequence.
6876	GM_122_B2_F05_MR	g507910	BLASTN	358	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6877	GM_122_B2_F05_T7	g507910	BLASTN	365	7e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6878	GM_122_B2_F09_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6879	GM_122_B2_F10_MR	g3777527	BLASTX	324	4e-28	67	(AF053008) gag-pol polyprotein [Glycine max] (D85597) polyprotein [Oryza australiensis]
6880	GM_122_B2_G01_T7	g2443320	BLASTX	225	2e-29	54	disease resistance protein RPM1 - Arabidopsis thaliana gi 963017 (X87851) disease resistance gene; pid:c183919 [Arabidopsis thaliana]
6881	GM_122_B2_G08_MR	g1361985	BLASTX	172	5e-11	33	(AF053008) envelope-like [Glycine max] (U68408) 5' end not determined experimentally [Zea mays]
6882	GM_122_B2_G09_T7	g3142379	BLASTX	343	2e-30	69	Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence, complete sequence [Arabidopsis thaliana]
6883	GM_122_B2_G11_MR	g3645899	BLASTX	191	6e-13	38	
6884	GM_122_B2_H02_T7	g3810584	BLASTN	442	6e-13	61	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6885	GM_122_B2_H03_T7	g2129618	BLASTX	223	2e-16	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6886	GM_122_B2_H06_MR	g3142328	BLASTN	1160	1e-45	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6887	GM_122_B2_H08_T7	g984307	BLASTN	1251	9e-55	90	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precursor...
6888	GM_123_A1_A03_MR	g1843462	BLASTX	204	3e-15	37	(L10211) isoliqurigenin 2'-O-methyltransferase [Medicago sativa]
6889	GM_123_A1_A05_T7	g2129618	BLASTX	220	4e-16	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6890	GM_123_A1_B05_T7	g3097320	BLASTN	554	5e-18	74	Glycine max gene for Bd 30K, complete cds
6891	GM_123_A1_B10_T7	g3319362	BLASTX	268	3e-21	49	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6892	GM_123_A1_C02_MR	g3193290	BLASTX	197	1e-23	47	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido...]
6893	GM_123_A1_C04_T7	g4063760	BLASTX	354	3e-30	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6894	GM_123_A1_C05_MR	g3859610	BLASTN	398	6e-11	66	Arabidopsis thaliana BAC T9E19
6895	GM_123_A1_C06_T7	g100484	BLASTX	356	6e-31	60	hypothetical protein - garden snapdragon
6896	GM_123_A1_C09_T7	g3097320	BLASTN	631	1e-21	75	Glycine max gene for Bd 30K, complete cds
6897	GM_123_A1_D03_MR	g133917	BLASTX	271	8e-23	92	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814 (Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf 1211235J ribosomal protein S2 [Nicotiana tabacum]
6898	GM_123_A1_D03_T7	g12212	BLASTN	1099	2e-48	93	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
6899	GM_123_A1_D04_MR	g461736	BLASTX	128	4e-22	89	MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR gi 478786 pir S29316 chaperonin 60 - cucurbit gi 12546 gnl PID e1188586 (X70868) chaperonin 60 [Cucurbita sp.]
6900	GM_123_A1_D06_T7	g2618688	BLASTX	161	6e-11	96	(AC002510) putative esterase D [Arabidopsis thaliana]
6901	GM_123_A1_D07_MR	g3930515	BLASTX	106	5e-09	37	(AF059674) putative gag protein [Nicotiana tabacum]
6902	GM_123_A1_D09_T7	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6903	GM_123_A1_D10_T7	g3461813	BLASTX	111	9e-12	64	(AC004138) putative sucrose/H+ symporter [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6904	GM_123_A1_F04_MR	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6905	GM_123_A1_E04_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6906	GM_123_A1_E07_T7	g3859610	BLASTN	580	4e-19	65	Arabidopsis thaliana BAC T9E19
6907	GM_123_A1_E09_MR	g4115365	BLASTX	158	2e-09	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
6908	GM_123_A1_E10_MR	g2995405	BLASTX	309	6e-34	61	(Y12432) polyprotein [Ananas comosus]
6909	GM_123_A1_E11_MR	g507910	BLASTN	378	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6910	GM_123_A1_F10_MR	g4063760	BLASTX	252	2e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6911	GM_123_A1_G01_T7	g1171978	BLASTX	461	6e-43	81	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) g1 304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] gi 2911051 gnl PID e1253339 (AL021961)
6912	GM_123_A1_G02_MR	g99726	BLASTX	122	1e-16	31	poly(A)-binding protein [Arabidopsis thaliana] hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
6913	GM_123_A1_G04_T7	g2864621	BLASTX	152	2e-09	46	hypothetical protein [Arabidopsis thaliana]
6914	GM_123_A1_G11_MR	g4115365	BLASTX	318	2e-26	55	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
6915	GM_123_A1_H03_T7	g4063756	BLASTN	456	1e-13	69	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence. complete sequence [Arabidopsis thaliana]
6916	GM_123_A1_H04_MR	g1769898	BLASTX	482	3e-45	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6917	GM_123_A1_H05_T7	g4063760	BLASTX	159	2e-09	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6918	GM_123_A1_H08_MR	g2522230	BLASTX	233	9e-19	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6919	GM_123_A1_H08_T7	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6920	GM_123_A1_H10_MR	g3142328	BLASTN	419	6e-12	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6921	GM_123_A1_H11_MR	g99922	BLASTX	168	2e-11	35	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
6922	GM_123_A1_H12_MR	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6923	GM_123_A2_A04_MR	g2129618	BLASTX	190	6e-13	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila g1 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6924	GM_123_A2_A12_T7	g3142328	BLASTN	410	1e-11	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U76261) unknown [Hordeum vulgare]
6925	GM_123_A2_B08_T7	g1666236	BLASTX	157	3e-10	32	Soybean seed lectin gene transposable element tgm1.
6926	GM_123_A2_B09_MR	g170080	BLASTN	487	5e-15	70	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6927	GM_123_A2_B12_T7	g2121303	BLASTN	457	1e-13	65	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens] (AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6928	GM_123_A2_C04_MR	g3695395	BLASTX	204	1e-14	39	A thaliana lectin receptor kinase gene (AC005561) putative POL3 protein [Arabidopsis thaliana]
6929	GM_123_A2_C04_T7	g1769896	BLASTN	486	5e-15	66	Glycine max BSR-101 satellite SB92 genomic sequence.
6930	GM_123_A2_D04_MR	g4063760	BLASTX	189	9e-13	43	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
6931	GM_123_A2_D10_T7	g507910	BLASTN	339	1e-08	68	(AB007466) reverse transcriptase-like protein [Vicia faba]
6932	GM_123_A2_F03_MR	g3650039	BLASTX	224	8e-17	34	G.max gene for catalase
6933	GM_123_A2_E04_MR	g2522228	BLASTX	170	2e-11	65	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
6934	GM_123_A2_F07_T7	g18559	BLASTN	649	2e-22	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6935	GM_123_A2_F01_MR	g3142328	BLASTN	681	7e-24	75	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6936	GM_123_A2_F02_MR	g2997694	BLASTX	206	6e-26	45	(AC005897) putative transposon [Arabidopsis thaliana]
6937	GM_123_A2_F05_T7	g4063760	BLASTX	124	5e-11	44	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
6938	GM_123_A2_F09_T7	g2129618	BLASTX	208	7e-15	42	Glycine max BSR-101 satellite SB92 genomic sequence.
6939	GM_123_A2_F10_MR	g4038056	BLASTX	115	5e-13	47	(D85597) polyprotein [Oryza australiensis]
6940	GM_123_A2_G01_T7	g3650039	BLASTX	215	8e-16	57	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
6941	GM_123_A2_G09_MR	g507910	BLASTN	621	2e-21	82	Glycine max gene for Bd 30K, complete cds
6942	GM_123_A2_H01_MR	g18768	BLASTN	428	5e-13	67	(AF110183) putative integrase [Oryza sativa]
6943	GM_123_A2_H04_T7	g1684913	BLASTX	188	1e-12	40	hypothetical protein - garden snapdragon
6944	GM_123_A2_H07_T7	g2443320	BLASTX	271	2e-21	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6945	GM_123_A2_H08_MR	g4092470	BLASTN	379	4e-10	62	Glycine max BSR-101 satellite SB92 genomic sequence.
6946	GM_123_A2_H08_T7	g3097320	BLASTN	360	3e-09	63	Glycine max gene for Bd 30K, complete cds
6947	GM_123_A2_H10_MR	g4140712	BLASTX	235	5e-19	49	(AF110183) putative integrase [Oryza sativa]
6948	GM_123_A2_H11_MR	g100484	BLASTX	248	2e-19	51	hypothetical protein - garden snapdragon
6949	GM_123_B1_A02_T7	g4063760	BLASTX	169	1e-10	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6950	GM_123_B1_A08_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6951	GM_123_B1_A12_MR	g3097320	BLASTN	433	1e-12	76	Glycine max gene for Bd 30K, complete cds
6952	GM_123_B1_B03_MR	g4063760	BLASTX	247	7e-19	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6953	GM_123_B1_B03_T7	g4063760	BLASTX	161	1e-09	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
6954	GM_123_B1_B11_MR	g3142328	BLASTN	832	1e-30	98	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 0
6955	GM_123_B1_B11_T7	g2244747	BLASTN	349	1e-08	71	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
6956	GM_123_B1_C06_MR	g2642431	BLASTX	189	1e-12	58	reverse transcriptase (copia-like retrotransposon) - soybean (fragment) >gi 169949 (M94493) reverse transcriptase [Glycine max]
6957	GM_123_B1_E02_T7	g478148	BLASTX	337	7e-30	91	Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. (AC005561) putative POL3 protein [Arabidopsis thaliana]
6958	GM_123_B1_E04_T7	g507910	BLASTN	355	2e-09	70	Glycine max gene for Bd 30K, complete cds
6959	GM_123_B1_E06_MR	g507910	BLASTN	482	4e-15	80	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
6960	GM_123_B1_E10_MR	g4063760	BLASTX	230	5e-17	68	(U22103) gag-protease polyprotein [Glycine max]
6961	GM_123_B1_F10_T7	g3097320	BLASTN	447	3e-13	73	(D12849) reverse transcriptase [Pinus thunbergiana]
6962	GM_123_B1_G01_T7	g4092470	BLASTN	440	8e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. (AF053008) envelope-like [Glycine max]
6963	GM_123_B1_G06_T7	g905361	BLASTX	352	9e-31	94	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6964	GM_123_B1_G07_T7	g217993	BLASTX	149	6e-10	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6965	GM_123_B1_G12_T7	g507910	BLASTN	443	2e-13	77	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
6966	GM_123_B1_H03_T7	g3142379	BLASTX	210	1e-15	59	(AF060192) putative resistance protein [Glycine max]
6967	GM_123_B1_H08_T7	g4063760	BLASTX	234	2e-17	63	Glycine max BSR-101 satellite SB92 genomic sequence. Glycine max BSR-101 satellite SB92 genomic sequence. Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence
6968	GM_123_B1_H11_T7	g1769899	BLASTX	212	1e-16	69	Glycine max cv. Dare nodulin 26 gene fragment. (Y08010) lectin receptor kinase [Arabidopsis thaliana]
6969	GM_123_B2_A03_T7	g2769655	BLASTN	379	4e-10	64	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
6970	GM_123_B2_A04_T7	g3091216	BLASTX	362	2e-32	57	P.falciapum complete gene map of plastid-like DNA (IR-B)
6971	GM_123_B2_A08_T7	g507910	BLASTN	400	2e-11	72	Glycine max gene for Bd 30K, complete cds
6972	GM_123_B2_B01_T7	g3176799	BLASTN	353	1e-09	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6973	GM_123_B2_B03_T7	g170029	BLASTN	407	2e-11	81	
6974	GM_123_B2_B06_T7	g1769898	BLASTX	145	9e-13	45	
6975	GM_123_B2_B07_T7	g2522227	BLASTX	223	9e-18	56	
6976	GM_123_B2_B12_T7	g1171591	BLASTN	356	5e-09	60	
6977	GM_123_B2_C01_T7	g3097320	BLASTN	1110	3e-43	80	
6978	GM_123_B2_C05_T7	g4063760	BLASTX	451	1e-40	59	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6979	GM_123_B2_C09_T7	g3097320	BLASTN	430	2e-12	72	Glycine max gene for Bd 30K, complete cds
6980	GM_123_B2_D01_T7	g170029	BLASTN	1714	1e-70	97	Glycine max cv. Dare nodulin 26 gene fragment.
6981	GM_123_B2_D06_T7	g2827715	BLASTX	331	6e-28	78	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
6982	GM_123_B2_D10_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6983	GM_123_B2_E04_T7	g4063760	BLASTX	170	1e-10	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6984	GM_123_B2_E09_T7	g4115370	BLASTN	393	1e-10	66	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]
6985	GM_123_B2_F01_MR	g1658457	BLASTX	155	2e-12	64	(U75248) reverse transcriptase [Gossypium barbadense]
6986	GM_123_B2_F05_T7	g4038056	BLASTX	189	8e-13	42	(AC005897) putative transposon [Arabidopsis thaliana]
6987	GM_123_B2_F08_T7	g3171875	BLASTN	432	2e-12	63	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylamine Monooxygenase (N-Oxide 3, EC1.14.1...
6988	GM_123_B2_G02_T7	g170029	BLASTN	434	1e-12	84	Glycine max cv. Dare nodulin 26 gene fragment.
6989	GM_123_B2_G06_T7	g2244877	BLASTX	227	3e-18	52	(Z97338) hypothetical protein [Arabidopsis thaliana]
6990	GM_123_B2_H03_T7	g3513747	BLASTX	364	4e-31	47	(AF080118) contains similarity to reverse transcriptases (Pfam, rvt.hmm, score: 11.19) [Arabidopsis thaliana]
6991	GM_123_B2_H09_T7	g507910	BLASTN	571	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6992	GM_124_A1_A04_T7	g2522228	BLASTX	154	1e-09	29	(AB007466) reverse transcriptase-like protein [Vicia faba]
6993	GM_124_A1_A05_MR	g3319351	BLASTX	278	4e-22	37	(AF077407) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
6994	GM_124_A1_A07_MR	g4063760	BLASTX	157	3e-09	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6995	GM_124_A1_A08_T7	g2522230	BLASTX	218	3e-17	36	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6996	GM_124_A1_A11_T7	g1055224	BLASTX	151	4e-10	43	(U20977) cellular nucleic acid binding protein [Xenopus laevis]
6997	GM_124_A1_B01_MR	g3258568	BLASTX	199	4e-14	45	(U89959) Unknown protein [Arabidopsis thaliana]
6998	GM_124_A1_B01_T7	g509768	BLASTN	438	6e-13	68	Glycine max seed-specific low molecular weight sulfur-rich protein.
6999	GM_124_A1_B03_MR	g2982452	BLASTX	564	5e-53	72	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
7000	GM_124_A1_B05_MR	g3599418	BLASTN	375	6e-10	70	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7001	GM_124_A1_B06_MR	g505129	BLASTN	386	2e-10	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7002	GM_124_A1_B06_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7003	GM_124_A1_B07_MR	g343755	BLASTN	339	6e-09	60	yeast (s.cerevisiae) mitochondrial atpase proteolipid (subunit 9) gene, 5' end.
7004	GM_124_A1_B11_T7	g2522228	BLASTX	386	5e-35	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
7005	GM_124_A1_C03_T7	g4019231	BLASTN	487	6e-15	64	Ateline herpesvirus 3 complete genome
7006	GM_124_A1_C06_T7	g2764526	BLASTN	629	2e-21	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
7007	GM_124_A1_C07_MR	g13596	BLASTN	332	7e-09	66	Yeast mit DNA for promoter upstream of tRNA-Leu gene 3 *Source:
7008	GM_124_A1_C09_T7	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7009	GM_124_A1_C11_MR	g2315737	BLASTN	368	1e-09	63	Caenorhabditis elegans cosmid R12A1
7010	GM_124_A1_C11_T7	g505129	BLASTN	291	2e-09	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7011	GM_124_A1_C12_T7	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
7012	GM_124_A1_D01_T7	g2764732	BLASTX	209	2e-15	81	(AJ002490) ndhB [Arabidopsis thaliana]
7013	GM_124_A1_D02_MR	g4063760	BLASTX	332	6e-28	52	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
7014	GM_124_A1_D02_T7	g4063760	BLASTX	292	1e-23	57	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
7015	GM_124_A1_D04_MR	g18559	BLASTN	375	6e-10	68	G.max gene for catalase
7016	GM_124_A1_D06_MR	g2367675	BLASTX	274	8e-22	43	(AF017040) Pol [Dictyostelium discoideum]
7017	GM_124_A1_D07_MR	g507910	BLASTX	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7018	GM_124_A1_D08_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7019	GM_124_A1_E04_T7	g396249	BLASTN	282	6e-09	72	S.douglasii mitochondrial ATP subunit 9 gene, complete CDS
7020	GM_124_A1_E05_T7	g4063760	BLASTX	524	2e-48	65	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
7021	GM_124_A1_E08_T7	g115471	BLASTX	180	9e-13	89	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) gi 100078 pir S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea gi 20673 (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]
7022	GM_124_A1_F09_MR	g507910	BLASTN	498	7e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7023	GM_124_A1_F09_T7	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7024	GM_124_A1_F11_T7	g3914002	BLASTX	187	8e-14	54	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279 (AF033862) Lon protease [Arabidopsis thaliana]
7025	GM_124_A1_F02_MR	g1653718	BLASTX	127	5e-10	38	(D90916) hypothetical protein [Synechocystis sp.]
7026	GM_124_A1_F02_T7	g3132696	BLASTX	266	6e-23	94	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]
7027	GM_124_A1_F03_MR	g505129	BLASTN	375	5e-10	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
7028	GM_124_A1_F04_MR	g2130082	BLASTX	155	9e-22	60	protein kinase Xa21 (EC 2.7.1.-) - rice gi 1122443 (U37133) receptor kinase-like protein [Oryza sativa] gi 2586085 (U72723) receptor kinase-like protein [Oryza longistaminata] gi 1586408 prf 2203451A receptor kinase-like protein [Oryza sativa]
7029	GM_124_A1_F08_MR	g3273127	BLASTN	349	9e-09	65	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-54, complete sequence [Plasmodium falciparum] (U22103) gag-protease polypeptide [Glycine max]
7030	GM_124_A1_F08_T7	g905361	BLASTX	252	7e-20	41	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7031	GM_124_A1_F09_MR	g3142328	BLASTN	1903	1e-79	94	LECTIN PRECURSOR (AGGLUTININ) (SBA) gi 282898 pir S27365 lectin precursor - soybean gi 170006 (K00821) lectin prepeptide [Glycine max]
7032	GM_124_A1_F11_MR	g126151	BLASTX	625	2e-60	96	Soybean lox1gm4 gene encoding lipxygenase 1-4 Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
7033	GM_124_A1_G01_MR	g441205	BLASTN	372	8e-10	72	(D85597) polyprotein [Oryza australiensis]
7034	GM_124_A1_G03_MR	g4092471	BLASTN	446	4e-13	68	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
7035	GM_124_A1_G04_MR	g2443320	BLASTX	341	8e-29	47	(U22103) gag-protease polyprotein [Glycine max]
7036	GM_124_A1_G05_T7	g3319362	BLASTX	430	1e-38	57	Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.
7037	GM_124_A1_G08_MR	g905361	BLASTX	424	9e-39	95	Glycine max telomere-associated sequence STAS5
7038	GM_124_A1_G10_MR	g389029	BLASTN	346	6e-09	57	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]
7039	GM_124_A1_G12_MR	g2801676	BLASTN	439	1e-13	65	(AC004238) putative phosphatidylinositol-glycan-class C (PIGC) [Arabidopsis thaliana]
7040	GM_124_A1_G12_T7	g3985931	BLASTN	495	2e-15	67	G.max gene for catalase (AC005561) putative POL3 protein [Arabidopsis thaliana]
7041	GM_124_A1_H04_MR	g3033393	BLASTX	231	1e-22	67	Glycine max BSR-101 satellite SB92 genomic sequence.
7042	GM_124_A1_H05_T7	g18559	BLASTN	553	5e-18	70	(AL021633) predicted protein [Arabidopsis thaliana]
7043	GM_124_A1_H06_MR	g4063760	BLASTX	287	4e-23	44	(D85597) polyprotein [Oryza australiensis]
7044	GM_124_A1_H07_MR	g507910	BLASTN	389	6e-11	72	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
7045	GM_124_A1_H08_T7	g2827514	BLASTX	197	4e-22	75	Glycine max copia-like retrotransposon Tgmr, complete sequence
7046	GM_124_B1_A05_MR	g2443320	BLASTX	238	7e-18	44	Homo sapiens clone GS114109, complete sequence [Homo sapiens]
7047	GM_124_B1_A06_T7	g421955	BLASTX	250	2e-20	60	
7048	GM_124_B1_A07_MR	g2104945	BLASTN	747	8e-27	68	
7049	GM_124_B1_A09_MR	g4156149	BLASTN	358	4e-09	64	

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
7050	GM_124_B1_B02_T7	g4063756	BLASTN	354	6e-09	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7051	GM_124_B1_B05_MR	g1769898	BLASTX	436	2e-40	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7052	GM_124_B1_B06_MR	g3063473	BLASTX	152	6e-09	64	(AC003981) F22O13.35 [Arabidopsis thaliana]
7053	GM_124_B1_B07_MR	g3097320	BLASTN	406	2e-11	72	Glycine max gene for Bd 30K, complete cds
7054	GM_124_B1_B08_T7	g2104945	BLASTN	457	1e-13	75	Glycine max copia-like retrotransposon Tgmr, complete sequence
7055	GM_124_B1_B12_MR	g3269291	BLASTX	166	2e-10	46	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]
7056	GM_124_B1_C02_MR	g2443320	BLASTX	287	4e-23	46	(D85597) polyprotein [Oryza australiensis]
7057	GM_124_B1_C03_MR	g3777527	BLASTX	683	3e-65	92	(AF053008) gag-pol polyprotein [Glycine max]
7058	GM_124_B1_C05_MR	g2995405	BLASTX	298	1e-24	51	(Y12432) polyprotein [Ananas comosus]
7059	GM_124_B1_C05_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7060	GM_124_B1_C07_MR	g2642431	BLASTX	321	1e-26	47	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
7061	GM_124_B1_C09_T7	g3891586	BLASTX	201	2e-15	49	Chain B, Complex Porcine Pancreatic TrypsinSOYBEAN TRYPSIN Inhibitor, Orthorhombic Crystal Form
7062	GM_124_B1_C12_T7	g4038056	BLASTX	190	6e-13	50	(AC005897) putative transposon [Arabidopsis thaliana]
7063	GM_124_B1_D05_MR	g4063760	BLASTX	233	2e-17	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7064	GM_124_B1_D05_T7	g4063760	BLASTX	190	7e-13	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7065	GM_124_B1_D09_MR	g2443320	BLASTX	181	8e-12	31	(D85597) polyprotein [Oryza australiensis]
7066	GM_124_B1_D09_T7	g1711306	BLASTX	105	5e-12	63	(Y09746) heat shock protein 70 [Hydra oligactis]
7067	GM_124_B1_D10_MR	g507910	BLASTN	361	1e-09	76	Glycine max BSR-101 satellite SB92 genomic sequence.
7068	GM_124_B1_D10_T7	g2245608	BLASTX	112	1e-09	61	(AF006007) heat shock cognate 70 kDa protein [Danio rerio]
7069	GM_124_B1_D12_MR	g2795792	BLASTN	350	9e-09	64	Homo sapiens DNA from chromosome 19, cosmid F20191, complete sequence [Homo sapiens]
7070	GM_124_B1_E08_MR	g1769898	BLASTX	107	3e-11	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7071	GM_124_B1_E09_MR	g1480927	BLASTN	464	4e-14	89	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
7072	GM_124_B1_F01_MR	g99922	BLASTX	536	6e-51	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
7073	GM_124_B1_F04_MR	g498931	BLASTX	317	1e-27	50	(Z12825) ORF167: homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
7074	GM_124_B1_F05_T7	g2564046	BLASTN	498	2e-15	72	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MG119, complete sequence [Arabidopsis thaliana]
7075	GM_124_B1_G04_MR	g2995405	BLASTX	307	2e-25	42	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7076	GM_124_B1_G06_MR	g3746568	BLASTX	106	1e-11	83	(AF061638) branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]
7077	GM_124_B1_G07_T7	g3319351	BLASTX	264	1e-20	70	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
7078	GM_124_B1_G11_MR	g2995405	BLASTX	295	3e-24	44	(Y12432) polyprotein [Ananas comosus]
7079	GM_124_B1_G12_MR	g2129618	BLASTX	218	6e-16	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7080	GM_124_B1_H06_T7	g100484	BLASTX	186	1e-12	45	hypothetical protein - garden snapdragon
7081	GM_125_B1_A05_MR	g12137	BLASTN	425	3e-12	66	Pea chloroplast DNA (4.7 kb) 5' to ATP-synthase a subunit gene
7082	GM_125_B1_A07_MR	g2522227	BLASTX	181	4e-13	47	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
7083	GM_125_B1_B03_MR	g3309619	BLASTX	165	3e-10	31	(AF074916) NBS/LRR disease resistance protein [Arabidopsis thaliana]
7084	GM_125_B1_B12_MR	g507910	BLASTN	391	5e-11	82	Glycine max BSR-101 satellite SB92 genomic sequence.
7085	GM_125_B1_C10_MR	g2995405	BLASTX	385	6e-34	62	(Y12432) polyprotein [Ananas comosus]
7086	GM_125_B1_D03_T7	g4150930	BLASTN	441	7e-13	63	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
7087	GM_125_B1_D04_T7	g4140712	BLASTX	210	2e-16	48	(AF110183) putative integrase [Oryza sativa]
7088	GM_125_B1_D07_MR	g3450889	BLASTX	411	1e-37	64	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
7089	GM_125_B1_E01_MR	g4063760	BLASTX	302	9e-25	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7090	GM_125_B1_E02_MR	g3426334	BLASTN	443	5e-13	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
7091	GM_125_B1_E10_MR	g3097320	BLASTN	839	6e-31	78	Glycine max gene for Bd 30K, complete cds
7092	GM_125_B1_H04_MR	g2982444	BLASTX	166	2e-10	36	(AL022224) CLV1 receptor kinase like protein [Arabidopsis thaliana]
7093	GM_125_B1_H08_T7	g1402881	BLASTX	204	2e-14	50	(X98130) non-ltr retrotransposon reverse transcriptase-like protein [Arabidopsis thaliana]
7094	GM_125_B2_F01_T7	g1171591	BLASTN	413	1e-11	64	P.falciparum complete gene map of plastid-like DNA (IR-B)
7095	GM_126_A1_A01_T7	g905361	BLASTX	207	5e-15	41	(U22103) gag-protease polyprotein [Glycine max]
7096	GM_126_A1_A03_MR	g1167523	BLASTX	372	4e-32	53	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
7097	GM_126_A1_A04_MR	g3377834	BLASTX	204	1e-14	35	(AF075598) No definition line found [Arabidopsis thaliana]
7098	GM_126_A1_B05_MR	g343917	BLASTN	362	3e-10	62	yeast (s.cerevisiae) mitochondrial rep1 region & repetitive unit.
7099	GM_126_A1_B05_T7	g3142328	BLASTN	1501	4e-61	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF053008) gag-pol polyprotein [Glycine max]
7100	GM_126_A1_B09_MR	g3777527	BLASTX	556	1e-51	98	Glycine max BSR-101 satellite SB92 genomic sequence.
7101	GM_126_A1_B09_T7	g507910	BLASTN	626	1e-21	84	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7102	GM_126_A1_B11_MR	g2894612	BLASTX	153	9e-11	56	(AL021889) putative protein [Arabidopsis thaliana]
7103	GM_126_A1_B12_T7	g3702731	BLASTN	393	1e-10	78	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]
7104	GM_126_A1_C10_MR	g1418331	BLASTX	280	6e-23	53	(X95909) receptor like protein kinase [Arabidopsis thaliana]
7105	GM_126_A1_D02_T7	g2443320	BLASTX	371	5e-32	60	(D85597) polyprotein [Oryza australiensis]
7106	GM_126_A1_D03_MR	g18768	BLASTN	411	3e-12	76	Soybean Tgm6 transposable element 3' end
7107	GM_126_A1_D03_T7	g3860247	BLASTX	153	4e-18	90	(AC005824) unknown protein [Arabidopsis thaliana]
7108	GM_126_A1_D06_T7	g4063760	BLASTX	201	5e-14	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7109	GM_126_A1_D10_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7110	GM_126_A1_D10_T7	g507910	BLASTN	386	8e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7111	GM_126_A1_D12_MR	g343950	BLASTN	270	7e-10	66	S.cerevisiae mitochondrion Tyr-tRNA gene.
7112	GM_126_A1_E02_T7	g3142328	BLASTN	1151	3e-45	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Y08010) lectin receptor kinase [Arabidopsis thaliana]
7113	GM_126_A1_E05_MR	g1769897	BLASTX	169	5e-11	37	(AC000348) T7N9.19 [Arabidopsis thaliana]
7114	GM_126_A1_F09_T7	g2213599	BLASTX	189	1e-12	44	(AF023472) peptide transporter [Hordeum vulgare]
7115	GM_126_A1_F03_T7	g2655098	BLASTX	205	7e-15	35	(AC004255) T1F9.12 [Arabidopsis thaliana]
7116	GM_126_A1_F05_T7	g3056591	BLASTX	177	1e-11	52	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7117	GM_126_A1_F06_T7	g1769897	BLASTX	172	2e-11	37	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
7118	GM_126_A1_F09_T7	g4092471	BLASTN	531	6e-17	68	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7119	GM_126_A1_F10_MR	g3599418	BLASTN	358	3e-09	73	Glycine max gene for Bd 30K, complete cds
7120	GM_126_A1_F10_T7	g3097320	BLASTN	569	1e-18	82	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7121	GM_126_A1_G04_MR	g4063760	BLASTX	131	4e-17	49	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
7122	GM_126_A1_G08_MR	g4092471	BLASTN	423	4e-12	71	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7123	GM_126_A1_G09_MR	g629693	BLASTX	354	1e-31	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7124	GM_126_A1_G11_T7	g4063760	BLASTX	284	7e-23	56	hypothetical protein [Arabidopsis thaliana]
7125	GM_126_A1_G12_MR	g2864621	BLASTX	185	6e-13	41	(Y13368) reverse transcriptase [Beta vulgaris]
7126	GM_126_A1_G12_T7	g2462134	BLASTX	162	2e-10	37	Glycine max satellite STR120-A.1.
7127	GM_126_A1_H02_T7	g1142699	BLASTN	271	4e-14	68	hypothetical protein - garden snapdragon
7128	GM_126_A1_H04_T7	g100484	BLASTX	348	4e-30	61	(U75192) germin-like protein [Arabidopsis thaliana]
7129	GM_126_A1_H05_MR	g1755162	BLASTX	286	2e-24	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7130	GM_126_A2_A05_T7	g4063760	BLASTX	254	1e-19	56	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7131	GM_126_A2_A07_T7	g3334667	BLASTX	149	5e-09	84	(Y10493) putative cytochrome P450 [Glycine max]
7132	GM_126_A2_A10_T7	g1620908	BLASTN	470	3e-15	82	Carrot mRNA for DcARF1, complete cds
7133	GM_126_A2_B07_T7	g905361	BLASTX	161	4e-10	40	(U22103) gag-protease polyprotein [Glycine max]
7134	GM_126_A2_B10_T7	g3142328	BLASTN	781	2e-28	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Z97337) hypothetical protein [Arabidopsis thaliana]
7135	GM_126_A2_D12_T7	g2244859	BLASTX	110	1e-10	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7136	GM_126_A2_E02_T7	g4063760	BLASTX	278	4e-23	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7137	GM_126_A2_E06_T7	g4063760	BLASTX	482	6e-44	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7138	GM_126_A2_E09_T7	g3599418	BLASTN	741	1e-26	81	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7139	GM_126_A2_E11_T7	g2980806	BLASTX	215	7e-16	61	(AL022197) putative protein [Arabidopsis thaliana]
7140	GM_126_A2_E12_MR	g3176777	BLASTN	420	5e-13	66	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 3' sequence
7141	GM_126_A2_F01_T7	g2104945	BLASTN	393	9e-11	66	Glycine max copia-like retrotransposon Tgm, complete sequence
7142	GM_126_A2_F06_T7	g2104945	BLASTN	429	2e-12	68	Glycine max copia-like retrotransposon Tgm, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
7143	GM_126_A2_F09_T7	g4063760	BLASTX	309	2e-25	58	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7144	GM_126_A2_F10_T7	g3142328	BLASTN	535	3e-17	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7145	GM_126_A2_F11_T7	g185559	BLASTN	520	1e-16	69	Gmax gene for catalase
7146	GM_126_A2_G06_T7	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
7147	GM_126_A2_G07_T7	g3142328	BLASTN	652	1e-22	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7148	GM_126_A2_H05_T7	g507910	BLASTN	355	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7149	GM_126_A2_H06_T7	g3860247	BLASTX	148	2e-16	93	(AC005824) unknown protein [Arabidopsis thaliana]
7150	GM_126_A2_H11_T7	g3935164	BLASTX	171	3e-11	46	(AC004557) F17L21.7 [Arabidopsis thaliana]
7151	GM_126_B1_A05_T7	g507910	BLASTN	415	4e-12	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7152	GM_126_B1_B03_T7	g3645899	BLASTX	158	2e-09	57	(U68408) 5' end not determined experimentally [Zea mays]
7153	GM_126_B1_C05_T7	g1769898	BLASTX	211	2e-15	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7154	GM_126_B1_D03_T7	g114532	BLASTX	245	2e-19	86	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (Y00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum]
7155	GM_126_B1_D08_T7	g30333399	BLASTX	159	7e-10	52	(AC004238) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7156	GM_126_B1_E04_T7	g507910	BLASTN	422	2e-12	85	Glycine max BSR-101 satellite SB92 genomic sequence.
7157	GM_126_B1_E12_T7	g99922	BLASTX	144	1e-08	54	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA): pid:e150225 [Glycine max]
7158	GM_126_B1_G01_T7	g507910	BLASTN	426	1e-12	79	Glycine max BSR-101 satellite SB92 genomic sequence.
7159	GM_126_B1_G06_T7	g1769898	BLASTX	236	4e-18	78	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7160	GM_127_A1_A01_MR	g2459426	BLASTX	152	3e-09	43	(AC002332) putative splicing factor U2AF large chain [Arabidopsis thaliana]
7161	GM_127_A1_A02_MR	g4063760	BLASTX	228	7e-17	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7162	GM_127_A1_B02_MR	g507910	BLASTN	438	4e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
7163	GM_127_A1_B07_MR	g507910	BLASTN	546	5e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7164	GM_127_A1_B10_MR	g3845204	BLASTN	385	2e-10	64	Plasmodium falciparum chromosome 2, section 37 of 73 of the complete sequence
7165	GM_127_A1_C01_MR	g3033389	BLASTX	156	3e-09	30	(AC004238) Cf-2, 1-like protein [Arabidopsis thaliana]
7166	GM_127_A1_C02_MR	g4063760	BLASTX	213	3e-15	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7167	GM_127_A1_C04_MR	g100484	BLASTX	290	8e-24	44	hypothetical protein - garden snapdragon
7168	GM_127_A1_C06_MR	g3645899	BLASTX	277	4e-22	50	(U68408) 5' end not determined experimentally [Zea mays]
7169	GM_127_A1_C10_MR	g100484	BLASTX	319	6e-27	58	hypothetical protein - garden snapdragon
7170	GM_127_A1_C12_MR	g3915037	BLASTX	322	6e-41	79	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi 2570067 gnl PID e1154401 (AJ001071) second sucrose synthase [Pisum sativum]
7171	GM_127_A1_D02_MR	g3777527	BLASTX	738	4e-71	95	(AF053008) gag-pol polyprotein [Glycine max]
7172	GM_127_A1_E01_MR	g296873	BLASTN	280	3e-10	64	W.makii mitochondrial DNA
7173	GM_127_A1_E02_MR	g3668069	BLASTX	218	5e-17	93	(U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
7174	GM_127_A1_E04_MR	g2245003	BLASTX	161	3e-10	34	(Z97341) similarity to a membrane-associated salt-inducible protein - Nicotiana tabacum [Arabidopsis thaliana]
7175	GM_127_A1_E05_MR	g4050011	BLASTN	434	1e-12	60	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
7176	GM_127_A1_E10_MR	g2828280	BLASTX	168	2e-10	82	(AL021687) putative protein [Arabidopsis thaliana] gi 2832633 gnl PID e1249651 (AL021711) putative protein [Arabidopsis thaliana]
7177	GM_127_A1_F04_MR	g3645899	BLASTX	287	3e-31	63	(U68408) 5' end not determined experimentally [Zea mays]
7178	GM_127_A1_F09_MR	g3426334	BLASTN	391	1e-10	65	Pisum sativum pectin methylesterase (repmel) gene, complete cds
7179	GM_127_A1_G04_MR	g507910	BLASTN	491	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
7180	GM_127_A1_G09_MR	g507910	BLASTN	342	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7181	GM_127_A1_G12_MR	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7182	GM_127_A1_H06_MR	g13533	BLASTN	251	1e-08	68	Yeast mitochondrial tRNA genes (several, map positions 3.5 to 8.6) encoding tRNAs for Lys, Arg, Gly, Asp, Ser, Arg, and Ala. (U68408) 5' end not determined experimentally [Zea mays]
7183	GM_127_A1_H08_MR	g3645899	BLASTX	184	1e-19	46	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]
7184	GM_127_A1_H09_MR	g2827718	BLASTX	254	1e-19	42	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300
7185	GM_127_A2_A01_MR	g2501353	BLASTX	219	7e-24	91	transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum] (AB004906) transposase [Ipomoea purpurea]
7186	GM_127_A2_A01_T7	g4063770	BLASTX	226	6e-17	39	Saccharomyces cerevisiae complete mitochondrial genome
7187	GM_127_A2_A04_MR	g4160362	BLASTN	349	1e-08	59	(AF058919) No definition line found [Arabidopsis thaliana]
7188	GM_127_A2_A05_T7	g3047127	BLASTX	236	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
7189	GM_127_A2_A06_MR	g507910	BLASTN	503	4e-16	81	(D85597) polyprotein [Oryza australiensis]
7190	GM_127_A2_A08_MR	g2443320	BLASTX	177	2e-11	34	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
7191	GM_127_A2_A09_MR	g2764526	BLASTN	410	1e-17	67	(AF013467) ARF6 [Arabidopsis thaliana]
7192	GM_127_A2_B01_MR	g4102600	BLASTX	127	8e-16	68	(AF053008) gag-pol polyprotein [Glycine max]
7193	GM_127_A2_B04_MR	g3777527	BLASTX	704	2e-67	95	(U76261) unknown [Hordeum vulgare]
7194	GM_127_A2_B06_MR	g1666236	BLASTX	144	9e-09	32	(AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]
7195	GM_127_A2_B11_T7	g3402690	BLASTX	174	6e-12	52	(AF053008) gag-pol polyprotein [Glycine max]
7196	GM_127_A2_B12_MR	g3777527	BLASTX	387	1e-33	94	(Y08502) orf119 [Arabidopsis thaliana]
7197	GM_127_A2_B12_T7	g1785736	BLASTX	139	8e-09	55	(AC004667) unknown protein [Arabidopsis thaliana]
7198	GM_127_A2_C02_T7	g3668080	BLASTX	217	1e-16	84	(U93272) pyrophosphate-dependent phosphofructo-1-kinase [Prunus armeniaca]
7199	GM_127_A2_C03_T7	g2688822	BLASTX	204	9e-16	93	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinae.hmm, score: 166.20) and to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 139.32) [Arabidopsis thaliana]
7200	GM_127_A2_C04_MR	g3193302	BLASTX	167	7e-11	38	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
7201	GM_127_A2_C04_T7	g4006833	BLASTX	289	3e-23	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7202	GM_127_A2_C05_T7	g4063760	BLASTX	205	2e-14	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7203	GM_127_A2_C07_MR	g1769897	BLASTX	188	7e-16	44	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7204	GM_127_A2_C07_T7	g3142328	BLASTN	581	3e-19	77	(AC002336) hypothetical protein [Arabidopsis thaliana]
7205	GM_127_A2_C12_T7	g2651305	BLASTX	157	5e-10	50	(AC000348) T7N9.6 [Arabidopsis thaliana]
7206	GM_127_A2_D02_MR	g2213586	BLASTX	232	8e-18	42	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387)
7207	GM_127_A2_D02_T7	g421955	BLASTX	184	5e-13	56	ORF4 [Solanum tuberosum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7208	GM_127_A2_D03_MR	g3142330	BLASTX	718	3e-70	94	(U96295) envelope-like [Glycine max]
7209	GM_127_A2_D04_T7	g421955	BLASTX	392	1e-35	54	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387)
7210	GM_127_A2_D07_MR	g1769899	BLASTX	224	4e-28	81	ORF4 [Solanum tuberosum]
7211	GM_127_A2_D08_MR	g3142379	BLASTX	443	5e-41	75	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7212	GM_127_A2_D10_MR	g1666236	BLASTX	196	1e-14	31	(AF053008) envelope-like [Glycine max]
7213	GM_127_A2_E02_T7	g3777527	BLASTX	729	4e-70	95	(U76261) unknown [Hordeum vulgare]
7214	GM_127_A2_E08_T7	g905361	BLASTX	176	1e-11	30	(AF053008) gag-pol polyprotein [Glycine max]
7215	GM_127_A2_E09_T7	g3243214	BLASTN	455	2e-13	65	(U22103) gag-protease polyprotein [Glycine max]
7216	GM_127_A2_E12_MR	g507910	BLASTN	345	6e-09	70	Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
7217	GM_127_A2_E12_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7218	GM_127_A2_F05_T7	g4063760	BLASTX	296	4e-24	53	Glycine max BSR-101 satellite SB92 genomic sequence.
7219	GM_127_A2_F06_T7	g4063760	BLASTX	272	1e-21	55	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
7220	GM_127_A2_F07_T7	g2443320	BLASTX	287	4e-23	45	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
7221	GM_127_A2_F09_MR	g857398	BLASTN	542	8e-21	81	(D85597) polyprotein [Oryza australiensis]
7222	GM_127_A2_F11_MR	g320569	BLASTX	153	3e-10	44	Soybean mRNA for mitotic cyclin b1-type, complete cds
7223	GM_127_A2_F11_T7	g4038056	BLASTX	151	8e-09	30	transposon TNT1 - Arabidopsis thaliana (fragment)
7224	GM_127_A2_F12_T7	g4063770	BLASTX	179	7e-12	36	(AC005897) putative transposon [Arabidopsis thaliana]
7225	GM_127_A2_G02_MR	g505129	BLASTN	365	1e-09	71	(AB004906) transposase [Ipomoea purpurea]
7226	GM_127_A2_G11_MR	g1769899	BLASTX	165	1e-11	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7227	GM_127_A2_G12_MR	g3777527	BLASTX	582	2e-54	94	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7228	GM_127_A2_H09_T7	g18559	BLASTN	667	1e-32	73	(AF053008) gag-pol polyprotein [Glycine max]
7229	GM_127_B1_A02_T7	g4063760	BLASTX	341	7e-29	61	G.max gene for catalase
7230	GM_127_B1_A04_MR	g3582342	BLASTX	266	8e-22	41	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
7231	GM_127_B1_A09_MR	g905361	BLASTX	155	1e-18	38	(AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
7232	GM_127_B1_A10_MR	g2995405	BLASTX	597	4e-57	60	(U22103) gag-protease polyprotein [Glycine max]
7233	GM_127_B1_B01_MR	g2443320	BLASTX	386	1e-33	55	(Y12432) polyprotein [Ananas comosus]
7234	GM_127_B1_B04_T7	g3249111	BLASTX	162	2e-10	52	(D85597) polyprotein [Oryza australiensis]
7235	GM_127_B1_B08_MR	g1370171	BLASTN	619	4e-22	77	(AC003114) T12M4.7 [Arabidopsis thaliana]
7236	GM_127_B1_C01_MR	g2464913	BLASTX	251	5e-20	43	L-japonicus mRNA for small GTP-binding protein, RAB1X. (Z99708) myo-inositol transport protein homolog [Arabidopsis thaliana]

Seq No	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7237	GM_127_B1_C02_MR	g1066856	BLASTN	313	2e-12	75	Glycine max acetyl coenzyme A carboxylase (ACCCase-B) gene, 5' end of cds.
7238	GM_127_B1_C10_MR	g2735017	BLASTX	311	5e-27	64	(U82481) K1 domain interacting kinase 1 [Zea mays]
7239	GM_127_B1_C12_MR	g4063760	BLASTX	209	7e-15	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7240	GM_127_B1_D08_MR	g1171642	BLASTX	198	7e-26	71	PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK gi 481206 pir S38326 protein kinase - Arabidopsis thaliana gi 166809 (L07248) protein kinase [Arabidopsis thaliana]
7241	GM_127_B1_D10_MR	g3540195	BLASTX	165	4e-10	63	(AC004260) Unknown protein [Arabidopsis thaliana]
7242	GM_127_B1_D10_T7	g4063760	BLASTX	481	1e-51	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7243	GM_127_B1_E02_MR	g2708743	BLASTX	270	3e-21	38	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
7244	GM_127_B1_E03_T7	g1000971	BLASTN	382	3e-10	65	Hansenula wingei mitochondrial DNA, complete sequence
7245	GM_127_B1_E05_MR	g3142328	BLASTN	1866	7e-78	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7246	GM_127_B1_E05_T7	g559273	BLASTN	368	1e-09	60	Saccharomyces cerevisiae mitochondrion oxi3 gene, aap1 gene, oli2 gene, ORF4, replication of origin (ori7 and ori2), and ORF5.
7247	GM_127_B1_E06_MR	g509768	BLASTN	450	2e-13	69	Glycine max seed-specific low molecular weight sulfur-rich protein.
7248	GM_127_B1_E07_MR	g4115365	BLASTX	139	3e-09	26	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
7249	GM_127_B1_E08_MR	g3915037	BLASTX	292	5e-30	80	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi 2570067 gnl PID e1154401 (AJ001071) second sucrose synthase [Pisum sativum]
7250	GM_127_B1_E09_MR	g3097320	BLASTN	478	1e-14	69	Glycine max gene for Bd 30K, complete cds
7251	GM_127_B1_E11_T7	g2708743	BLASTX	180	1e-11	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
7252	GM_127_B1_E12_T7	g2316016	BLASTX	320	2e-26	62	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
7253	GM_127_B1_F02_MR	g130582	BLASTX	214	2e-15	34	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
7254	GM_127_B1_F05_MR	g1778822	BLASTN	492	3e-16	77	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
7255	GM_127_B1_F06_MR	g4063756	BLASTN	609	2e-20	62	Glycine max early light-induced protein (ELIP) mRNA, complete cds
7256	GM_127_B1_F08_T7	g905361	BLASTX	410	3e-37	90	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana] (U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7257	GM_127_B1_F10_T7	g2979597	BLASTN	384	3e-10	61	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
7258	GM_127_B1_G04_T7	g18695	BLASTN	389	1e-10	74	Soybean nodulin 22 gene
7259	GM_127_B1_G05_MR	g2828182	BLASTN	548	7e-19	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]
7260	GM_127_B1_G06_MR	g3777527	BLASTX	756	5e-73	94	(AF053008) gag-pol polyprotein [Glycine max]
7261	GM_127_B1_H04_MR	g2129618	BLASTX	151	4e-12	30	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7262	GM_127_B1_H07_MR	g18559	BLASTN	484	7e-15	68	G.max gene for catalase
7263	GM_127_B1_H09_T7	g2864625	BLASTX	180	6e-12	68	(AI021811) putative protein [Arabidopsis thaliana]
7264	GM_127_B1_H12_T7	g3513745	BLASTX	217	2e-15	36	(AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
7265	GM_127_B2_A04_MR	g3873182	BLASTN	433	2e-12	64	Homo sapiens chromosome 17, clone hRPK2.35_1_10, complete sequence [Homo sapiens]
7266	GM_127_B2_A06_T7	g2253579	BLASTX	103	5e-10	64	(U78721) hypothetical protein [Arabidopsis thaliana]
7267	GM_127_B2_B01_MR	g3142328	BLASTN	392	1e-10	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7268	GM_127_B2_B02_MR	g905361	BLASTX	137	1e-14	68	(U22103) gag-protease polyprotein [Glycine max]
7269	GM_127_B2_B10_MR	g3281850	BLASTX	135	3e-09	83	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]
7270	GM_127_B2_C01_T7	g4160362	BLASTN	449	1e-14	60	Saccharomyces cerevisiae complete mitochondrial genome
7271	GM_127_B2_C04_MR	g836954	BLASTX	292	6e-24	72	(U20948) receptor protein kinase [Ipomoea trifida]
7272	GM_127_B2_C06_T7	g1204057	BLASTN	417	8e-12	60	Caenorhabditis elegans cosmid C04B4, complete sequence [Caenorhabditis elegans]
7273	GM_127_B2_C07_MR	g99755	BLASTX	331	2e-33	54	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
7274	GM_127_B2_C11_T7	g2995405	BLASTX	200	5e-14	41	(Y12432) polyprotein [Ananas comosus]
7275	GM_127_B2_D03_T7	g3695387	BLASTX	212	7e-18	59	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
7276	GM_127_B2_D07_T7	g3097320	BLASTN	993	6e-38	78	Glycine max gene for Bd 30K, complete cds
7277	GM_127_B2_D10_T7	g3282159	BLASTN	374	7e-10	58	Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
7278	GM_127_B2_D12_MR	g1170781	BLASTX	214	6e-30	80	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) gi 629615 pir S47177 lactoylglutathione lyase (EC 4.4.1.5) - soybean gi 505585 (X68819) lactoylglutathione lyase [Glycine max] (AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana] (AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana] Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence (U76261) unknown [Hordeum vulgare] (AF007270) similar to the peptidase family S16 [Arabidopsis thaliana] transforming protein (myb) homolog - Arabidopsis thaliana gi 217859 gnl PID d1002205 (D10936) ATMYB1 protein [Arabidopsis thaliana] (Z97336) reverse transcriptase-like protein [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana] Glycine max BSR-101 satellite SB92 genomic sequence. Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region G.max gene for catalase P.falciparum complete gene map of plastid-like DNA (IR-B) (AC005561) putative POL3 protein [Arabidopsis thaliana] probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum] Human DNA sequence from clone 87808 on chromosome Xq21.1-21.33. Contains an EST, STSs, a GSS and genomic marker DXS472, complete sequence [Homo sapiens]
7279	GM_127_B2_E01_T7	g3193320	BLASTX	156	5e-16	54	
7280	GM_127_B2_E06_T7	g3193320	BLASTX	149	4e-13	52	
7281	GM_127_B2_E09_MR	g3845321	BLASTN	377	5e-10	63	
7282	GM_127_B2_E10_T7	g1666236	BLASTX	256	3e-21	34	
7283	GM_127_B2_E12_T7	g2191174	BLASTX	173	6e-26	64	
7284	GM_127_B2_F06_MR	g282873	BLASTX	171	1e-11	60	
7285	GM_127_B2_F12_T7	g2244803	BLASTX	229	2e-18	42	
7286	GM_127_B2_G03_T7	g507910	BLASTN	371	4e-10	72	
7287	GM_127_B2_G12_T7	g4063756	BLASTN	614	1e-20	64	
7288	GM_127_B2_H03_MR	g507910	BLASTN	394	3e-11	73	
7289	GM_127_B2_H04_MR	g505129	BLASTN	427	2e-12	65	
7290	GM_127_B2_I110_T7	g18559	BLASTN	1119	1e-43	74	
7291	GM_128_A2_A04_T7	g1171591	BLASTN	380	4e-10	63	
7292	GM_128_A2_A06_T7	g4063760	BLASTX	157	2e-10	37	
7293	GM_128_A2_A10_MR	g629693	BLASTX	161	2e-10	33	
7294	GM_128_A2_A11_MR	g3821044	BLASTN	374	7e-10	66	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7295	GM_128_A2_A11_T7	g2196878	BLASTX	104	7e-09	52	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]
7296	GM_128_A2_B01_MR	g4063760	BLASTX	485	3e-44	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7297	GM_128_A2_B01_T7	g2196878	BLASTX	295	1e-27	77	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]
7298	GM_128_A2_B02_T7	g3810595	BLASTX	284	9e-23	41	(AC005398) putative reverse transcriptase [Arabidopsis thaliana]
7299	GM_128_A2_B04_T7	g2245029	BLASTX	155	4e-09	52	(Z97341) limonene cyclase homolog [Arabidopsis thaliana]
7300	GM_128_A2_B10_T7	g1170644	BLASTX	166	1e-10	35	RING CANAL PROTEIN (KELCH PROTEIN) gi 577276 (L08483) ring canal protein [Drosophila melanogaster]
7301	GM_128_A2_C02_MR	g3599418	BLASTN	391	1e-10	76	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7302	GM_128_A2_C04_MR	g3738114	BLASTN	367	1e-09	62	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
7303	GM_128_A2_C07_T7	g1769898	BLASTX	341	1e-29	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7304	GM_128_A2_C09_MR	g3810596	BLASTX	221	3e-16	42	(AC005398) reverse transcriptase-like protein [Arabidopsis thaliana]
7305	GM_128_A2_D07_MR	g4115365	BLASTX	255	1e-19	41	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
7306	GM_128_A2_D07_T7	g1769897	BLASTX	225	4e-17	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7307	GM_128_A2_D11_MR	g629693	BLASTX	165	6e-11	32	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7308	GM_128_A2_F01_MR	g18559	BLASTN	699	1e-24	73	G.max gene for catalase
7309	GM_128_A2_F02_T7	g2522228	BLASTX	398	3e-36	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
7310	GM_128_A2_E04_MR	g3142379	BLASTX	338	6e-30	72	(AF053008) envelope-like [Glycine max]
7311	GM_128_A2_E06_MR	g2129618	BLASTX	204	2e-14	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7312	GM_128_A2_E10_MR	g18559	BLASTN	465	5e-14	69	G.max gene for catalase
7313	GM_128_A2_E12_MR	g3142328	BLASTN	518	2e-16	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7314	GM_128_A2_F04_MR	g2129618	BLASTX	154	6e-19	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7315	GM_128_A2_F08_MR	g2832901	BLASTN	286	9e-12	65	Cajanus cajan copia-like retrotransposon.Panzee
7316	GM_128_A2_G03_MR	g4092471	BLASTN	499	2e-15	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
7317	GM_128_A2_G05_T7	g905361	BLASTX	149	9e-09	83	(U22103) gag-protease polyprotein [Glycine max]
7318	GM_128_A2_G06_MR	g507910	BLASTN	353	2e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7319	GM_128_A2_G07_T7	g4106406	BLASTN	428	4e-13	64	Sorghum bicolor centromere specific element pHind22, complete sequence
7320	GM_128_A2_G08_T7	g1769897	BLASTX	322	8e-28	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7321	GM_128_A2_H01_T7	g3786009	BLASTX	164	1e-22	58	(AC005499) unknown protein [Arabidopsis thaliana]
7322	GM_128_A2_H06_MR	g507910	BLASTN	592	4e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
7323	GM_128_A2_H06_T7	g507910	BLASTN	395	3e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7324	GM_128_A2_H08_MR	g507910	BLASTN	693	1e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
7325	GM_128_B1_A05_MR	g4063760	BLASTX	585	5e-55	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7326	GM_128_B1_A07_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
7327	GM_128_B1_A08_T7	g2462058	BLASTX	232	1e-18	58	(Y13389) reverse transcriptase [Antirrhinum majus]
7328	GM_128_B1_B02_MR	g4159703	BLASTN	373	8e-10	66	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence [Arabidopsis thaliana]
7329	GM_128_B1_B08_T7	g2522228	BLASTX	135	4e-11	83	(AB007466) reverse transcriptase-like protein [Vicia faba]
7330	GM_128_B1_B09_MR	g4063756	BLASTN	533	5e-17	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7331	GM_128_B1_B10_MR	g3645899	BLASTX	221	3e-16	38	(U68408) 5' end not determined experimentally [Zea mays]
7332	GM_128_B1_B12_MR	g1769898	BLASTX	327	2e-38	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7333	GM_128_B1_C08_MR	g18559	BLASTN	521	1e-16	74	G max gene for catalase
7334	GM_128_B1_D02_MR	g3193221	BLASTN	1126	5e-44	94	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7335	GM_128_B1_D03_MR	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7336	GM_128_B1_D03_T7	g3777527	BLASTX	621	3e-59	93	(AF053008) gag-pol polyprotein [Glycine max]
7337	GM_128_B1_D09_T7	g2832611	BLASTN	362	3e-09	63	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)
7338	GM_128_B1_E06_T7	g3688328	BLASTX	262	7e-22	50	(AJ228325) reverse transcriptase [Ginkgo biloba]
7339	GM_128_B1_E09_MR	g18559	BLASTN	512	4e-16	70	G max gene for catalase
7340	GM_128_B1_E09_T7	g1666236	BLASTX	165	4e-11	31	(U76261) unknown [Hordeum vulgare]
7341	GM_128_B1_F03_MR	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7342	GM_128_B1_F03_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7343	GM_128_B1_F05_MR	g4063756	BLASTN	441	7e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7344	GM_128_B1_F05_T7	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
7345	GM_128_B1_F09_T7	g1167523	BLASTX	135	2e-09	40	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
7346	GM_128_B1_F12_T7	g3695294	BLASTN	371	9e-10	69	Glycine max module-specific glutamine synthetase gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7347	GM_128_B1_G07_MR	g505129	BLASTN	360	3e-09	63	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
7348	GM_128_B1_G10_MR	g507910	BLASTN	521	6e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7349	GM_128_B1_H02_MR	g4063760	BLASTX	464	5e-42	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7350	GM_128_B1_H03_MR	g1350783	BLASTX	301	9e-25	54	RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR gi 282883 pir S27756 receptor-like protein kinase precursor - Arabidopsis thaliana gi 166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana] gi 2842492 gnl PID e1250067 (A1.021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]
7351	GM_128_B1_H08_T7	g3201680	BLASTX	211	1e-25	86	(AF060941) extra-large G-protein [Arabidopsis thaliana]
7352	GM_128_B1_H09_MR	g4115534	BLASTX	276	1e-25	49	(AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
7353	GM_128_B1_H09_T7	g3241916	BLASTN	403	4e-11	65	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]
7354	GM_128_B2_A01_T7	g100484	BLASTX	316	1e-26	56	hypothetical protein - garden snapdragon
7355	GM_128_B2_A07_T7	g4063760	BLASTX	270	2e-21	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7356	GM_128_B2_A08_MR	g3777527	BLASTX	291	2e-23	46	(AF053008) gag-pol polypeptide [Glycine max]
7357	GM_128_B2_A08_T7	g3550435	BLASTN	555	4e-18	64	Hordeum vulgare Hotr1 gene
7358	GM_128_B2_A12_MR	g2495590	BLASTX	154	1e-09	71	HYPOTHETICAL 51.8 KD PROTEIN IN PHOH-CSGG INTERGENIC REGION gi 1787262 (AE000204) o452; This 452 aa ORF is 31 pct identical (20 gaps) to 179 residues of an approx. 248 aa protein YHUH_STRGR SW: P24222 [Escherichia coli]
7359	GM_128_B2_B02_MR	g18559	BLASTN	789	9e-29	74	G max gene for catalase
7360	GM_128_B2_B02_T7	g2995405	BLASTX	522	9e-49	64	(Y12432) polypeptide [Ananas comosus]
7361	GM_128_B2_B04_T7	g2462058	BLASTX	220	2e-17	41	(Y13389) reverse transcriptase [Antirrhinum majus]
7362	GM_128_B2_B06_MR	g3695395	BLASTX	228	3e-17	44	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
7363	GM_128_B2_B07_MR	g3600036	BLASTX	139	5e-12	87	(AF080119) contains similarity to protein kinase domains (Pfam: pkase.hmm, score: 227.04) [Arabidopsis thaliana]
7364	GM_128_B2_B10_MR	g3513745	BLASTX	247	1e-18	35	(AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
7365	GM_128_B2_B10_T7	g343945	BLASTN	390	1e-11	62	Yeast (S.cerevisiae) mitochondrial var1 gene, 5' flank.
7366	GM_128_B2_B12_T7	g4063760	BLASTX	369	7e-32	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7367	GM_128_B2_C04_T7	g505129	BLASTN	448	3e-13	64	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
7368	GM_128_B2_C06_MR	g2522230	BLASTX	324	2e-28	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
7369	GM_128_B2_C08_MR	g2443320	BLASTX	434	9e-39	50	(D85597) polyprotein [Oryza australiensis]
7370	GM_128_B2_C10_MR	g4038037	BLASTX	178	1e-11	27	(AC005936) hypothetical protein [Arabidopsis thaliana]
7371	GM_128_B2_C10_T7	g170029	BLASTN	399	5e-11	64	Glycine max cv. Dare nodulin 26 gene fragment.
7372	GM_128_B2_C11_MR	g2558658	BLASTX	191	8e-17	37	(AC002354) No definition line found [Arabidopsis thaliana]
7373	GM_128_B2_D08_T7	g3548804	BLASTX	378	3e-33	57	(AC005313) unknown protein [Arabidopsis thaliana]
7374	GM_128_B2_D11_T7	g2970554	BLASTN	482	9e-15	85	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
7375	GM_128_B2_E01_MR	g3135274	BLASTX	271	3e-22	42	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]
7376	GM_128_B2_E01_T7	g2522228	BLASTX	464	3e-43	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
7377	GM_128_B2_E02_T7	g4139038	BLASTX	166	5e-10	40	(AF072272) resistance protein candidate RGC2K [Lactuca sativa]
7378	GM_128_B2_E05_MR	g2213582	BLASTX	447	4e-40	56	(AC000348) T7N9.2 [Arabidopsis thaliana]
7379	GM_128_B2_E05_T7	g170080	BLASTN	463	6e-14	73	Soybean seed lectin gene transposable element tgm1.
7380	GM_128_B2_E06_MR	g507910	BLASTN	629	8e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7381	GM_128_B2_E06_T7	g18559	BLASTN	596	5e-20	70	G.max gene for catalase
7382	GM_128_B2_E07_T7	g3142328	BLASTN	735	3e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7383	GM_128_B2_E09_T7	g3777527	BLASTX	697	1e-66	91	(AF053008) gag-pol polyprotein [Glycine max]
7384	GM_128_B2_E11_MR	g3892709	BLASTX	176	1e-11	82	(AL033545) putative protein [Arabidopsis thaliana]
7385	GM_128_B2_E12_T7	g3319362	BLASTX	296	3e-26	49	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
7386	GM_128_B2_F05_MR	g2564750	BLASTN	372	9e-10	64	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7387	GM_128_B2_F05_T7	g1806143	BLASTN	348	7e-09	72	M.sativa mRNA for cdc2 kinase homologue, cdc2MSE.
7388	GM_128_B2_F10_MR	g3128209	BLASTX	680	4e-66	80	(AC004077) unknown protein [Arabidopsis thaliana]
7389	GM_128_B2_F12_MR	g505129	BLASTN	362	2e-09	64	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
7390	GM_128_B2_F12_T7	g2522230	BLASTX	200	3e-15	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
7391	GM_128_B2_G02_MR	g169910	BLASTN	615	3e-21	87	Soybean actin 3 gene (SAc3), complete cds.
7392	GM_128_B2_G02_T7	g3873182	BLASTN	437	1e-12	63	Homo sapiens chromosome 17, clone hRPK.235_L_10, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7393	GM_128_B2_G03_T7	g99922	BLASTX	317	1e-27	60	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA): pid:e150225 [Glycine max]
7394	GM_128_B2_G06_T7	g4056456	BLASTX	290	7e-25	80	(AC005990) Strong similarity to gb U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF 00107. ESTs gb T43674, gb H77006 and gb AA395179 come from this gene. [Arabidopsis thaliana]
7395	GM_128_B2_G07_MR	g2995405	BLASTX	204	1e-37	66	(Y12432) polyprotein [Ananas comosus]
7396	GM_128_B2_G11_T7	g421955	BLASTX	369	3e-33	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
7397	GM_128_B2_G12_T7	g3757517	BLASTX	149	2e-10	34	(AC005167) putative salt-inducible protein [Arabidopsis thaliana]
7398	GM_128_B2_H05_T7	g507910	BLASTN	471	1e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7399	GM_128_B2_H09_MR	g1785729	BLASTN	621	5e-21	61	A.thaliana mitochondrial genome, part B
7400	GM_128_B2_H09_T7	g3941729	BLASTN	405	3e-11	61	Homo sapiens chromosome 7 BAC clone F5, complete sequence [Homo sapiens]
7401	GM_129_A1_D10_MR	g905360	BLASTN	423	3e-12	88	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
7402	GM_129_A1_E07_MR	g2443320	BLASTX	157	3e-09	48	(D85597) polyprotein [Oryza australiensis]
7403	GM_129_A2_A05_MR	g3777526	BLASTN	450	2e-13	66	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
7404	GM_129_A2_A07_T7	g13606	BLASTN	283	9e-10	68	Yeast mitochondrial gene for transfer RNA-Trp >gi 343974 gb K03310 YSTMTTGWX Saccharomyces cerevisiae mitochondrial Trp-tRNA gene.
7405	GM_129_A2_A08_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7406	GM_129_A2_A08_T7	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7407	GM_129_A2_A11_T7	g3758836	BLASTN	361	3e-09	61	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
7408	GM_129_A2_A12_T7	g2642431	BLASTX	320	2e-26	48	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
7409	GM_129_A2_B01_MR	g2894587	BLASTN	383	3e-10	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-112, complete sequence [Plasmodium falciparum]
7410	GM_129_A2_B02_MR	g3845327	BLASTN	289	3e-10	63	Plasmodium falciparum chromosome 2, section 68 of 73 of the complete sequence
7411	GM_129_A2_B03_MR	g3097320	BLASTN	717	2e-25	77	Glycine max gene for Bd 30K, complete cds
7412	GM_129_A2_B09_MR	g155854	BLASTN	414	4e-12	61	Babesia bigemina antigen (Bbg 1.1) mRNA, 3' end.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
7413	GM_129_A2_B10_T7	g3426334	BLASTN	375	6e-10	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
7414	GM_129_A2_B11_MR	g134646	BLASTX	201	3e-19	92	SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (FE) gi 169955 (M64267) Fe-superoxide dismutase [Glycine max] gi 228415 prf 1803527A Fe superoxide dismutase [Glycine max] (AC005561) putative POL3 protein [Arabidopsis thaliana]
7415	GM_129_A2_B12_MR	g4063760	BLASTX	332	6e-28	59	Glycine max BSR-101 satellite SB92 genomic sequence.
7416	GM_129_A2_B12_T7	g507910	BLASTN	373	3e-10	70	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
7417	GM_129_A2_C06_T7	g2129709	BLASTX	236	1e-17	42	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
7418	GM_129_A2_C07_T7	g2522227	BLASTX	183	2e-13	38	Glycine max BSR-101 satellite SB92 genomic sequence.
7419	GM_129_A2_C12_T7	g507910	BLASTN	357	2e-09	70	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]
7420	GM_129_A2_D01_T7	g3549652	BLASTX	269	4e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7421	GM_129_A2_D02_T7	g4063760	BLASTX	148	2e-09	32	Glycine max gene for Bd 30K, complete cds
7422	GM_129_A2_D04_MR	g3097320	BLASTN	427	3e-12	63	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
7423	GM_129_A2_D05_T7	g2160694	BLASTX	246	2e-21	83	Glycine max gene for Bd 30K, complete cds
7424	GM_129_A2_D06_T7	g3097320	BLASTN	564	2e-18	73	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7425	GM_129_A2_D09_MR	g2129618	BLASTX	243	1e-18	45	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7426	GM_129_A2_D10_MR	g3142328	BLASTN	1138	1e-44	77	Glycine max gene for Bd 30K, complete cds
7427	GM_129_A2_E02_MR	g3097320	BLASTN	470	3e-14	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7428	GM_129_A2_E04_MR	g507910	BLASTN	576	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7429	GM_129_A2_E04_T7	g507910	BLASTN	572	3e-19	81	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7430	GM_129_A2_E07_MR	g3810596	BLASTX	273	8e-22	49	(U22103) gag-protease polyprotein [Glycine max]
7431	GM_129_A2_E08_MR	g905361	BLASTX	334	9e-29	78	Glycine max BSR-101 satellite SB92 genomic sequence.
7432	GM_129_A2_E08_T7	g507910	BLASTN	433	6e-13	77	hypothetical protein YPL086c - yeast (Saccharomyces cerevisiae) gi 1151240 (U43281) Lpg22p [Saccharomyces cerevisiae]
7433	GM_129_A2_E09_T7	g2132182	BLASTX	262	4e-21	83	(D85597) polyprotein [Oryza australiensis]
7434	GM_129_A2_E12_T7	g2443320	BLASTX	178	9e-16	42	(AJ006771) beta-galactosidase [Cicer arietinum]
7435	GM_129_A2_F01_MR	g3204134	BLASTX	193	4e-29	96	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7436	GM_129_A2_F07_T7	g1769899	BLASTX	189	4e-22	73	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
7437	GM_129_A2_F08_MR	g2522226	BLASTN	691	2e-24	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7438	GM_129_A2_F10_MR	g4063760	BLASTX	390	4e-34	56	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
7439	GM_129_A2_F11_MR	g1167523	BLASTX	91	5e-09	50	(U68408) 5' end not determined experimentally [Zea mays]
7440	GM_129_A2_F12_T7	g3645899	BLASTX	146	1e-13	41	

Seq No.	ClonID	NCBI gi	Method	Score	P-value	% Ident	Description
7441	GM_129_A2_G05_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7442	GM_129_A2_G05_T7	g507910	BLASTN	361	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7443	GM_129_A2_H01_MR	g3142328	BLASTN	691	3e-24	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7444	GM_129_A2_H04_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7445	GM_129_A2_H05_T7	g3645899	BLASTX	213	8e-28	51	(U68408) 5' end not determined experimentally [Zea mays]
7446	GM_129_A2_H06_MR	g507910	BLASTN	604	1e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7447	GM_129_A2_H06_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7448	GM_129_B1_A01_MR	g2522227	BLASTX	150	1e-17	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
7449	GM_129_B1_A03_MR	g507910	BLASTN	401	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7450	GM_129_B1_A03_T7	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7451	GM_129_B1_A06_MR	g3142328	BLASTN	625	3e-21	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7452	GM_129_B1_A06_T7	g35599418	BLASTN	467	4e-14	70	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7453	GM_129_B1_A07_MR	g3845197	BLASTN	365	2e-09	57	Plasmidium falciparum chromosome 2, section 35 of 73 of the complete sequence
7454	GM_129_B1_A07_T7	g1769897	BLASTX	317	3e-27	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7455	GM_129_B1_A08_MR	g2129618	BLASTX	184	4e-14	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7456	GM_129_B1_A09_MR	g4063760	BLASTX	536	9e-50	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7457	GM_129_B1_A11_T7	g3688600	BLASTX	174	2e-11	58	(AB009030) beta-Amyrin Synthase [Panax ginseng]
7458	GM_129_B1_A12_T7	g18559	BLASTN	355	5e-09	66	G-max gene for catalase
7459	GM_129_B1_B02_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7460	GM_129_B1_B02_T7	g507910	BLASTN	366	6e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7461	GM_129_B1_B03_T7	g507910	BLASTN	369	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7462	GM_129_B1_B05_MR	g2244916	BLASTX	154	3e-09	21	(Z97339) hypothetical protein [Arabidopsis thaliana]
7463	GM_129_B1_B05_T7	g3097320	BLASTN	476	2e-14	69	Glycine max gene for Bd 30K, complete cds
7464	GM_129_B1_B06_MR	g2555576	BLASTN	333	7e-09	66	small auxin up RNA gene cluster: orf 6B [Glycine max=soybeans, cv. Wayne, Genomic, 665 nt]
7465	GM_129_B1_B11_MR	g3142328	BLASTN	1290	2e-51	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7466	GM_129_B1_B12_MR	g4159702	BLASTN	579	4e-19	69	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2N11, complete sequence [Arabidopsis thaliana]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
7467	GM_129_B1_C01_T7	g3513745	BLASTX	214	3e-15	28	(AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
7468	GM_129_B1_C02_T7	g2801677	BLASTN	748	1e-27	72	Glycine max telomere-associated sequence STAS6
7469	GM_129_B1_C08_MR	g2982571	BLASTN	384	2e-10	59	Plasmodium falci-parum DNA *** SEQUENCING IN PROGRESS *** from contig 3-97, complete sequence [Plasmodium falci-parum]
7470	GM_129_B1_C10_MR	g507910	BLASTN	414	4e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7471	GM_129_B1_C10_T7	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7472	GM_129_B1_C11_MR	g905361	BLASTX	723	1e-70	96	(U22103) gag-protease polypeptide [Glycine max]
7473	GM_129_B1_D03_MR	g1040717	BLASTN	396	4e-19	67	D.polychroa microsattelite sequence (clone Dp ch1 F3)
7474	GM_129_B1_D03_T7	g130582	BLASTX	422	2e-37	62	RETROVIRUS-RELATED POL. POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
7475	GM_129_B1_D11_MR	g535454	BLASTX	196	1e-14	43	(U13940) cysteine proteinase [Alnus glutinosa]
7476	GM_129_B1_D11_T7	g535454	BLASTX	182	6e-13	58	(U13940) cysteine proteinase [Alnus glutinosa]
7477	GM_129_B1_D12_T7	g3142328	BLASTN	769	7e-28	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7478	GM_129_B1_F01_MR	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7479	GM_129_B1_F01_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7480	GM_129_B1_F02_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7481	GM_129_B1_E06_MR	g4063756	BLASTN	529	7e-17	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7482	GM_129_B1_E10_MR	g3947433	BLASTN	468	4e-14	64	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
7483	GM_129_B1_E12_T7	g1171583	BLASTN	356	5e-09	63	P.falci-parum complete gene map of plastid-like DNA (IR-A)
7484	GM_129_B1_F05_MR	g3645899	BLASTX	292	9e-24	62	(U68408) 5' end not determined experimentally [Zea mays]
7485	GM_129_B1_G04_T7	g18559	BLASTN	886	4e-33	75	G.max gene for catalase
7486	GM_129_B1_G06_MR	g3599418	BLASTN	355	5e-09	64	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7487	GM_129_B1_G08_MR	g507910	BLASTN	353	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7488	GM_129_B1_G08_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7489	GM_129_B1_G10_T7	g507910	BLASTN	380	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7490	GM_129_B1_G11_MR	g507910	BLASTN	515	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
7491	GM_129_B1_G11_T7	g4063760	BLASTX	288	3e-23	51	(AC005561) putative POL.3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7492	GM_129_B1_G12_MR	g1654140	BLASTX	260	2e-20	69	(U37840) lipoxigenase [Lycopersicon esculentum]
7493	GM_129_B1_H01_MR	g1174779	BLASTX	249	7e-20	88	TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR gi 166894 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
7494	GM_129_B1_H03_T7	g2129613	BLASTX	135	8e-10	42	homeotic protein BEL1 - Arabidopsis thaliana gi 1122533 (U39944) BELL1 [Arabidopsis thaliana]
7495	GM_129_B1_H08_MR	g4115365	BLASTX	277	5e-22	50	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
7496	GM_129_B1_H09_MR	g3142328	BLASTN	1987	2e-83	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7497	GM_129_B1_H10_MR	g507910	BLASTN	515	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
7498	GM_129_B1_H10_T7	g4063760	BLASTX	281	2e-22	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7499	GM_129_B1_H11_T7	g3097320	BLASTN	432	2e-12	69	Glycine max gene for Bd 30K, complete cds
7500	GM_129_B1_H12_MR	g2500199	BLASTX	185	6e-38	100	RAC-LIKE GTP BINDING PROTEIN RHO1 gi 477010 pir A47525 ras-related small GTP-binding protein Rho1Ps - garden pea gi 1263170 (L19093) GTP-binding protein [Pisum sativum] (U68408) 5' end not determined experimentally [Zea mays]
7501	GM_129_B2_A01_T7	g3645899	BLASTX	297	1e-29	49	Glycine max BSR-101 satellite SB92 genomic sequence.
7502	GM_129_B2_A05_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7503	GM_129_B2_A05_T7	g507910	BLASTN	409	7e-12	73	(Y12777) acyl-CoA synthetase-like protein [Homo sapiens]
7504	GM_129_B2_B01_MR	g2960069	BLASTX	155	2e-09	60	(AF110183) putative integrase [Oryza sativa]
7505	GM_129_B2_B08_MR	g4140712	BLASTX	197	6e-15	38	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
7506	GM_129_B2_C09_MR	g2462749	BLASTX	289	6e-24	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
7507	GM_129_B2_D02_MR	g2924729	BLASTN	362	3e-09	65	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
7508	GM_129_B2_D08_T7	g2708743	BLASTX	241	4e-18	36	(AF053008) gag-pol polyprotein [Glycine max]
7509	GM_129_B2_D11_T7	g3777527	BLASTX	520	3e-56	95	Glycine max pol gene for reverse transcriptase, partial sequence
7510	GM_129_B2_D12_MR	g218268	BLASTN	437	3e-13	78	G. max gene for catalase
7511	GM_129_B2_E02_MR	g18559	BLASTN	694	2e-24	75	(D12839) reverse transcriptase [Glycine max]
7512	GM_129_B2_E03_MR	g218269	BLASTX	247	3e-20	71	(U96295) envelope-like [Glycine max]
7513	GM_129_B2_E04_T7	g3142330	BLASTX	593	6e-57	84	Glycine max BSR-101 satellite SB92 genomic sequence.
7514	GM_129_B2_E09_MR	g507910	BLASTN	411	6e-12	74	M.fusca microsatellite DNA, MFGT22 region
7515	GM_129_B2_E10_T7	g4138185	BLASTN	418	1e-12	67	(X02600) unidentified open reading frame II (146 aa) [Drosophila melanogaster]
7516	GM_129_B2_E11_MR	g1335695	BLASTX	208	5e-22	46	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7517	GM_129_B2_E12_MR	g4115365	BLASTX	164	5e-10	43	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
7518	GM_129_B2_F04_T7	g1171583	BLASTN	360	3e-09	61	P.falcapur complete gene map of plastid-like DNA (IR-A)
7519	GM_129_B2_F08_T7	g3033389	BLASTX	242	2e-18	38	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
7520	GM_129_B2_F11_MR	g3777527	BLASTX	295	8e-24	45	(AF053008) gag-pol polyprotein [Glycine max]
7521	GM_129_B2_G01_MR	g117188	BLASTX	312	5e-27	50	CYTCHROME P450 LXXIA1 (ARP-2) gi 81423 pir A35867 cytochrome P450 71A1 - avocado
7522	GM_129_B2_G07_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7523	GM_129_B2_G07_T7	g507910	BLASTN	348	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7524	GM_129_B2_G08_T7	g4092470	BLASTN	713	4e-25	71	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
7525	GM_129_B2_G09_T7	g4063760	BLASTX	247	1e-25	60	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
7526	GM_129_B2_G12_T7	g454847	BLASTN	411	1e-11	75	Glycine max ribosomal protein S11 gene, complete cds
7527	GM_129_B2_H03_T7	g3097320	BLASTN	528	7e-17	71	Glycine max gene for Bd 30K, complete cds
7528	GM_129_B2_H08_MR	g3142328	BLASTN	559	6e-40	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7529	GM_129_B2_H09_MR	g4063760	BLASTX	201	5e-14	37	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
7530	GM_129_B2_H11_MR	g507910	BLASTN	389	6e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
7531	GM_129_B2_H12_T7	g2462058	BLASTX	286	2e-24	51	(Y13389) reverse transcriptase [Antirrhinum majus]
7532	GM_130_A1_A01_MR	g507910	BLASTN	501	5e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7533	GM_130_A1_B09_MR	g13373	BLASTN	395	1e-11	61	Terminal inverted repeat from Paramecium mitochondrion >gi 342968 gb J01432 PARMTDIN1 paramecium species 1 mitochondria dimer initiation region dna.
7534	GM_130_A1_B11_MR	g3777527	BLASTX	229	1e-19	63	(AF053008) gag-pol polyprotein [Glycine max]
7535	GM_130_A1_C02_MR	g3097320	BLASTN	710	4e-25	81	Glycine max gene for Bd 30K, complete cds
7536	GM_130_A1_C04_MR	g1644402	BLASTX	174	8e-12	49	(U73524) putative ATP/GTP-binding protein [Homo sapiens]
7537	GM_130_A1_E06_MR	g1483218	BLASTX	130	5e-13	43	(X99793) induced upon wounding stress [Arabidopsis thaliana]
7538	GM_130_A1_G11_MR	g3845197	BLASTN	394	9e-11	62	Plasmodium falcapur chromosome 2, section 35 of 73 of the complete sequence
7539	GM_130_B1_A01_T7	g4050011	BLASTN	425	3e-12	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
7540	GM_130_B1_A02_MR	g2624372	BLASTN	375	6e-10	62	Plasmodium falcapur DNA *** SEQUENCING IN PROGRESS
7541	GM_130_B1_A02_T7	g3250687	BLASTX	127	4e-14	40	*** from contig 3-64, complete sequence [Plasmodium falcapur] (AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
7542	GM_130_B1_A03_MR	g18559	BLASTN	412	1e-11	70	G-max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7543	GM_130_B1_A05_T7	g3979928	BLASTN	400	5e-11	63	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
7544	GM_130_B1_A06_T7	g21059	BLASTN	425	4e-13	66	P.vulgaris PvVPE2 mRNA for pectin esterase.
7545	GM_130_B1_A07_MR	g507910	BLASTN	359	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7546	GM_130_B1_A11_MR	g2522226	BLASTN	483	7e-15	63	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
7547	GM_130_B1_B04_T7	g3738114	BLASTN	359	3e-09	65	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
7548	GM_130_B1_B06_MR	g3142379	BLASTX	299	1e-25	67	(AF053008) envelope-like [Glycine max]
7549	GM_130_B1_B07_T7	g629693	BLASTX	183	7e-13	45	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7550	GM_130_B1_B08_T7	g3021268	BLASTX	329	1e-27	44	(AL022347) putative protein [Arabidopsis thaliana]
7551	GM_130_B1_B10_MR	g2522228	BLASTX	222	4e-17	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
7552	GM_130_B1_B10_T7	g1769898	BLASTX	239	2e-18	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7553	GM_130_B1_B12_T7	g3033400	BLASTX	216	5e-34	93	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
7554	GM_130_B1_C02_MR	g3645899	BLASTX	206	1e-14	42	(U68408) 5' end not determined experimentally [Zea mays]
7555	GM_130_B1_C02_T7	g2708743	BLASTX	203	4e-14	31	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
7556	GM_130_B1_C04_T7	g3513747	BLASTX	204	2e-18	33	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
7557	GM_130_B1_C08_MR	g2194123	BLASTX	125	1e-15	70	(AC002062) Similar to Secale chloroplast ribosomal protein L12 (gb SCL121A). EST gb H36579 comes from this gene. [Arabidopsis thaliana]
7558	GM_130_B1_D01_T7	g2995405	BLASTX	574	2e-54	59	(Y12432) polyprotein [Ananas comosus]
7559	GM_130_B1_D02_MR	g3492857	BLASTN	454	2e-13	65	Homo sapiens 12q24.2 PAC RPC11-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence [Homo sapiens]
7560	GM_130_B1_D04_MR	g1666236	BLASTX	166	3e-11	39	(U76261) unknown [Hordeum vulgare]
7561	GM_130_B1_D05_MR	g3777527	BLASTX	338	2e-28	45	(AF053008) gag-pol polyprotein [Glycine max]
7562	GM_130_B1_D07_T7	g4038056	BLASTX	399	2e-35	51	(AC005897) putative transposon [Arabidopsis thaliana]
7563	GM_130_B1_D09_MR	g2429543	BLASTX	173	5e-11	43	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans])
7564	GM_130_B1_D11_MR	g3250687	BLASTX	158	2e-10	34	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
7565	GM_130_B1_E01_MR	g2462936	BLASTX	303	3e-26	46	(Y12321) open reading frame 2 [Brassica oleracea]
7566	GM_130_B1_E03_MR	g100488	BLASTX	199	5e-14	44	TNP2 protein - garden snapdragon

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
7567	GM_130_B1_E04_MR	g3406033	BLASTN	393	1e-10	67	Homo sapiens 12p13.3 RPC14-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence [Homo sapiens]
7568	GM_130_B1_E05_T7	g3176806	BLASTN	389	2e-11	62	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
7569	GM_130_B1_E08_MR	g99755	BLASTX	381	3e-34	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
7570	GM_130_B1_E11_MR	g1066856	BLASTN	459	1e-13	87	Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene, 5' end of cds.
7571	GM_130_B1_F01_MR	g1666236	BLASTX	191	5e-14	30	(U76261) unknown [Hordeum vulgare]
7572	GM_130_B1_F02_T7	g3687234	BLASTX	182	5e-12	35	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
7573	GM_130_B1_F03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7574	GM_130_B1_F03_T7	g3777527	BLASTX	794	4e-77	98	(AF053008) gag-pol polyprotein [Glycine max]
7575	GM_130_B1_F05_MR	g2828184	BLASTN	545	1e-17	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; MSN9, complete sequence [Arabidopsis thaliana]
7576	GM_130_B1_F07_MR	g2642431	BLASTX	335	4e-28	50	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
7577	GM_130_B1_F10_T7	g507910	BLASTN	578	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7578	GM_130_B1_F11_T7	g18559	BLASTN	464	5e-14	76	G.max gene for catalase
7579	GM_130_B1_F12_MR	g2443320	BLASTX	452	1e-40	48	(D85597) polyprotein [Oryza australiensis]
7580	GM_130_B1_G05_MR	g507910	BLASTN	365	7e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
7581	GM_130_B1_G05_T7	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
7582	GM_130_B1_G10_MR	g1431738	BLASTN	676	9e-24	76	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
7583	GM_130_B1_G12_MR	g2239134	BLASTX	168	7e-15	65	(Y13729) NDH-A protein [Hordeum vulgare]
7584	GM_130_B1_H01_MR	g4063756	BLASTN	478	1e-14	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7585	GM_130_B1_H02_MR	g1666236	BLASTX	240	1e-19	32	(U76261) unknown [Hordeum vulgare]
7586	GM_130_B1_H02_T7	g3980359	BLASTN	372	9e-10	60	Human DNA sequence from clone 34417 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence [Homo sapiens]
7587	GM_130_B1_H03_T7	g1142701	BLASTN	1299	2e-52	84	Glycine max satellite STR120-A.3.
7588	GM_130_B1_H04_T7	g905361	BLASTX	219	2e-16	30	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7589	GM_130_B1_H05_MR	g100484	BLASTX	325	1e-27	43	hypothetical protein - garden snapdragon
7590	GM_130_B1_H06_T7	g2465923	BLASTX	175	3e-21	79	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
7591	GM_130_B1_H08_MR	g3063461	BLASTX	168	1e-10	33	(AC003981) F22O13.23 [Arabidopsis thaliana]
7592	GM_130_B1_H10_MR	g629693	BLASTX	150	3e-15	36	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7593	GM_130_B1_H11_MR	g2979597	BLASTN	716	3e-25	65	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
7594	GM_130_B1_H12_MR	g3695395	BLASTX	230	6e-19	40	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
7595	GM_130_B1_H12_T7	g3777527	BLASTX	687	1e-65	96	(AF053008) gag-pol polyprotein [Glycine max]
7596	GM_130_B2_A01_MR	g2129618	BLASTX	172	3e-12	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7597	GM_130_B2_A05_MR	g905361	BLASTX	305	1e-25	96	(U22103) gag-protease polyprotein [Glycine max]
7598	GM_130_B2_A06_MR	g507910	BLASTN	339	1e-08	69	Glycine max BSR-101 satellite SB92 genomic sequence.
7599	GM_130_B2_A06_T7	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7600	GM_130_B2_A07_T7	g3142328	BLASTN	844	3e-31	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U22103) gag-protease polyprotein [Glycine max]
7601	GM_130_B2_A08_T7	g905361	BLASTX	524	1e-49	96	Glycine max BSR-101 satellite SB92 genomic sequence.
7602	GM_130_B2_A11_T7	g507910	BLASTN	617	3e-21	83	Soybean chloroplast psb A gene coding for photosystem II thylakoid membrane protein
7603	GM_130_B2_B05_MR	g11565	BLASTN	556	1e-18	91	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7604	GM_130_B2_B07_MR	g4063760	BLASTX	272	1e-21	53	(Y13389) reverse transcriptase [Antirrhinum majus]
7605	GM_130_B2_C01_T7	g2462058	BLASTX	266	3e-22	52	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
7606	GM_130_B2_C03_MR	g2997694	BLASTX	196	7e-15	38	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7607	GM_130_B2_C06_T7	g3142328	BLASTN	586	1e-19	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7608	GM_130_B2_C07_MR	g100484	BLASTX	340	3e-29	52	hypothetical protein - garden snapdragon
7609	GM_130_B2_C07_T7	g18559	BLASTN	366	1e-09	75	G.max gene for catalase
7610	GM_130_B2_C08_T7	g3142328	BLASTN	700	1e-24	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7611	GM_130_B2_C09_T7	g3142328	BLASTN	1306	3e-52	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7612	GM_130_B2_C10_T7	g507910	BLASTN	720	6e-26	88	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7613	GM_130_B2_C12_MR	g507910	BLASTN	561	1e-18	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7614	GM_130_B2_D02_MR	g2522227	BLASTX	199	3e-15	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
7615	GM_130_B2_D03_T7	g4063760	BLASTX	537	8e-50	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7616	GM_130_B2_D07_MR	g3763850	BLASTN	524	1e-16	65	Glycine max GmENOD93 gene for early nodulin, complete cds
7617	GM_130_B2_D11_MR	g505129	BLASTN	361	2e-09	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7618	GM_130_B2_E05_MR	g2129618	BLASTX	218	6e-16	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7619	GM_130_B2_E05_T7	g2244803	BLASTX	208	2e-19	42	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]
7620	GM_130_B2_E07_MR	g1066856	BLASTN	456	1e-13	67	Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene, 5' end of cds.
7621	GM_130_B2_F09_MR	g3599418	BLASTN	559	3e-18	83	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7622	GM_130_B2_E12_MR	g18559	BLASTN	361	3e-09	68	G-max gene for catalase
7623	GM_130_B2_F07_MR	g4063760	BLASTX	557	5e-52	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7624	GM_130_B2_F10_MR	g3097320	BLASTN	428	2e-12	72	Glycine max gene for Bd 30K, complete cds
7625	GM_130_B2_G05_T7	g130398	BLASTX	187	1e-12	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
7626	GM_130_B2_H04_MR	g3777527	BLASTX	669	1e-66	97	(TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
7627	GM_130_B2_H06_MR	g3097320	BLASTN	480	1e-14	77	(AF053008) gag-pol polyprotein [Glycine max]
7628	GM_130_B2_H09_T7	g905361	BLASTX	432	1e-39	95	Glycine max gene for Bd 30K, complete cds
7629	GM_131_A1_A05_T7	g1769898	BLASTX	241	1e-18	58	(U22103) gag-protease polyprotein [Glycine max]
7630	GM_131_A1_B03_MR	g2276311	BLASTN	367	1e-09	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7631	GM_131_A1_D01_MR	g3650039	BLASTX	149	8e-09	57	Human DNA sequence from PAC 431A14 on chromosome 6p21. Contains CYCLOPHILIN (PEPTIDYLPROLYL ISOMERASE) like and CIP1 (WAF1, CDKN1, CDKN1, MDA-6, SD11, PIC1, CAP20) genes. Contains probable GTPase and receptor genes and E...
7632	GM_131_A1_D02_MR	g3204133	BLASTN	416	7e-12	84	(AC005396) putative Er/Spm transposon protein, 5' partial [Arabidopsis thaliana]
7633	GM_131_A1_E09_T7	g507910	BLASTN	384	9e-11	77	Cicer arretinum mRNA for beta-galactosidase, partial Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7634	GM_131_A1_F01_MR	g3695395	BLASTX	174	2e-11	46	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
7635	GM_131_A1_G06_T7	g3097836	BLASTN	434	1e-12	62	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
7636	GM_131_A1_H01_MR	g130582	BLASTX	155	4e-09	63	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
7637	GM_131_B1_A09_T7	g100484	BLASTX	364	7e-32	56	hypothetical protein - garden snapdragon
7638	GM_131_B1_B02_T7	g3845197	BLASTN	410	2e-11	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
7639	GM_131_B1_B07_T7	g3097320	BLASTN	586	2e-19	75	Glycine max gene for Bd 30K, complete cds
7640	GM_131_B1_C01_T7	g1871202	BLASTN	372	9e-10	67	Human chromosome 16p13 BAC clone CTT987SK-3H8 complete sequence [Homo sapiens]
7641	GM_131_B1_C03_T7	g2979574	BLASTN	484	8e-15	64	Homo sapiens Chromosome 16 BAC clone CTT987SK-A-279B10, complete sequence [Homo sapiens]
7642	GM_131_B1_C07_T7	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7643	GM_131_B1_C11_T7	g2961349	BLASTX	225	1e-16	50	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
7644	GM_131_B1_D11_T7	g3142328	BLASTN	939	1e-35	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7645	GM_131_B1_F07_T7	g3097320	BLASTN	458	1e-13	73	Glycine max gene for Bd 30K, complete cds
7646	GM_131_B1_G07_T7	g18559	BLASTN	348	1e-08	74	G.max gene for catalase
7647	GM_131_B1_G09_T7	g3023281	BLASTX	377	1e-38	61	HIGH AFFINITY AMMONIUM TRANSPORTER gi 2065194 gnl PID e223603 (X95098) ammonium transporter [Lycopersicon esculentum]
7648	GM_131_B1_H01_T7	g4063760	BLASTX	377	9e-33	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7649	GM_131_B2_A01_MR	g3142328	BLASTN	777	3e-28	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7650	GM_131_B2_A06_MR	g3142328	BLASTN	1225	1e-48	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7651	GM_131_B2_A07_MR	g505129	BLASTN	351	1e-11	73	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7652	GM_131_B2_A09_MR	g3845298	BLASTN	403	3e-11	67	Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7653	GM_131_B2_A10_MR	g1769898	BLASTX	336	5e-29	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7654	GM_131_B2_B06_MR	g2995405	BLASTX	333	3e-28	45	(Y12432) polyprotein [Ananas comosus]
7655	GM_131_B2_B11_MR	g1769897	BLASTX	179	4e-12	32	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7656	GM_131_B2_C11_T7	g3777527	BLASTX	636	3e-60	95	(AF053008) gag-pol polyprotein [Glycine max]
7657	GM_131_B2_D01_MR	g100488	BLASTX	128	8e-09	37	TNP2 protein - garden snapdragon
7658	GM_131_B2_D04_T7	g1091678	BLASTX	140	1e-11	36	activator-like transposable element [Pennisetum glaucum]
7659	GM_131_B2_D06_MR	g541825	BLASTX	124	6e-11	80	protein kinase - spinach gi 457711 (Z30332) protein kinase [Spinacia oleracea]
7660	GM_131_B2_D10_T7	g3142328	BLASTN	1727	2e-71	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U68408) 5' end not determined experimentally [Zea mays]
7661	GM_131_B2_D12_T7	g3645899	BLASTX	173	3e-15	41	Glycine max gene for Bd 30K, complete cds
7662	GM_131_B2_E01_MR	g3097320	BLASTN	620	5e-21	80	(U68408) 5' end not determined experimentally [Zea mays]
7663	GM_131_B2_E03_T7	g3645899	BLASTX	275	3e-27	49	(AC002062) Strong similarity to Zea mays retrotransposon
7664	GM_131_B2_E04_T7	g2194136	BLASTX	370	6e-32	48	Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
7665	GM_131_B2_F06_MR	g3142328	BLASTN	1621	1e-66	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005171) putative retrotransposon [Arabidopsis thaliana]
7666	GM_131_B2_E09_T7	g3779026	BLASTX	324	5e-27	47	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
7667	GM_131_B2_E11_T7	g3650039	BLASTX	136	5e-14	36	[Arabidopsis thaliana]
7668	GM_131_B2_F01_MR	g4038056	BLASTX	294	4e-24	50	(AC005897) putative transposon [Arabidopsis thaliana]
7669	GM_131_B2_F06_T7	g3947433	BLASTN	439	9e-13	73	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
7670	GM_131_B2_G03_T7	g2815075	BLASTN	380	4e-10	60	Caenorhabditis elegans cosmid Y38H8A, complete sequence [Caenorhabditis elegans]
7671	GM_131_B2_G05_MR	g1769898	BLASTX	331	2e-28	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7672	GM_131_B2_G05_T7	g3319351	BLASTX	207	1e-14	38	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
7673	GM_131_B2_G07_MR	g4126312	BLASTN	456	1e-13	63	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
7674	GM_131_B2_G09_MR	g18559	BLASTN	448	3e-13	70	G-max gene for catalase
7675	GM_131_B2_G09_T7	g2522228	BLASTX	124	3e-10	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
7676	GM_131_B2_G11_MR	g3738114	BLASTN	466	5e-14	66	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7677	GM_131_B2_G12_T7	g3777527	BLASTX	334	6e-31	74	(AF053008) gag-pol polyprotein [Glycine max]
7678	GM_131_B2_H03_MR	g2213606	BLASTN	420	6e-12	58	Genomic sequence for Arabidopsis thaliana BAC F2119, complete sequence [Arabidopsis thaliana]
7679	GM_131_B2_H04_MR	g507910	BLASTN	373	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7680	GM_131_B2_H06_MR	g2245044	BLASTX	174	2e-20	52	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
7681	GM_132_A1_A10_T7	g3882355	BLASTX	189	1e-13	77	(U92460) pdr1 [Arabidopsis thaliana]
7682	GM_132_A1_E03_T7	g507910	BLASTN	569	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7683	GM_132_A1_F01_MR	g1658456	BLASTN	350	2e-09	66	Gossypium barbadense strain Griza 84, gypsy retrotransposon, reverse transcriptase gene, partial cds.
7684	GM_132_A1_F03_MR	g342952	BLASTN	409	2e-12	64	paramécie species 1.168 mt dna dimer: replication init. region.
7685	GM_132_A1_F04_T7	g2522227	BLASTX	207	5e-16	54	(AB007466) retrotransposon-like gene: the first amino acid was determined to be glycine [Vicia faba]
7686	GM_132_A1_F12_T7	g3452140	BLASTX	191	2e-14	73	(AJ004901) resistance protein [Glycine max]
7687	GM_132_A1_H01_T7	g3582328	BLASTX	170	6e-11	39	(AC005496) hypothetical protein [Arabidopsis thaliana]
7688	GM_132_A1_H02_T7	g3298547	BLASTX	180	4e-12	42	(AC004681) putative condensin protein [Arabidopsis thaliana]
7689	GM_132_A1_H11_T7	g3142328	BLASTN	692	2e-24	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7690	GM_132_A2_A02_T7	g3097320	BLASTN	1011	9e-39	78	Glycine max gene for Bd 30K, complete cds
7691	GM_132_A2_A05_MR	g905361	BLASTX	697	5e-68	93	(U22103) gag-protease polyprotein [Glycine max]
7692	GM_132_A2_A05_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7693	GM_132_A2_A11_MR	g3645899	BLASTX	155	2e-12	50	(U68408) 5' end not determined experimentally [Zea mays]
7694	GM_132_A2_A11_T7	g3777527	BLASTX	313	9e-33	49	(AF053008) gag-pol polyprotein [Glycine max]
7695	GM_132_A2_B03_T7	g3513745	BLASTX	213	4e-15	33	(AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
7696	GM_132_A2_B04_T7	g1769898	BLASTX	176	4e-17	52	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7697	GM_132_A2_B05_MR	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
7698	GM_132_A2_B05_T7	g4063760	BLASTX	219	7e-16	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7699	GM_132_A2_C01_MR	g18559	BLASTN	1004	2e-38	73	G.max gene for catalase
7700	GM_132_A2_C02_MR	g3608155	BLASTX	117	2e-13	60	(AC005314) putative RNA helicase [Arabidopsis thaliana]
7701	GM_132_A2_C02_T7	g3377834	BLASTX	216	6e-16	36	(AF075598) No definition line found [Arabidopsis thaliana]
7702	GM_132_A2_C03_T7	g422418	BLASTX	228	6e-17	43	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
7703	GM_132_A2_C05_T7	g3645899	BLASTX	280	2e-22	57	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7704	GM_132_A2_C07_T7	g3241916	BLASTN	505	9e-16	68	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]
7705	GM_132_A2_C08_T7	g4006831	BLASTX	229	9e-27	41	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
7706	GM_132_A2_C09_MR	g3777527	BLASTX	289	3e-23	52	(AF053008) gag-pol polyprotein [Glycine max]
7707	GM_132_A2_D02_MR	g343022	BLASTN	733	3e-26	83	Pea chloroplast photosystem II gene encoding the D2 and 44kd chlorophyll a-binding proteins, complete cds.
7708	GM_132_A2_D03_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7709	GM_132_A2_D03_T7	g507910	BLASTN	623	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7710	GM_132_A2_D06_MR	g131301	BLASTX	246	3e-20	86	PHOTOSYSTEM II D2 PROTEIN (PHOTOSYSTEM Q(A) PROTEIN) gi 72664 pir F2NTD2 photosystem II protein D2 - common tobacco chloroplast gi 1076691 pir S52397 photosystem II protein D2 - garden snapdragon chloroplast gi 11824 (Z00044) PSII D2 protein [Nicotiana tabacum] gi 669100 (X84155) photosystem I subunit [Antirrhinum majus] gi 225284 prf 1211235V photosystem II D2 protein [Nicotiana tabacum]
7711	GM_132_A2_D10_MR	g99922	BLASTX	272	1e-28	66	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA): pid:e150225 [Glycine max]
7712	GM_132_A2_E05_T7	g1785701	BLASTX	103	2e-09	33	(Y08501) orf154 [Arabidopsis thaliana]
7713	GM_132_A2_E08_T7	g3810596	BLASTX	138	7e-09	32	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7714	GM_132_A2_F03_MR	g4038057	BLASTX	179	7e-12	39	(AC005897) hypothetical protein [Arabidopsis thaliana]
7715	GM_132_A2_F04_T7	g3608144	BLASTX	118	2e-13	72	(AC005314) unknown protein [Arabidopsis thaliana]
7716	GM_132_A2_F06_T7	g3599418	BLASTN	493	2e-15	88	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7717	GM_132_A2_F08_T7	g1769898	BLASTX	399	5e-36	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7718	GM_132_A2_G01_T7	g1666236	BLASTX	294	3e-25	34	(U76261) unknown [Hordeum vulgare]
7719	GM_132_A2_G02_MR	g2160169	BLASTX	143	6e-18	48	(AC000132) No definition line found [Arabidopsis thaliana]
7720	GM_132_A2_G03_MR	g3777527	BLASTX	240	5e-18	38	(AF053008) gag-pol polyprotein [Glycine max]
7721	GM_132_A2_G06_T7	g3176795	BLASTN	430	4e-13	60	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
7722	GM_132_A2_G08_T7	g4160362	BLASTN	357	4e-09	61	Saccharomyces cerevisiae complete mitochondrial genome
7723	GM_132_A2_H09_MR	g3834323	BLASTX	192	5e-14	42	(AC005679) F9K20.25 [Arabidopsis thaliana]
7724	GM_132_A2_H10_MR	g18559	BLASTN	427	3e-12	74	G.max gene for catalase
7725	GM_132_B1_A03_T7	g507910	BLASTN	629	8e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
7726	GM_132_B1_A04_T7	g2791289	BLASTX	358	1e-30	49	(AJ000387) protease [Drosophila melanogaster]
7727	GM_132_B1_A11_T7	g507910	BLASTN	404	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
7728	GM_132_B1_A12_T7	g2506276	BLASTX	225	5e-17	64	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) gi 2129561 pir S71235 chaperonin-60 alpha chain - Arabidopsis thaliana gi 1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana]
7729	GM_132_B1_B01_T7	g2129618	BLASTX	161	1e-11	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7730	GM_132_B1_B02_MR	g3449327	BLASTN	419	7e-12	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]
7731	GM_132_B1_B03_MR	g3810596	BLASTX	255	7e-20	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7732	GM_132_B1_B05_MR	g3810596	BLASTX	179	9e-12	45	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7733	GM_132_B1_B06_MR	g2443320	BLASTX	252	2e-19	47	(D85597) polyprotein [Oryza australiensis]
7734	GM_132_B1_B10_MR	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
7735	GM_132_B1_B11_T7	g1326016	BLASTX	188	1e-12	58	TY3-2 orfB
7736	GM_132_B1_C05_MR	g4063760	BLASTX	321	8e-27	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7737	GM_132_B1_C06_MR	g2660670	BLASTX	360	4e-31	76	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]
7738	GM_132_B1_C06_T7	g2827663	BLASTX	149	8e-09	35	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]
7739	GM_132_B1_C07_MR	g3142300	BLASTX	284	9e-23	65	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb I29224 from S. cerevisiae. ESTs gb R64908 and gb T88158, gb N38703 and gb AA651043 come from this gene. [Arabidopsis thaliana]
7740	GM_132_B1_C08_MR	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
7741	GM_132_B1_C08_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7742	GM_132_B1_C10_MR	g507910	BLASTN	678	5e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
7743	GM_132_B1_C11_T7	g170605	BLASTN	546	4e-18	64	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
7744	GM_132_B1_D01_T7	g3142328	BLASTN	812	8e-30	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U68408) 5' end not determined experimentally [Zea mays]
7745	GM_132_B1_D02_MR	g3645899	BLASTX	196	2e-14	46	Glycine max BSR-101 satellite SB92 genomic sequence.
7746	GM_132_B1_D04_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7747	GM_132_B1_D04_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7748	GM_132_B1_D06_MR	g2129618	BLASTX	161	7e-10	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7749	GM_132_B1_D10_MR	g18559	BLASTN	352	6e-09	65	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7750	GM_132_B1_E01_MR	g3142328	BLASTN	494	2e-15	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Y12432) polyprotein [Ananas comosus]
7751	GM_132_B1_E05_T7	g2995405	BLASTX	147	2e-10	44	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
7752	GM_132_B1_E10_MR	g2244915	BLASTX	228	5e-17	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7753	GM_132_B1_E11_MR	g1769898	BLASTX	225	4e-17	60	(Y12432) polyprotein [Ananas comosus]
7754	GM_132_B1_F02_T7	g2995405	BLASTX	410	3e-40	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA);
7755	GM_132_B1_F03_MR	g99922	BLASTX	368	9e-43	76	pid:e150225 [Glycine max]
7756	GM_132_B1_F05_MR	g2462749	BLASTX	226	4e-17	57	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
7757	GM_132_B1_F06_MR	g3599418	BLASTN	380	3e-10	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7758	GM_132_B1_G02_T7	g1769898	BLASTX	334	8e-29	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7759	GM_132_B1_G03_MR	g3047103	BLASTX	146	7e-09	84	(AF058919) regions of weak similarity to l-asparaginase [Arabidopsis thaliana]
7760	GM_132_B1_G08_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7761	GM_132_B1_G08_T7	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7762	GM_132_B1_G10_MR	g3810596	BLASTX	300	1e-24	51	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7763	GM_132_B1_H06_T7	g507910	BLASTN	622	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7764	GM_132_B1_H07_T7	g3377856	BLASTX	351	5e-30	53	(AF076274) contains similarity to reverse transcriptase (Pfam: zfvrt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zfcchc.hmm, score: 12.35) [Arabidopsis thaliana]
7765	GM_132_B1_H08_T7	g1703318	BLASTX	111	4e-13	65	ANNEXIN-LIKE PROTEIN RJ4 gi 1362037 pir S56674 annexin homolog RJ4 (clone RJ4) - garden strawberry (fragment) gi 643076 (U19941) annexin [Fragaria x ananassa]
7766	GM_132_B1_H10_T7	g4038037	BLASTX	155	4e-09	29	(AC005936) hypothetical protein [Arabidopsis thaliana]
7767	GM_132_B1_H11_T7	g2584827	BLASTN	309	6e-11	60	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]
7768	GM_132_B2_A02_T7	g3777527	BLASTX	229	7e-17	76	(AF053008) gag-pol polyprotein [Glycine max]
7769	GM_132_B2_A04_MR	g507910	BLASTN	529	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
7770	GM_132_B2_A08_MR	g507910	BLASTN	406	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7771	GM_132_B2_B03_T7	g2522227	BLASTX	199	3e-15	52	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
7772	GM_132_B2_B06_MR	g3461836	BLASTX	206	8e-19	72	(AC005315) putative protein kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
7773	GM_132_B2_B09_MR	g3142328	BLASTN	813	7e-30	98	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7774	GM_132_B2_B12_MR	g3142328	BLASTN	1330	2e-53	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
7775	GM_132_B2_C01_MR	g4063760	BLASTX	156	3e-09	37	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387)
7776	GM_132_B2_C02_T7	g421955	BLASTX	183	2e-21	52	ORF4 [Solanum tuberosum]
7777	GM_132_B2_C03_MR	g2462058	BLASTX	385	7e-35	54	(Y13389) reverse transcriptase [Antirrhinum majus]
7778	GM_132_B2_C04_MR	g3738114	BLASTN	398	6e-11	59	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
7779	GM_132_B2_C07_MR	g1142703	BLASTN	903	3e-34	91	Glycine max satellite STR120-B.1.
7780	GM_132_B2_C09_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7781	GM_132_B2_C10_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence
7782	GM_132_B2_C10_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7783	GM_132_B2_D03_MR	g3023751	BLASTX	177	3e-14	64	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) gi 1076772 pir S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat gi 854626 (X86903) peptidylprolyl isomerase [Triticum aestivum]
7784	GM_132_B2_D10_T7	g1769898	BLASTX	200	1e-24	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7785	GM_132_B2_D12_MR	g18559	BLASTN	1098	9e-43	75	G.max gene for catalase
7786	GM_132_B2_E05_MR	g100484	BLASTX	244	3e-22	46	hypothetical protein - garden snapdragon
7787	GM_132_B2_E05_T7	g3777527	BLASTX	541	4e-50	91	(AF053008) gag-pol polypeptide [Glycine max]
7788	GM_132_B2_E08_MR	g3097320	BLASTN	415	9e-12	72	Glycine max gene for Bd 30K, complete cds
7789	GM_132_B2_F02_T7	g1480927	BLASTN	395	6e-11	79	Glycine max cdc2 protein kinase (cdc2(1)) nonprocessed pseudogene
7790	GM_132_B2_F03_T7	g18737	BLASTN	374	6e-10	81	Glycine max RPRP3 gene for repetitive proline-rich protein 3
7791	GM_132_B2_F05_MR	g99755	BLASTX	406	4e-37	53	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 163556 (X53973) reverse transcriptase [Arabidopsis thaliana]
7792	GM_132_B2_F07_MR	g3820757	BLASTN	400	3e-11	65	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
7793	GM_132_B2_G01_MR	g508826	BLASTN	362	2e-09	64	Drosophila melanogaster Oregon-R mitochondrial A+T region.
7794	GM_132_B2_G02_T7	g18559	BLASTN	769	8e-28	79	G.max gene for catalase
7795	GM_132_B2_G05_MR	g3047068	BLASTX	192	3e-13	39	(AF058825) similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7796	GM_132_B2_G10_MR	g1167523	BLASTX	107	7e-17	46	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
7797	GM_132_B2_G11_MR	g2995405	BLASTX	493	1e-45	69	(Y12432) polyprotein [Ananas comosus]
7798	GM_132_B2_H02_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7799	GM_132_B2_H09_MR	g3097320	BLASTN	465	5e-14	68	Glycine max gene for Bd 30K, complete cds
7800	GM_133_A1_A02_T7	g507910	BLASTN	539	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
7801	GM_133_A1_A05_T7	g905361	BLASTX	116	9e-13	31	(U22103) gag-protease polyprotein [Glycine max]
7802	GM_133_A1_B09_T7	g507910	BLASTN	395	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7803	GM_133_A1_B10_T7	g3097320	BLASTN	837	7e-31	79	Glycine max gene for Bd 30K, complete cds
7804	GM_133_A1_B11_MR	g2443320	BLASTX	193	4e-13	36	(D85597) polyprotein [Oryza australiensis]
7805	GM_133_A1_B12_MR	g99922	BLASTX	324	2e-28	76	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
7806	GM_133_A1_C01_T7	g3097320	BLASTN	467	4e-14	70	Glycine max gene for Bd 30K, complete cds
7807	GM_133_A1_C06_MR	g4038056	BLASTX	266	4e-21	47	(AC005897) putative transposon [Arabidopsis thaliana]
7808	GM_133_A1_C12_T7	g4063760	BLASTX	173	7e-18	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7809	GM_133_A1_D05_T7	g3695395	BLASTX	104	1e-10	51	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
7810	GM_133_A1_D06_MR	g507910	BLASTN	522	6e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7811	GM_133_A1_E07_T7	g2464905	BLASTX	240	1e-19	59	(Z99708) minor allergen [Arabidopsis thaliana]
7812	GM_133_A1_E12_T7	g728905	BLASTX	202	5e-14	46	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) gi 1078206 pir S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast [Saccharomyces cerevisiae] gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] gi 595560 (U12980) Drs2p: Membrane spanning Ca-ATPase (P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]
7813	GM_133_A1_F02_T7	g2522228	BLASTX	239	5e-19	57	(AB007466) reverse transcriptase-like protein [Vicia faba]
7814	GM_133_A1_F04_T7	g18559	BLASTN	705	6e-25	76	G.max gene for catalase
7815	GM_133_A1_F12_T7	g3777527	BLASTX	252	4e-29	53	(AF053008) gag-pol polyprotein [Glycine max]
7816	GM_133_A1_G02_MR	g2129618	BLASTX	185	2e-12	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7817	GM_133_A1_G03_MR	g4038056	BLASTX	194	2e-23	49	(AC005897) putative transposon [Arabidopsis thaliana]
7818	GM_133_A1_G04_MR	g170606	BLASTN	494	1e-15	65	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
7819	GM_133_A1_G08_T7	g3097320	BLASTN	504	9e-16	78	Glycine max gene for Bd 30K, complete cds
7820	GM_133_A1_H02_MR	g3142328	BLASTN	789	7e-58	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
7821	GM_133_A1_H05_MR	g294042	BLASTN	409	2e-11	62	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
7822	GM_133_A1_H10_T7	g2264307	BLASTN	774	6e-28	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]
7823	GM_133_A2_A02_MR	g2995405	BLASTX	407	3e-36	68	(Y12432) polyprotein [Ananas comosus]
7824	GM_133_A2_A05_MR	g3650039	BLASTX	152	4e-09	36	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
7825	GM_133_A2_A06_MR	g629693	BLASTX	305	2e-26	60	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7826	GM_133_A2_B03_MR	g18559	BLASTN	511	4e-16	71	G max gene for catalase
7827	GM_133_A2_B06_T7	g629693	BLASTX	283	4e-24	61	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7828	GM_133_A2_B11_MR	g3777527	BLASTX	497	2e-45	92	(AF053008) gag-pol polyprotein [Glycine max]
7829	GM_133_A2_B11_T7	g3142379	BLASTX	310	6e-27	66	(AF053008) envelope-like [Glycine max]
7830	GM_133_A2_C02_T7	g3810595	BLASTX	279	3e-22	42	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
7831	GM_133_A2_C03_MR	g1685003	BLASTX	230	8e-18	40	(U32643) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]
7832	GM_133_A2_C04_MR	g3645899	BLASTX	133	4e-11	43	(U68408) 5' end not determined experimentally [Zea mays]
7833	GM_133_A2_C04_T7	g3142379	BLASTX	260	3e-21	59	(AF053008) envelope-like [Glycine max]
7834	GM_133_A2_C05_MR	g132086	BLASTX	290	7e-25	100	RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR gi 68053 pir RKSYS ribulose-bisphosphate carboxylase (F5C 4.1.1.39) small chain precursor SRS1 - soybean gi 18742 (V00458) rubpase [Glycine max]
7835	GM_133_A2_C06_T7	g3097320	BLASTN	1180	2e-46	82	Glycine max gene for Bd 30K, complete cds
7836	GM_133_A2_C08_MR	g507910	BLASTN	424	2e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence
7837	GM_133_A2_C08_T7	g507910	BLASTN	447	1e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence
7838	GM_133_A2_C09_T7	g2895634	BLASTN	395	4e-11	64	Zerene eurydice large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
7839	GM_133_A2_C11_MR	g3845281	BLASTN	324	5e-09	65	Plasmodium falciparum chromosome 2, section 56 of 73 of the complete sequence
7840	GM_133_A2_D02_T7	g1666236	BLASTX	200	5e-15	37	(U76261) unknown [Hordeum vulgare]
7841	GM_133_A2_D07_T7	g3395443	BLASTX	291	6e-25	47	(AC004683) putative ammonium transporter, 3' partial [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7842	GM_133_A2_D08_T7	g3600054	BLASTX	169	3e-11	34	(AF080120) No definition line found [Arabidopsis thaliana]
7843	GM_133_A2_D09_MR	g1888357	BLASTX	177	2e-11	67	(X98130) alpha-mannosidase [Arabidopsis thaliana] gi 1890154 gnl PID e307744 (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]
7844	GM_133_A2_D09_T7	g2323254	BLASTN	373	8e-10	64	Human Chromosome X, complete sequence [Homo sapiens]
7845	GM_133_A2_E02_MR	g507910	BLASTN	609	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7846	GM_133_A2_E02_T7	g4063756	BLASTN	361	3e-09	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7847	GM_133_A2_E03_MR	g3810596	BLASTX	212	3e-15	34	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7848	GM_133_A2_E05_MR	g3599418	BLASTN	1118	1e-43	87	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7849	GM_133_A2_F02_T7	g18559	BLASTN	715	2e-25	73	G.max gene for catalase
7850	GM_133_A2_F03_MR	g1142701	BLASTN	975	9e-38	81	Glycine max satellite STR120-A.3.
7851	GM_133_A2_F05_T7	g507910	BLASTN	577	2e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7852	GM_133_A2_F09_MR	g1619300	BLASTX	168	6e-12	47	(X95269) LRR protein [Lycopersicon esculentum]
7853	GM_133_A2_F11_T7	g1524341	BLASTN	362	8e-10	73	S.douglasii mitochondrial tRNAPro and tRNAArg genes
7854	GM_133_A2_F12_T7	g2522230	BLASTX	239	2e-19	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
7855	GM_133_A2_G01_MR	g905361	BLASTX	194	1e-13	40	(U22103) gag-protease polyprotein [Glycine max]
7856	GM_133_A2_G04_MR	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7857	GM_133_A2_G04_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
7858	GM_133_A2_G05_T7	g1813979	BLASTX	325	1e-28	76	(Y10860) hypothetical protein [Musa acuminata]
7859	GM_133_A2_G08_T7	g3142328	BLASTN	961	1e-36	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Z95352) AtMlo-h1 [Arabidopsis thaliana]
7860	GM_133_A2_G10_MR	g2765817	BLASTX	157	9e-10	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7861	GM_133_A2_G11_T7	g4063760	BLASTX	281	1e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7862	GM_133_A2_H05_MR	g4063760	BLASTX	423	1e-37	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7863	GM_133_A2_H08_T7	g4063760	BLASTX	225	1e-16	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7864	GM_133_B1_A04_MR	g3695387	BLASTX	151	1e-08	50	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
7865	GM_133_B1_A07_T7	g3820757	BLASTN	387	1e-10	66	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
7866	GM_133_B1_A08_T7	g1769898	BLASTX	183	2e-12	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7867	GM_133_B1_A09_T7	g507910	BLASTN	420	2e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7868	GM_133_B1_B04_MR	g2995405	BLASTX	309	1e-25	63	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
7869	GM_133_B1_C02_T7	g2462134	BLASTX	187	5e-13	39	(Y13368) reverse transcriptase [Beta vulgaris]
7870	GM_133_B1_C03_MR	g4063760	BLASTX	309	2e-25	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7871	GM_133_B1_C03_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7872	GM_133_B1_C05_MR	g2502084	BLASTN	623	4e-22	77	Vigna radiata adenosine triphosphatase mRNA, partial cds
7873	GM_133_B1_C05_T7	g4056421	BLASTX	352	2e-31	76	(AC005322) Similar to gb Z30094 basic transcription factor 2, 44 kD subunit from Homo sapiens. EST gb W43325 comes from this gene. [Arabidopsis thaliana]
7874	GM_133_B1_C11_MR	g3097320	BLASTN	1258	6e-50	84	Glycine max gene for Bd 30K, complete cds
7875	GM_133_B1_D03_MR	g3777527	BLASTX	313	2e-27	71	(AF053008) gag-pol polypeptide [Glycine max]
7876	GM_133_B1_D04_T7	g3513747	BLASTX	182	8e-12	44	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
7877	GM_133_B1_D12_T7	g2129473	BLASTX	238	2e-19	48	arabinogalactan-like protein - loblolly pine gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda]
7878	GM_133_B1_E01_T7	g2642431	BLASTX	156	5e-09	38	(AC002391) putative retrotransposon polypeptide [Arabidopsis thaliana]
7879	GM_133_B1_E02_MR	g2505878	BLASTX	298	7e-25	62	(Y12776) gene5; most likely [Arabidopsis thaliana]
7880	GM_133_B1_E02_T7	g2252836	BLASTX	201	3e-14	52	(AF013293) contains weak similarity to S. cerevisiae BOB1 protein (PIR:S45444) [Arabidopsis thaliana]
7881	GM_133_B1_E06_MR	g3319362	BLASTX	234	1e-17	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
7882	GM_133_B1_E06_T7	g3513747	BLASTX	283	2e-22	51	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
7883	GM_133_B1_E07_T7	g507910	BLASTN	573	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7884	GM_133_B1_E11_T7	g3882297	BLASTX	135	9e-09	67	(AB018331) KIAA0788 protein [Homo sapiens]
7885	GM_133_B1_F03_MR	g3810596	BLASTX	247	5e-19	35	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7886	GM_133_B1_F04_MR	g3142328	BLASTN	891	2e-33	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7887	GM_133_B1_F04_T7	g3142328	BLASTN	870	2e-32	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7888	GM_133_B1_F07_MR	g3097320	BLASTN	556	4e-18	72	Glycine max gene for Bd 30K, complete cds
7889	GM_133_B1_F08_T7	g3461846	BLASTX	155	5e-09	44	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
7890	GM_133_B1_F09_T7	g507910	BLASTN	442	2e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7891	GM_133_B1_F11_MR	g2443320	BLASTX	196	2e-13	39	(D85597) polyprotein [Oryza australiensis]
7892	GM_133_B1_F12_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7893	GM_133_B1_G02_T7	g185559	BLASTN	803	2e-29	77	G-max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
7894	GM_133_B1_G03_MR	g641905	BLASTX	241	1e-19	59	(U19267) cysteine proteinase [Zinnia elegans]
7895	GM_133_B1_G06_MR	g132674	BLASTX	86	6e-13	40	50S RIBOSOMAL PROTEIN L14 gi 94724 pir S15437 ribosomal protein L14 - Thermus aquaticus gi 48104 (X56552) ribosomal protein L14 [Thermus aquaticus] gi 755806 (Z37993) ribosomal protein L14 [Thermus thermophilus]
7896	GM_133_B1_G10_MR	g18559	BLASTN	835	8e-31	78	G.max gene for catalase
7897	GM_133_B1_H05_T7	g629693	BLASTX	275	3e-23	60	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7898	GM_133_B1_H11_MR	g3510505	BLASTX	210	6e-15	48	(AF030881) pol polyprotein [Fugu rubripes]
7899	GM_133_B2_A03_MR	g3695387	BLASTX	283	8e-23	72	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
7900	GM_133_B2_A03_T7	g3142328	BLASTN	847	2e-31	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7901	GM_133_B2_A04_MR	g3097320	BLASTN	639	7e-22	73	Glycine max gene for Bd 30K, complete cds
7902	GM_133_B2_A07_MR	g507910	BLASTN	422	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7903	GM_133_B2_A07_T7	g18559	BLASTN	924	7e-35	78	G.max gene for catalase
7904	GM_133_B2_A10_T7	g3930515	BLASTX	121	7e-09	47	(AF059674) putative gag protein [Nicotiana tabacum]
7905	GM_133_B2_B01_T7	g3650039	BLASTX	220	2e-16	42	(AC005396) putative Em/Spm transposon protein, 5' partial [Arabidopsis thaliana]
7906	GM_133_B2_B02_T7	g1142701	BLASTN	1267	6e-51	84	Glycine max satellite STR120-A.3.
7907	GM_133_B2_B04_MR	g507910	BLASTN	666	2e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
7908	GM_133_B2_B07_MR	g2443320	BLASTX	262	6e-26	53	(D85597) polyprotein [Oryza australiensis]
7909	GM_133_B2_B07_T7	g2995405	BLASTX	410	1e-36	63	(Y12432) polyprotein [Ananas comosus]
7910	GM_133_B2_C06_MR	g18559	BLASTN	871	2e-32	75	G.max gene for catalase
7911	GM_133_B2_C07_T7	g2995405	BLASTX	312	2e-28	47	(Y12432) polyprotein [Ananas comosus]
7912	GM_133_B2_D08_MR	g3645899	BLASTX	139	7e-18	48	(U68408) 5' end not determined experimentally [Zea mays]
7913	GM_133_B2_D10_MR	g2924777	BLASTX	247	6e-19	39	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]
7914	GM_133_B2_E01_MR	g2129618	BLASTX	216	1e-15	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7915	GM_133_B2_E02_MR	g4063760	BLASTX	433	8e-39	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7916	GM_133_B2_E02_T7	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7917	GM_133_B2_E05_MR	g4063760	BLASTX	163	5e-17	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7918	GM_133_B2_E05_T7	g3142328	BLASTN	1775	1e-73	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF051230) heat shock protein [Picea mariana]
7919	GM_133_B2_E07_MR	g2982291	BLASTX	146	1e-09	57	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7920	GM_133_B2_E09_MR	g1769897	BLASTX	317	3e-27	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7921	GM_133_B2_E12_T7	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
7922	GM_133_B2_F01_T7	g4063760	BLASTX	472	7e-43	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7923	GM_133_B2_F02_T7	g3777527	BLASTX	626	4e-59	96	(AF053008) gag-pol polyprotein [Glycine max]
7924	GM_133_B2_F05_MR	g4063760	BLASTX	255	1e-19	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7925	GM_133_B2_G02_T7	g3142328	BLASTN	961	1e-36	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7926	GM_133_B2_G03_MR	g2769655	BLASTN	525	1e-16	66	Human DNA sequence from PAC 1271.4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Contain...
7927	GM_133_B2_G04_MR	g1769897	BLASTX	233	6e-18	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7928	GM_133_B2_H05_T7	g18559	BLASTN	786	1e-28	75	G.max gene for catalase
7929	GM_133_B2_H09_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7930	GM_133_B2_H09_T7	g3777527	BLASTX	584	1e-54	94	(AF053008) gag-pol polyprotein [Glycine max]
7931	GM_133_B2_H10_MR	g4063760	BLASTX	122	8e-09	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7932	GM_133_B2_H11_T7	g421954	BLASTX	259	1e-20	46	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
7933	GM_134_A1_A06_MR	g507910	BLASTN	378	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7934	GM_134_A1_A10_T7	g4063760	BLASTX	258	4e-20	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7935	GM_134_A1_B01_MR	g507910	BLASTN	423	2e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7936	GM_134_A1_B01_T7	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7937	GM_134_A1_B04_MR	g3097320	BLASTN	552	6e-18	75	Glycine max gene for Bd 30K, complete cds
7938	GM_134_A1_B07_MR	g18695	BLASTN	474	1e-14	75	Soybean nodulin 22 gene
7939	GM_134_A1_B08_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7940	GM_134_A1_B08_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7941	GM_134_A1_B12_T7	g2522228	BLASTX	154	1e-09	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
7942	GM_134_A1_C08_MR	g169934	BLASTN	1501	1e-61	99	G.max (soybean) atpH gene encoding CFO-ATPase subunit III, chloroplast gene encoding chloroplast protein, complete cds. (AC004481) ankyrin-like protein [Arabidopsis thaliana]
7943	GM_134_A1_C09_MR	g3337361	BLASTX	240	6e-20	56	(Y13632) dem [Lycopersicon esculentum]
7944	GM_134_A1_C11_T7	g2190419	BLASTX	250	1e-19	48	(AF053008) gag-pol polyprotein [Glycine max]
7945	GM_134_A1_D01_MR	g3777527	BLASTX	708	7e-68	96	Glycine max BSR-101 satellite SB92 genomic sequence.
7946	GM_134_A1_D03_MR	g507910	BLASTN	380	1e-10	75	(AF053093) disease resistance protein [Lycopersicon esculentum]
7947	GM_134_A1_D10_T7	g3894383	BLASTX	278	3e-22	47	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
7948	GM_134_A1_D11_MR	g3746069	BLASTX	224	2e-16	35	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7949	GM_134_A1_E08_MR	g3869063	BLASTN	489	5e-15	66	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17022, complete sequence [Arabidopsis thaliana]
7950	GM_134_A1_E11_MR	g3746069	BLASTX	200	7e-14	33	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
7951	GM_134_A1_F04_T7	g3426334	BLASTN	590	1e-19	67	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
7952	GM_134_A1_F07_MR	g2462058	BLASTX	258	2e-21	42	(Y13389) reverse transcriptase [Antirrhinum majus]
7953	GM_134_A1_F10_T7	g3097320	BLASTN	526	9e-17	74	Glycine max gene for Bd 30K, complete cds
7954	GM_134_A1_G01_T7	g3721855	BLASTN	381	3e-10	70	Panax ginseng OSCPNY2 mRNA for beta-Amyrin Synthase, complete cds
7955	GM_134_A1_G04_MR	g3549652	BLASTX	144	8e-09	90	(A1224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]
7956	GM_134_A1_G05_T7	g345511	BLASTX	179	7e-12	34	retrovirus-related copia polyprotein - fruit fly (Drosophila simulans) (fragments)
7957	GM_134_A1_G06_MR	g2129618	BLASTX	212	3e-15	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7958	GM_134_A1_G10_T7	g3513745	BLASTX	196	3e-13	39	(AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
7959	GM_134_A1_H01_T7	g2462058	BLASTX	353	2e-31	54	(Y13389) reverse transcriptase [Antirrhinum majus]
7960	GM_134_A1_H06_MR	g4038056	BLASTX	277	3e-22	43	(AC005897) putative transposon [Arabidopsis thaliana]
7961	GM_134_A1_H06_T7	g1769898	BLASTX	156	1e-09	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7962	GM_134_A1_H07_MR	g2765817	BLASTX	157	8e-10	64	(Z95352) AtMlo-h1 [Arabidopsis thaliana]
7963	GM_134_A1_H10_MR	g3097320	BLASTN	1320	9e-53	82	Glycine max gene for Bd 30K, complete cds
7964	GM_134_A1_H11_T7	g2522228	BLASTX	165	1e-24	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
7965	GM_134_A2_A01_MR	g2995405	BLASTX	331	4e-28	53	(Y12432) polyprotein [Ananas comosus]
7966	GM_134_A2_A04_MR	g3810596	BLASTX	244	1e-18	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7967	GM_134_A2_A06_MR	g4038056	BLASTX	141	1e-13	32	(AC005897) putative transposon [Arabidopsis thaliana]
7968	GM_134_A2_A07_T7	g2351064	BLASTN	723	1e-25	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22
7969	GM_134_A2_A11_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
7970	GM_134_A2_A11_T7	g507910	BLASTN	492	1e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7971	GM_134_A2_B03_T7	g3097320	BLASTN	764	1e-27	76	Glycine max gene for Bd 30K, complete cds
7972	GM_134_A2_B04_MR	g170080	BLASTN	285	1e-09	63	Soybean seed lectin gene transposable element tgm1.
7973	GM_134_A2_B08_T7	g3097320	BLASTN	896	2e-33	79	Glycine max gene for Bd 30K, complete cds
7974	GM_134_A2_B12_MR	g18559	BLASTN	794	6e-29	73	G.max gene for catalase
7975	GM_134_A2_B12_T7	g2828185	BLASTN	391	1e-10	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]
7976	GM_134_A2_C03_T7	g18559	BLASTN	793	6e-29	77	G.max gene for catalase

Seq No.	ClonID	NCBI gi	Method	Score	P-value	% Ident	Description
7977	GM_134_A2_C06_MR	g3645899	BLASTX	213	4e-22	49	(U68408) 5' end not determined experimentally [Zea mays]
7978	GM_134_A2_D01_MR	g2995405	BLASTX	328	9e-28	52	(Y12432) polyprotein [Ananas comosus]
7979	GM_134_A2_D02_T7	g507910	BLASTN	392	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7980	GM_134_A2_D03_MR	g3002939	BLASTX	102	3e-14	100	(AF043426) RNA polymerase II second largest subunit [Peperomia caperata]
7981	GM_134_A2_D04_MR	g1707007	BLASTX	231	2e-17	37	(U7821) hypothetical protein [Arabidopsis thaliana]
7982	GM_134_A2_D05_T7	g1076755	BLASTX	492	1e-45	80	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
7983	GM_134_A2_D08_MR	g169934	BLASTN	1257	2e-50	90	G.max (soybean) aph gene encoding CFO-ATPase subunit III. chloroplast gene encoding chloroplast protein, complete cds.
7984	GM_134_A2_E02_MR	g18559	BLASTN	460	8e-14	68	G.max gene for catalase
7985	GM_134_A2_E06_T7	g18683	BLASTN	397	5e-11	74	G.max N-20t gene
7986	GM_134_A2_E07_MR	g3097320	BLASTN	525	1e-16	78	Glycine max gene for Bd 30K, complete cds
7987	GM_134_A2_E08_T7	g3097320	BLASTN	681	8e-24	75	Glycine max gene for Bd 30K, complete cds
7988	GM_134_A2_E09_T7	g3269281	BLASTX	272	9e-22	49	(AL030978) putative protein [Arabidopsis thaliana]
7989	GM_134_A2_F02_MR	g3845197	BLASTN	357	4e-09	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
7990	GM_134_A2_F04_MR	g2582971	BLASTX	156	4e-12	54	(D83711) TKRP125 [Nicotiana tabacum]
7991	GM_134_A2_F05_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7992	GM_134_A2_F06_MR	g1666236	BLASTX	167	3e-11	30	(U76261) unknown [Hordeum vulgare]
7993	GM_134_A2_F10_T7	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7994	GM_134_A2_F11_MR	g3777527	BLASTX	409	6e-36	60	(AF053008) gag-pol polyprotein [Glycine max]
7995	GM_134_A2_F11_T7	g1167523	BLASTX	189	1e-12	47	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
7996	GM_134_A2_G01_MR	g1171499	BLASTX	282	5e-24	69	(Z68913) reverse transcriptase [Beta vulgaris]
7997	GM_134_A2_G01_T7	g1658457	BLASTX	225	6e-18	61	(U75248) reverse transcriptase [Gossypium barbadense]
7998	GM_134_A2_G03_MR	g4063760	BLASTX	383	2e-33	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7999	GM_134_A2_G05_MR	g4056428	BLASTX	163	3e-10	73	(AC005322) Similar to gb U43629 integral membrane protein from Beta vulgaris and a member of sugar transporter family PF 00083. [Arabidopsis thaliana]
8000	GM_134_A2_G06_T7	g2407789	BLASTN	431	2e-12	63	Glycine max grr1 (grr1) mRNA, complete cds
8001	GM_134_A2_G07_MR	g2462134	BLASTX	117	5e-14	44	(Y13368) reverse transcriptase [Beta vulgaris]
8002	GM_134_A2_G09_T7	g18559	BLASTN	860	6e-32	79	G.max gene for catalase
8003	GM_134_A2_H01_T7	g18559	BLASTN	554	4e-18	72	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8004	GM_134_A2_H06_T7	g2129618	BLASTX	210	4e-15	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana] (AF053008) gag-pol polyprotein [Glycine max]
8005	GM_134_A2_H07_T7	g3777527	BLASTX	490	1e-44	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8006	GM_134_B1_A05_MR	g3142328	BLASTN	1023	2e-39	92	Glycine max BSR-101 satellite SB92 genomic sequence.
8007	GM_134_B1_A09_MR	g507910	BLASTN	484	3e-15	76	Yeast (Saccharomyces) mitochondrial Ser-tRNA and ATPase proteolipid genes.
8008	GM_134_B1_A11_T7	g343938	BLASTN	349	9e-09	61	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U76261) unknown [Hordeum vulgare]
8009	GM_134_B1_B03_MR	g3142328	BLASTN	1645	9e-68	89	G.max gene for catalase
8010	GM_134_B1_B04_MR	g1666236	BLASTX	172	7e-12	28	Speyeria morionia large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
8011	GM_134_B1_B06_T7	g18559	BLASTN	796	5e-29	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8012	GM_134_B1_B08_MR	g2895632	BLASTN	244	7e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8013	GM_134_B1_B10_T7	g507910	BLASTN	409	7e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8014	GM_134_B1_B12_T7	g507910	BLASTN	573	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8015	GM_134_B1_C03_T7	g1167523	BLASTX	226	1e-17	43	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
8016	GM_134_B1_C05_MR	g13619	BLASTN	356	7e-10	63	Saccharomyces douglasii mitDNA for tRNA(fMet and put. tRNA synthesis locus (TSL)
8017	GM_134_B1_C05_T7	g1931643	BLASTX	210	1e-15	47	(U95973) DnaJ isolog [Arabidopsis thaliana]
8018	GM_134_B1_D01_MR	g2982303	BLASTX	168	1e-14	71	(AF051236) hypothetical protein [Picea mariana]
8019	GM_134_B1_D01_T7	g3834323	BLASTX	188	5e-25	63	(AC005679) F9K20.25 [Arabidopsis thaliana]
8020	GM_134_B1_D04_MR	g1170897	BLASTX	308	1e-41	75	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR gi 1076276 pir S52039 NAD-malate dehydrogenase - cucumber gi 695311 (L31900) glyoxysomal malate dehydrogenase [Cucumis sativus]
8021	GM_134_B1_D04_T7	g13767	BLASTN	452	3e-14	62	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8022	GM_134_B1_D05_MR	g13764	BLASTN	388	2e-11	65	Torulopsis glabrata mitochondrial DNA for ATPase 8 downstream of cytochrome oxidase 1 gene >gi 343953 gb M11874 YSLMTIG03 Yeast (T. glabrata) mitochondrial DNA between cytochrome oxidase subunit I and ATPase subunit 8 genes.
8023	GM_134_B1_D05_T7	g2499498	BLASTX	319	1e-43	86	PHOSPHOGLYCERATE KINASE, CYTOSOLIC gi 1161602 gnl PID e151093 (Z48976) phosphoglycerate kinase (PGK) [Nicotiana tabacum]
8024	GM_134_B1_D08_MR	g2129618	BLASTX	180	7e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8025	GM_134_B1_D08_T7	g13584	BLASTN	399	2e-11	61	Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I
8026	GM_134_B1_D11_MR	g3142328	BLASTN	1413	4e-57	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
8027	GM_134_B1_D11_T7	g3650039	BLASTX	155	2e-09	33	(U76261) unknown [Hordeum vulgare]
8028	GM_134_B1_E01_MR	g1666236	BLASTX	161	1e-10	28	(AC000103) F21J9.24 [Arabidopsis thaliana]
8029	GM_134_B1_E03_T7	g2213632	BLASTX	159	3e-10	43	Glycine max BSR-101 satellite SB92 genomic sequence.
8030	GM_134_B1_E04_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8031	GM_134_B1_E04_T7	g507910	BLASTN	409	7e-12	73	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
8032	GM_134_B1_E08_MR	g1431738	BLASTN	558	2e-18	93	(U22103) gag-protease polypeptide [Glycine max]
8033	GM_134_B1_F02_MR	g905361	BLASTX	544	2e-55	94	(AF053008) envelope-like [Glycine max]
8034	GM_134_B1_F03_MR	g3142379	BLASTX	333	2e-29	60	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8035	GM_134_B1_F05_T7	g2129618	BLASTX	153	5e-09	33	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
8036	GM_134_B1_F07_MR	g505129	BLASTN	282	1e-10	63	(AL023094) putative ketoacyl-CoA synthase [Arabidopsis thaliana]
8037	GM_134_B1_F08_T7	g3096920	BLASTX	107	6e-09	34	Caenorhabditis elegans cosmid F52D1
8038	GM_134_B1_F10_MR	g2435558	BLASTN	375	7e-10	64	Glycine max BSR-101 satellite SB92 genomic sequence.
8039	GM_134_B1_F11_T7	g507910	BLASTN	542	7e-18	80	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8040	GM_134_B1_G01_T7	g1769898	BLASTX	146	8e-13	46	Glycine max BSR-101 satellite SB92 genomic sequence.
8041	GM_134_B1_G03_MR	g507910	BLASTN	367	6e-10	72	(U76261) unknown [Hordeum vulgare]
8042	GM_134_B1_G10_MR	g1666236	BLASTX	144	9e-09	28	Soybean Tgm6 transposable element 3' end
8043	GM_134_B1_G11_MR	g18768	BLASTN	482	2e-15	68	Glycine max BSR-101 satellite SB92 genomic sequence.
8044	GM_134_B1_H05_T7	g507910	BLASTN	508	2e-16	77	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8045	GM_134_B1_H08_MR	g18559	BLASTN	792	7e-29	73	G.max gene for catalase
8046	GM_135_A1_A03_MR	g100484	BLASTX	310	5e-26	56	hypothetical protein - garden snapdragon
8047	GM_135_A1_A04_MR	g170606	BLASTN	743	4e-27	70	Broad bean (V faba) BamHI repetitive element, 1750 bp family.
8048	GM_135_A1_A06_T7	g1213629	BLASTX	245	2e-19	51	(X95091) pectinesterase [Prunus persica]
8049	GM_135_A1_A09_MR	g1871173	BLASTN	450	3e-13	61	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence
8050	GM_135_A1_A10_T7	g629693	BLASTX	153	1e-09	45	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8051	GM_135_A1_B04_MR	g2335186	BLASTN	387	2e-10	61	Human Xq28 cosmid U126G1, U142F2, U69B6, U1145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence [Homo sapiens]
8052	GM_135_A1_B05_MR	g2443320	BLASTX	167	3e-10	39	(D85597) polyprotein [Oryza australiensis]
8053	GM_135_A1_B10_T7	g1769898	BLASTX	394	9e-38	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8054	GM_135_A1_B11_MR	g1710401	BLASTX	307	8e-27	83	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) gi 1044912 (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]
8055	GM_135_A1_B12_T7	g2129618	BLASTX	178	1e-11	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8056	GM_135_A1_C09_T7	g2443889	BLASTX	163	4e-10	45	similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
8057	GM_135_A1_C11_MR	g1666236	BLASTX	205	1e-15	35	(U76261) unknown [Hordeum vulgare]
8058	GM_135_A1_C11_T7	g629693	BLASTX	311	4e-27	60	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8059	GM_135_A1_C12_MR	g3869065	BLASTN	389	1e-10	67	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]
8060	GM_135_A1_C12_T7	g2598587	BLASTX	124	5e-10	86	(Y15366) cycloartenol synthase [Medicago truncatula]
8061	GM_135_A1_D01_T7	g3319372	BLASTX	207	7e-16	37	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
8062	GM_135_A1_D02_MR	g2583121	BLASTX	144	3e-09	77	(AC002387) putative phosphotransferase [Arabidopsis thaliana]
8063	GM_135_A1_D07_MR	g3241935	BLASTN	477	2e-14	63	Arabidopsis thaliana chromosome IV from 19 cM, complete sequence [Arabidopsis thaliana]
8064	GM_135_A1_D09_T7	g507910	BLASTN	362	9e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8065	GM_135_A1_D12_MR	g3645899	BLASTX	351	4e-30	61	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8066	GM_135_A1_E05_T7	g1006806	BLASTN	757	1e-27	70	Vigna radiata 1-aminocyclopropane-1-carboxylic acid synthase (VRACS7) mRNA, complete cds.
8067	GM_135_A1_F01_MR	g100484	BLASTX	262	2e-22	51	hypothetical protein - garden snapdragon
8068	GM_135_A1_F05_T7	g170083	BLASTN	419	3e-12	70	Soybean (clone E15) urease (ure) gene, exons 2,3 and 4 and partial cds.
8069	GM_135_A1_F08_T7	g2129618	BLASTX	227	6e-17	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8070	GM_135_A1_F11_T7	g3777527	BLASTX	140	2e-18	62	(AF053008) gag-pol polyprotein [Glycine max]
8071	GM_135_A1_G01_MR	g3142328	BLASTN	1175	3e-46	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8072	GM_135_A1_G04_T7	g4039114	BLASTN	470	3e-14	66	Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds
8073	GM_135_A1_G07_T7	g99922	BLASTX	361	2e-32	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8074	GM_135_A1_G12_T7	g4115357	BLASTX	143	3e-12	39	(AC005957) hypothetical protein [Arabidopsis thaliana]
8075	GM_135_A1_H01_MR	g2760165	BLASTN	675	2e-23	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; MAC9, complete sequence [Arabidopsis thaliana]
8076	GM_135_A1_H02_MR	g507910	BLASTN	500	6e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8077	GM_135_A1_H03_MR	g4063760	BLASTX	404	7e-40	71	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8078	GM_135_A1_H05_T7	g3513747	BLASTX	173	8e-11	45	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
8079	GM_135_A1_H08_T7	g99922	BLASTX	535	8e-51	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8080	GM_135_A1_H10_MR	g100484	BLASTX	298	1e-24	58	hypothetical protein - garden snapdragon
8081	GM_135_A1_H11_T7	g556672	BLASTN	349	8e-09	71	S.cereale (Halo) chloroplast mRNA for heat-shock protein
8082	GM_135_B1_A07_T7	g13767	BLASTN	405	4e-12	69	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
8083	GM_135_B1_A08_MR	g2522228	BLASTX	304	2e-26	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
8084	GM_135_B1_B02_MR	g3645899	BLASTX	251	2e-19	47	(U68408) 5' end not determined experimentally [Zea mays]
8085	GM_135_B1_B09_T7	g3337367	BLASTX	196	4e-14	36	(AC004481) hypothetical protein [Arabidopsis thaliana]
8086	GM_135_B1_B10_MR	g3142328	BLASTN	956	2e-36	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8087	GM_135_B1_B12_T7	g507910	BLASTN	536	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8088	GM_135_B1_C02_MR	g559276	BLASTN	405	2e-11	63	Saccharomyces cerevisiae mitochondrion transfer RNA-Ser1 (tRNA-Ser) gene and var1 gene, complete cds.
8089	GM_135_B1_C07_T7	g18559	BLASTN	913	2e-34	76	G.max gene for catalase
8090	GM_135_B1_C09_T7	g3650035	BLASTX	172	6e-11	51	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
8091	GM_135_B1_C11_T7	g1934969	BLASTN	369	1e-09	65	P.falciparum mRNA for AARP1 protein, partial
8092	GM_135_B1_C12_T7	g3142328	BLASTN	878	8e-33	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U68408) 5' end not determined experimentally [Zea mays]
8093	GM_135_B1_D10_T7	g3645899	BLASTX	327	2e-27	52	(U22103) gag-protease polyprotein [Glycine max]
8094	GM_135_B1_D11_MR	g905361	BLASTX	425	7e-39	96	(Y13368) reverse transcriptase [Beta vulgaris]
8095	GM_135_B1_D12_MR	g2462134	BLASTX	205	5e-15	37	Glycine max gene for Bd 30K, complete cds
8096	GM_135_B1_D12_T7	g3097320	BLASTN	705	7e-25	81	G.max gene for catalase
8097	GM_135_B1_E03_T7	g18559	BLASTN	355	5e-09	72	Glycine max satellite STR120-B.1.
8098	GM_135_B1_E04_T7	g1142703	BLASTN	275	1e-13	75	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8099	GM_135_B1_E06_MR	g4063760	BLASTX	364	2e-31	63	Glycine max gene for Bd 30K, complete cds
8100	GM_135_B1_E11_MR	g3097320	BLASTN	543	2e-17	75	Glycine max gene for Bd 30K, complete cds
8101	GM_135_B1_E12_T7	g3097320	BLASTN	874	2e-32	78	Glycine max gene for Bd 30K, complete cds
8102	GM_135_B1_F03_MR	g3777527	BLASTX	139	9e-09	41	(AF053008) gag-pol polyprotein [Glycine max]
8103	GM_135_B1_F03_T7	g1785740	BLASTX	114	7e-09	31	(Y08502) orf170 [Arabidopsis thaliana]
8104	GM_135_B1_F04_MR	g2245073	BLASTN	406	3e-11	68	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
8105	GM_135_B1_F06_MR	g984307	BLASTN	1137	3e-47	91	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psal), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precursor...
8106	GM_135_B1_F08_T7	g4115563	BLASTX	220	1e-16	41	(AB013598) UDP-glucose:anthocyanin 5-O-glucosyltransferase [Verbena x hybrida]
8107	GM_135_B1_F11_MR	g3688172	BLASTX	162	1e-11	50	(AL031804) putative protein [Arabidopsis thaliana]
8108	GM_135_B1_F12_MR	g18559	BLASTN	856	9e-32	75	G.max gene for catalase
8109	GM_135_B1_F12_T7	g2462936	BLASTX	171	3e-12	35	(Y12321) open reading frame 2 [Brassica oleracea]
8110	GM_135_B1_G08_MR	g4063760	BLASTX	420	3e-37	71	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8111	GM_135_B1_G08_T7	g507910	BLASTN	400	2e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8112	GM_135_B1_G11_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
8113	GM_135_B1_G11_T7	g507910	BLASTN	647	1e-22	86	Glycine max BSR-101 satellite SB92 genomic sequence.
8114	GM_135_B1_H07_MR	g3643588	BLASTN	493	3e-15	67	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8115	GM_135_B1_H09_MR	g905361	BLASTX	414	1e-37	92	(U22103) gag-protease polyprotein [Glycine max]
8116	GM_135_B1_H09_T7	g417499	BLASTX	155	3e-09	76	AUTOANTIGEN PM-SCL gi 284357 pir A43920 nucleolar 100K polymyositis-scleroderma protein 2 - human gi 179283 (L01457)
							PM-Scl autoantigen [Homo sapiens]
8117	GM_135_B1_H10_MR	g507910	BLASTN	695	8e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
8118	GM_135_B1_H10_T7	g507910	BLASTN	559	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8119	GM_135_B1_H11_MR	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8120	GM_136_A1_A03_MR	g3047068	BLASTX	194	2e-13	38	(AF058825) similar to maize transposon MuDR (GIB:M76978) [Arabidopsis thaliana]
8121	GM_136_A1_A09_MR	g2522228	BLASTX	373	1e-33	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
8122	GM_136_A1_A11_MR	g1666236	BLASTX	198	8e-15	33	(U76261) unknown [Hordeum vulgare]
8123	GM_136_A1_B01_MR	g3924609	BLASTX	127	1e-12	46	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
8124	GM_136_A1_B03_MR	g3513745	BLASTX	214	3e-15	39	(AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
8125	GM_136_A1_B05_MR	g2995405	BLASTX	315	2e-26	52	(Y12432) polyprotein [Ananas comosus]
8126	GM_136_A1_B05_T7	g3142379	BLASTX	273	1e-22	80	(AF053008) envelope-like [Glycine max]
8127	GM_136_A1_B07_T7	g3426334	BLASTN	367	1e-09	59	Pisum sativum pectin methylesterase (rcpml) gene, complete cds
8128	GM_136_A1_C03_MR	g18559	BLASTN	1161	1e-45	86	G.max gene for catalase
8129	GM_136_A1_C05_T7	g3777527	BLASTX	508	6e-50	95	(AF053008) gag-pol polyprotein [Glycine max]
8130	GM_136_A1_D03_MR	g100484	BLASTX	242	1e-18	47	hypothetical protein - garden snapdragon
8131	GM_136_A1_D04_T7	g2961349	BLASTX	237	7e-18	52	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
8132	GM_136_A1_D07_MR	g629693	BLASTX	131	6e-10	54	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8133	GM_136_A1_D11_MR	g18559	BLASTN	767	9e-28	75	G.max gene for catalase
8134	GM_136_A1_D12_T7	g3097320	BLASTN	431	2e-12	72	Glycine max gene for Bd 30K, complete cds
8135	GM_136_A1_E01_T7	g3777527	BLASTX	350	1e-29	79	(AF053008) gag-pol polyprotein [Glycine max]
8136	GM_136_A1_E02_T7	g905361	BLASTX	288	9e-24	73	(U22103) gag-protease polyprotein [Glycine max]
8137	GM_136_A1_E06_MR	g18559	BLASTN	396	6e-11	73	G.max gene for catalase
8138	GM_136_A1_E12_MR	g905361	BLASTX	313	2e-26	74	(U22103) gag-protease polyprotein [Glycine max]
8139	GM_136_A1_F01_MR	g3522945	BLASTX	175	1e-11	47	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]
8140	GM_136_A1_F01_T7	g4140712	BLASTX	159	6e-11	33	(AF110183) putative integrase [Oryza sativa]
8141	GM_136_A1_F04_T7	g2522227	BLASTX	211	2e-16	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8142	GM_136_A1_F06_T7	g1769898	BLASTX	254	4e-20	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8143	GM_136_A1_F07_MR	g3250687	BLASTX	251	1e-20	41	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
8144	GM_136_A1_F07_T7	g2245104	BLASTX	226	1e-16	64	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
8145	GM_136_A1_F08_T7	g1769898	BLASTX	298	7e-25	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8146	GM_136_A1_F11_MR	g507910	BLASTN	467	2e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8147	GM_136_A1_G01_MR	g507910	BLASTN	620	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8148	GM_136_A1_G07_MR	g3645899	BLASTX	216	1e-15	45	(U68408) 5' end not determined experimentally [Zea mays]
8149	GM_136_A1_G08_T7	g1769897	BLASTX	167	7e-11	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8150	GM_136_A1_G09_T7	g4038056	BLASTX	270	2e-21	49	(AC005897) putative transposon [Arabidopsis thaliana]
8151	GM_136_A1_G10_T7	g507910	BLASTN	398	2e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8152	GM_136_A1_H01_MR	g1666236	BLASTX	189	9e-14	29	(U76261) unknown [Hordeum vulgare]
8153	GM_136_A1_H05_T7	g3810596	BLASTX	200	5e-14	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
8154	GM_136_A1_H07_MR	g4063760	BLASTX	351	6e-30	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8155	GM_136_A1_H09_MR	g100484	BLASTX	326	1e-27	54	hypothetical protein - garden snapdragon
8156	GM_136_A2_A05_T7	g629693	BLASTX	342	2e-30	55	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8157	GM_136_A2_A07_MR	g4038056	BLASTX	216	1e-15	44	(AC005897) putative transposon [Arabidopsis thaliana]
8158	GM_136_A2_A08_T7	g1666236	BLASTX	208	6e-16	30	(U76261) unknown [Hordeum vulgare]
8159	GM_136_A2_A11_MR	g18559	BLASTN	821	3e-30	77	G-max gene for catalase
8160	GM_136_A2_B05_T7	g170080	BLASTN	679	8e-24	97	Soybean seed lectin gene transposable element tgm1.
8161	GM_136_A2_B10_MR	g3097320	BLASTN	500	1e-15	72	Glycine max gene for Bd 30K, complete cds
8162	GM_136_A2_C04_MR	g4063760	BLASTX	316	3e-26	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8163	GM_136_A2_C12_MR	g13536	BLASTN	403	2e-11	68	Yeast (S. cerevisiae) mitochondrial genes for several tRNAs (Thr2), Cys(2) and His). >gi 343930 gb K00537 YSCMTTGO1 Yeast (S.cerevisiae) mitochondrial cap-oxi1 region: Thr-2, Cys-2 and His-tRNA genes.
8164	GM_136_A2_C12_T7	g2842479	BLASTX	162	2e-10	57	(AL021749) hypothetical protein [Arabidopsis thaliana]
8165	GM_136_A2_D01_T7	g4038056	BLASTX	399	2e-35	51	(AC005897) putative transposon [Arabidopsis thaliana]
8166	GM_136_A2_D02_T7	g2104945	BLASTN	431	2e-12	76	Glycine max copia-like retrotransposon Tgmr, complete sequence
8167	GM_136_A2_D03_MR	g2688299	BLASTX	191	7e-23	56	(AE001145) prolyl-tRNA synthetase (proS) [Borrelia burgdorferi]
8168	GM_136_A2_D07_MR	g4063760	BLASTX	249	4e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8169	GM_136_A2_D07_T7	g507910	BLASTN	660	3e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
8170	GM_136_A2_D08_MR	g3142328	BLASTN	785	1e-28	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence.
8171	GM_136_A2_D09_MR	g507910	BLASTN	350	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8172	GM_136_A2_D09_T7	g507910	BLASTN	380	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8173	GM_136_A2_E04_MR	g3004543	BLASTN	325	6e-09	62	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence.
8174	GM_136_A2_E04_T7	g662904	BLASTX	118	4e-10	59	nitrate reductase (NADH) [Cichorium intybus]
8175	GM_136_A2_E05_T7	g18695	BLASTN	399	4e-11	71	Soybean nodulin 22 gene
8176	GM_136_A2_E07_T7	g18559	BLASTN	350	8e-09	72	G.max gene for catalase
8177	GM_136_A2_E09_MR	g2244804	BLASTX	213	7e-16	48	(Z97336) Ste20-like kinase homolog [Arabidopsis thaliana]
8178	GM_136_A2_F07_MR	g2642431	BLASTX	160	2e-09	47	(AC002391) putative retrotransposon polypeptide [Arabidopsis thaliana]
8179	GM_136_A2_F09_T7	g3426334	BLASTN	349	9e-09	66	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
8180	GM_136_A2_G01_MR	g2522227	BLASTX	162	6e-11	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8181	GM_136_A2_G04_MR	g1171583	BLASTN	387	2e-10	68	P.falciptarum complete gene map of plastid-like DNA (IR-A)
8182	GM_136_A2_H08_T7	g421955	BLASTX	273	5e-23	54	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
8183	GM_136_A2_H09_MR	g99922	BLASTX	494	2e-46	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8184	GM_136_A2_H10_MR	g3128195	BLASTX	176	4e-12	81	(AC004521) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] gi 3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]
8185	GM_136_B1_A01_MR	g99755	BLASTX	185	6e-21	48	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
8186	GM_136_B1_A04_T7	g18695	BLASTN	401	3e-11	71	Soybean nodulin 22 gene
8187	GM_136_B1_B04_MR	g507910	BLASTN	659	4e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
8188	GM_136_B1_B06_T7	g18660	BLASTN	635	8e-22	77	G.max hsp22 gene for low MW heat shock protein
8189	GM_136_B1_B07_MR	g212878	BLASTN	393	6e-11	66	Gallus gallus vitellogenin gene coding for phosvitin, exons 23 and 24.
8190	GM_136_B1_B08_MR	g507910	BLASTN	477	6e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
8191	GM_136_B1_B08_T7	g507910	BLASTN	491	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8192	GM_136_B1_B11_MR	g1666236	BLASTX	199	6e-15	30	(U76261) unknown [Hordeum vulgare]
8193	GM_136_B1_C06_T7	g3777527	BLASTX	389	1e-39	96	(AF053008) gag-pol polypeptide [Glycine max]
8194	GM_136_B1_C11_T7	g2129618	BLASTX	193	3e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8195	GM_136_B1_D02_MR	g905361	BLASTX	333	1e-28	79	(U22103) gag-protease polypeptide [Glycine max]
8196	GM_136_B1_D03_MR	g4063760	BLASTX	105	7e-11	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8197	GM_136_B1_D04_MR	g4063760	BLASTX	299	2e-24	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8198	GM_136_B1_D05_MR	g1360090	BLASTX	121	1e-09	66	(X95576) C1C-N1 gene product [Nicotiana tabacum]
8199	GM_136_B1_D06_MR	g1142702	BLASTN	437	3e-13	73	Glycine max satellite STR120-A.4.
8200	GM_136_B1_D11_MR	g547684	BLASTX	583	6e-56	95	HEAT SHOCK PROTEIN 82 gi 100336 pir S18865 heat shock protein 82 - common tobacco (fragment) gi 19880 (X63195) heat shock protein 82 [Nicotiana tabacum]
8201	GM_136_B1_D11_T7	g905361	BLASTX	387	1e-34	82	(U22103) gag-protease polypeptide [Glycine max]
8202	GM_136_B1_E05_MR	g507910	BLASTN	378	2e-10	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8203	GM_136_B1_E07_MR	g421955	BLASTX	178	3e-12	44	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
8204	GM_136_B1_E11_MR	g1813979	BLASTX	286	2e-27	58	(Y10860) hypothetical protein [Musa acuminata]
8205	GM_136_B1_F01_MR	g3845197	BLASTN	357	4e-09	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
8206	GM_136_B1_F01_T7	g3097320	BLASTN	912	3e-34	79	Glycine max gene for Bd 30K, complete cds
8207	GM_136_B1_F06_MR	g3777527	BLASTX	242	7e-35	77	(AF053008) gag-pol polypeptide [Glycine max]
8208	GM_136_B1_F08_T7	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8209	GM_136_B1_F12_MR	g2315153	BLASTX	173	8e-12	72	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
8210	GM_136_B1_F12_T7	g3645899	BLASTX	319	1e-26	58	(U68408) 5' end not determined experimentally [Zea mays]
8211	GM_136_B1_G02_MR	g905361	BLASTX	426	5e-39	96	(U22103) gag-protease polypeptide [Glycine max]
8212	GM_136_B1_G04_MR	g2522227	BLASTX	227	3e-18	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8213	GM_136_B1_G07_T7	g1236920	BLASTN	356	4e-09	64	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
8214	GM_136_B1_G09_T7	g3947733	BLASTX	329	1e-28	53	(AJ009719) NL25 [Solanum tuberosum]
8215	GM_136_B1_G10_T7	g99922	BLASTX	494	2e-46	74	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8216	GM_136_B1_H01_MR	g1666236	BLASTX	156	4e-10	32	(U76261) unknown [Hordeum vulgare]
8217	GM_136_B1_H02_T7	g3645899	BLASTX	216	4e-18	47	(U68408) 5' end not determined experimentally [Zea mays]
8218	GM_136_B1_H07_MR	g4063760	BLASTX	449	2e-40	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8219	GM_137_A1_A09_T7	g3047086	BLASTX	126	4e-12	46	(AF058914) similar to reverse transcriptase (Pfam: transcript_fact_hmm, score: 72.31) [Arabidopsis thaliana]
8220	GM_137_A1_C07_T7	g2618605	BLASTN	534	4e-17	79	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8221	GM_137_A1_C10_T7	g3386613	BLASTX	92	4e-10	94	(AC004665) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
8222	GM_137_A1_D09_T7	g507910	BLASTN	568	5e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8223	GM_137_A1_E03_T7	g4038056	BLASTX	269	2e-21	54	(AC005897) putative transposon [Arabidopsis thaliana]
8224	GM_137_A1_E05_T7	g507910	BLASTN	355	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8225	GM_137_A1_F07_T7	g2443320	BLASTX	114	2e-11	52	(D85597) polyprotein [Oryza australiensis]
8226	GM_137_A1_E10_T7	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
8227	GM_137_A1_F07_T7	g3142328	BLASTN	972	4e-37	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8228	GM_137_A1_F09_T7	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8229	GM_137_A1_G01_T7	g3599418	BLASTN	358	3e-09	75	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
8230	GM_137_A1_G06_T7	g18559	BLASTN	762	2e-27	71	G.max gene for catalase
8231	GM_137_A1_G08_T7	g3550090	BLASTX	147	6e-16	48	(AF072640) reverse transcriptase [Lycopersicon esculentum]
8232	GM_137_A1_G09_T7	g905361	BLASTX	189	4e-13	39	(U22103) gag-protease polyprotein [Glycine max]
8233	GM_137_A1_H04_T7	g18559	BLASTN	868	3e-32	74	G.max gene for catalase
8234	GM_137_A1_H06_T7	g3319362	BLASTX	169	1e-10	35	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
8235	GM_137_A1_H08_T7	g3930515	BLASTX	115	3e-10	46	(AF059674) putative gag protein [Nicotiana tabacum]
8236	GM_137_A1_H11_T7	g18559	BLASTN	871	2e-32	75	G.max gene for catalase
8237	GM_137_A2_A08_MR	g4063760	BLASTX	206	2e-14	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8238	GM_137_A2_A09_T7	g2264320	BLASTN	436	1e-12	60	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
8239	GM_137_A2_B03_MR	g533086	BLASTX	278	1e-23	75	(U07605) precursor delta-9-stearoyl-acyl carrier protein desaturase [Thunbergia alata]
8240	GM_137_A2_B07_T7	g3269291	BLASTX	141	1e-14	69	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]
8241	GM_137_A2_B09_T7	g4063760	BLASTX	155	4e-09	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8242	GM_137_A2_B12_MR	g2129618	BLASTX	100	3e-11	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8243	GM_137_A2_C04_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8244	GM_137_A2_D04_T7	g4038056	BLASTX	186	2e-12	50	(AC005897) putative transposon [Arabidopsis thaliana]
8245	GM_137_A2_F06_MR	g1480927	BLASTN	986	4e-38	86	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
8246	GM_137_A2_F10_MR	g100484	BLASTX	183	4e-14	48	hypothetical protein - garden snapdragon

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8247	GM_137_A2_F10_T7	g130582	BLASTX	153	8e-09	42	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
8248	GM_137_A2_G06_T7	g3097320	BLASTN	383	3e-10	72	Glycine max gene for Bd 30K, complete cds
8249	GM_137_A2_G10_T7	g3777527	BLASTX	429	6e-41	90	(AF053008) gag-pol polyprotein [Glycine max]
8250	GM_137_A2_H10_T7	g4063756	BLASTN	404	3e-11	73	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8251	GM_137_A2_H12_T7	g507910	BLASTN	550	3e-18	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8252	GM_137_B1_A05_T7	g100484	BLASTX	314	2e-26	54	hypothetical protein - garden snapdragon
8253	GM_137_B1_A09_MR	g507910	BLASTN	391	5e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8254	GM_137_B1_B01_T7	g2961384	BLASTX	181	1e-23	67	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]
8255	GM_137_B1_B05_T7	g9933	BLASTN	380	3e-10	64	P.falciparum pfec2 gene for p34cdc2 protein kinase
8256	GM_137_B1_B06_T7	g3046854	BLASTN	376	6e-10	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]
8257	GM_137_B1_B08_T7	g2522228	BLASTX	382	1e-34	61	(AB007466) reverse transcriptase-like protein [Vicia faba]
8258	GM_137_B1_B12_MR	g2443320	BLASTX	199	1e-13	51	(D85597) polyprotein [Oryza australiensis]
8259	GM_137_B1_C11_T7	g507910	BLASTN	508	2e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8260	GM_137_B1_C12_MR	g507910	BLASTN	382	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8261	GM_137_B1_D06_T7	g3426334	BLASTN	416	8e-12	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
8262	GM_137_B1_D07_MR	g99730	BLASTX	245	2e-19	51	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Kashmir) (fragment) gi 1345512 gnl PID c73215 (X53975) orf 3 [Arabidopsis thaliana]
8263	GM_137_B1_D07_T7	g4063756	BLASTN	449	3e-13	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8264	GM_137_B1_E02_MR	g507910	BLASTN	366	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8265	GM_137_B1_E02_T7	g3142328	BLASTN	755	3e-27	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 33.26) [Arabidopsis thaliana]
8266	GM_137_B1_F04_MR	g3319363	BLASTX	276	4e-22	54	(U68408) 5' end not determined experimentally [Zea mays]
8267	GM_137_B1_E04_T7	g3645899	BLASTX	351	4e-30	62	Glycine max copia-like retrotransposon Tgm1, complete sequence
8268	GM_137_B1_E11_MR	g2104945	BLASTN	400	4e-11	66	Glycine max BSR-101 satellite SB92 genomic sequence.
8269	GM_137_B1_F01_MR	g507910	BLASTN	476	7e-15	74	

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
8270	GM_137_B1_F03_MR	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8271	GM_137_B1_F06_T7	g18559	BLASTN	614	8e-21	76	G.max gene for catalase
8272	GM_137_B1_F07_MR	g4092470	BLASTN	459	1e-13	66	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
8273	GM_137_B1_F08_MR	g3695395	BLASTX	199	3e-14	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
8274	GM_137_B1_F08_T7	g3645899	BLASTX	170	9e-11	36	(U68408) 5' end not determined experimentally [Zea mays]
8275	GM_137_B1_F12_T7	g3142328	BLASTN	741	1e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8276	GM_137_B1_G02_T7	g18559	BLASTN	836	7e-31	73	G.max gene for catalase
8277	GM_137_B1_G10_T7	g18559	BLASTN	1156	2e-45	91	G.max gene for catalase
8278	GM_137_B1_H01_MR	g2443320	BLASTX	241	3e-18	49	(D85597) polyprotein [Oryza australiensis]
8279	GM_137_B1_H02_T7	g2828182	BLASTN	417	8e-12	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]
8280	GM_137_B1_H04_MR	g1480927	BLASTN	882	3e-33	84	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
8281	GM_137_B1_H06_MR	g4063760	BLASTX	135	4e-15	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8282	GM_137_B2_A04_MR	g507910	BLASTN	541	8e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8283	GM_137_B2_A04_T7	g4063760	BLASTX	335	3e-28	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8284	GM_137_B2_A05_MR	g507910	BLASTN	356	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8285	GM_137_B2_A06_MR	g469192	BLASTN	377	4e-10	65	Arabidopsis thaliana mRNA for amidophosphoribosyltransferase, complete cds
8286	GM_137_B2_A07_MR	g2982251	BLASTX	192	2e-14	70	(AF051208) putative RNA-binding protein [Picea mariana]
8287	GM_137_B2_A11_MR	g3097320	BLASTN	455	1e-13	70	Glycine max gene for Bd 30K, complete cds
8288	GM_137_B2_B01_MR	g4063760	BLASTX	414	1e-36	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8289	GM_137_B2_B01_T7	g507910	BLASTN	385	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8290	GM_137_B2_B02_MR	g18559	BLASTN	371	9e-10	72	G.max gene for catalase
8291	GM_137_B2_B02_T7	g629693	BLASTX	157	4e-10	32	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8292	GM_137_B2_B03_T7	g2443320	BLASTX	339	1e-28	52	(D85597) polyprotein [Oryza australiensis]
8293	GM_137_B2_B05_MR	g100484	BLASTX	246	4e-19	44	hypothetical protein - garden snapdragon
8294	GM_137_B2_B09_T7	g4063760	BLASTX	153	7e-09	33	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8295	GM_137_B2_B12_MR	g2651310	BLASTX	272	4e-22	48	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8296	GM_137_B2_B12_T7	g3377848	BLASTX	213	4e-16	51	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
8297	GM_137_B2_C01_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8298	GM_137_B2_C01_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8299	GM_137_B2_C03_MR	g2344903	BLASTX	287	1e-24	75	(AC002388) triacylglycerol lipase isolog [Arabidopsis thaliana] gi 3341700 (AC003672) putative triacylglycerol lipase [Arabidopsis thaliana]
8300	GM_137_B2_C04_MR	g3142379	BLASTX	261	2e-21	59	(AF053008) envelope-like [Glycine max]
8301	GM_137_B2_C05_T7	g3097320	BLASTN	1111	3e-43	82	Glycine max gene for Bd 30K, complete cds
8302	GM_137_B2_C12_T7	g629693	BLASTX	251	1e-20	56	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8303	GM_137_B2_D11_MR	g2342684	BLASTX	399	2e-36	56	(AC000106) F7G19.14 [Arabidopsis thaliana]
8304	GM_137_B2_D12_T7	g1871187	BLASTX	197	1e-13	84	(U90439) unknown protein [Arabidopsis thaliana]
8305	GM_137_B2_E03_MR	g3935183	BLASTX	253	8e-23	66	(AC004557) F17L21.26 [Arabidopsis thaliana]
8306	GM_137_B2_E07_T7	g1769898	BLASTX	370	9e-33	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8307	GM_137_B2_E08_MR	g3241917	BLASTN	463	7e-14	65	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]
8308	GM_137_B2_E09_MR	g3449334	BLASTN	311	4e-10	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
8309	GM_137_B2_E09_T7	g2980777	BLASTX	198	3e-14	55	(AL022198) putative protein [Arabidopsis thaliana]
8310	GM_137_B2_F02_T7	g2443348	BLASTX	309	2e-36	81	(AB001379) cytochrome P450 [Glycyrrhiza echinata]
8311	GM_137_B2_F03_MR	g1168471	BLASTX	196	5e-24	78	PROTEIN KINASE APK1B gi 2160295 gnl PID d1001485 (D10152) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]
8312	GM_137_B2_F09_T7	g3319362	BLASTX	429	2e-38	66	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
8313	GM_137_B2_F11_MR	g3236250	BLASTX	251	1e-20	95	(AC004684) hypothetical protein [Arabidopsis thaliana]
8314	GM_137_B2_G01_T7	g2995405	BLASTX	330	5e-28	55	(Y12432) polypeptide [Ananas comosus]
8315	GM_137_B2_G02_T7	g3645899	BLASTX	359	6e-31	57	(U68408) 5' end not determined experimentally [Zea mays]
8316	GM_137_B2_G03_T7	g3033389	BLASTX	206	1e-14	42	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
8317	GM_137_B2_G06_MR	g1167523	BLASTX	358	1e-30	55	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
8318	GM_137_B2_G11_T7	g4063760	BLASTX	171	3e-13	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8319	GM_137_B2_G12_T7	g1915988	BLASTN	353	5e-09	66	Tritrichomonas foetus putative protein tyrosine phosphatase, complete cds, and putative serine/threonine protein kinase genes, partial cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8320	GM_137_B2_H04_MR	g507910	BLASTN	596	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8321	GM_137_B2_H06_MR	g905361	BLASTX	652	3e-63	97	(U22103) gag-protease polyprotein [Glycine max]
8322	GM_137_B2_H07_T7	g2764526	BLASTN	472	3e-14	61	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
8323	GM_137_B2_H10_T7	g3645899	BLASTX	341	5e-29	56	(U68408) 5' end not determined experimentally [Zea mays]
8324	GM_138_A2_A02_MR	g343945	BLASTN	380	4e-11	60	Yeast (S.cerevisiae) mitochondrial var1 gene, 5' flank.
8325	GM_138_A2_A05_MR	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8326	GM_138_A2_A05_T7	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8327	GM_138_A2_A06_MR	g2970554	BLASTN	354	6e-09	70	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
8328	GM_138_A2_A07_T7	g4063760	BLASTX	298	1e-25	47	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8329	GM_138_A2_A11_MR	g2522228	BLASTX	452	5e-42	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
8330	GM_138_A2_A12_MR	g3264544	BLASTN	605	3e-20	62	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
8331	GM_138_A2_B11_MR	g905361	BLASTX	787	2e-77	95	(U22103) gag-protease polyprotein [Glycine max]
8332	GM_138_A2_B11_T7	g18768	BLASTN	525	2e-17	66	Soybean Tgm6 transposable element 3' end
8333	GM_138_A2_C03_T7	g1871180	BLASTX	243	7e-20	80	(U90439) unknown protein [Arabidopsis thaliana]
8334	GM_138_A2_C04_MR	g4003339	BLASTN	365	2e-09	62	Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence [Homo sapiens]
8335	GM_138_A2_C09_MR	g3097320	BLASTN	430	2e-12	72	Glycine max gene for Bd 30K, complete cds
8336	GM_138_A2_C12_T7	g3645899	BLASTX	184	7e-24	42	(U68408) 5' end not determined experimentally [Zea mays]
8337	GM_138_A2_D02_T7	g3097320	BLASTN	925	7e-35	81	Glycine max gene for Bd 30K, complete cds
8338	GM_138_A2_D03_T7	g343945	BLASTN	363	2e-10	58	Yeast (S.cerevisiae) mitochondrial var 1 gene, 5' flank.
8339	GM_138_A2_D04_MR	g4063760	BLASTX	389	4e-34	56	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8340	GM_138_A2_D06_MR	g4160362	BLASTN	363	2e-09	61	Saccharomyces cerevisiae complete mitochondrial genome
8341	GM_138_A2_D06_T7	g342953	BLASTN	514	3e-17	68	paramecium species 4.5 la mt dna dimer: replication init. region.
8342	GM_138_A2_D08_T7	g100484	BLASTX	320	4e-27	43	hypothetical protein - garden snail
8343	GM_138_A2_D09_MR	g507910	BLASTN	389	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8344	GM_138_A2_E03_MR	g3337395	BLASTN	508	7e-16	62	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
8345	GM_138_A2_E05_MR	g3510505	BLASTX	264	1e-20	40	(AF030881) pol polyprotein [Fugu rubripes]
8346	GM_138_A2_E07_MR	g3599418	BLASTN	476	1e-14	93	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
8347	GM_138_A2_E07_T7	g505129	BLASTN	356	4e-09	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8348	GM_138_A2_E08_MR	g2995405	BLASTX	459	2e-44	57	(Y12432) polyprotein [Ananas comosus]
8349	GM_138_A2_E10_MR	g4063756	BLASTN	546	1e-17	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8350	GM_138_A2_E12_MR	g3097320	BLASTN	439	8e-13	74	Glycine max gene for Bd 30K, complete cds
8351	GM_138_A2_F02_MR	g3845089	BLASTN	366	2e-09	60	Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence
8352	GM_138_A2_F02_T7	g1666236	BLASTX	265	3e-22	34	(U76261) unknown [Hordeum vulgare]
8353	GM_138_A2_F05_MR	g99755	BLASTX	458	1e-42	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
8354	GM_138_A2_F06_T7	g3142328	BLASTN	2143	1e-90	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF004216) ethylene-insensitive3 [Arabidopsis thaliana] gi 2224935 (AF004217) ethylene-insensitive3 [Arabidopsis thaliana]
8355	GM_138_A2_F12_MR	g2224933	BLASTX	806	2e-79	86	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
8356	GM_138_A2_G02_MR	g505129	BLASTN	430	2e-12	68	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
8357	GM_138_A2_G02_T7	g4115365	BLASTX	127	4e-09	29	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL.H148), complete sequence [Homo sapiens]
8358	GM_138_A2_G08_MR	g3097836	BLASTN	427	3e-12	43	Homo sapiens clone DJ56J10, complete sequence [Homo sapiens] (AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
8359	GM_138_A2_G10_MR	g4156152	BLASTN	389	1e-10	62	(AC003680) unknown protein [Arabidopsis thaliana] gi 3386623
8360	GM_138_A2_H02_T7	g3319362	BLASTX	380	3e-33	71	(AC004665) unknown protein [Arabidopsis thaliana]
8361	GM_138_A2_H04_MR	g2979562	BLASTX	193	9e-24	82	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8362	GM_138_A2_H05_MR	g99922	BLASTX	203	7e-20	68	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSAII project)
8363	GM_138_A2_H07_MR	g2911063	BLASTN	351	8e-09	90	(AF053008) gag-pol polyprotein [Glycine max]
8364	GM_138_B2_A03_T7	g3777527	BLASTX	553	3e-51	93	(AF053008) gag-pol polyprotein [Glycine max]
8365	GM_138_B2_B04_MR	g3777527	BLASTX	384	2e-33	98	(U22103) gag-protease polyprotein [Glycine max]
8366	GM_138_B2_B04_T7	g905361	BLASTX	550	2e-52	46	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
8367	GM_138_B2_B07_MR	g2961349	BLASTX	174	4e-11	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8368	GM_138_B2_B08_T7	g1769898	BLASTX	387	1e-34	79	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M)
8369	GM_138_B2_B09_T7	g1431738	BLASTN	493	2e-15		

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
8370	GM_138_B2_C08_MR	g3142289	BLASTX	249	4e-27	53	(AC002411) Strong similarity to beta-keto-CoA synthase gb U37088 from <i>Simmondsia chinensis</i> . [Arabidopsis thaliana]
8371	GM_138_B2_C09_T7	g4063760	BLASTX	435	6e-39	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8372	GM_138_B2_C11_T7	g3176798	BLASTN	381	5e-11	62	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite. 5' sequence
8373	GM_138_B2_C12_MR	g1769898	BLASTX	196	7e-14	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8374	GM_138_B2_D01_T7	g2443320	BLASTX	257	7e-20	49	(D85597) polyprotein [Oryza australiensis]
8375	GM_138_B2_D02_MR	g100484	BLASTX	234	8e-18	62	hypothetical protein - garden snapdragon
8376	GM_138_B2_D05_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence
8377	GM_138_B2_D07_T7	g2522227	BLASTX	127	9e-09	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8378	GM_138_B2_D09_MR	g4063760	BLASTX	189	2e-14	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8379	GM_138_B2_D10_MR	g507910	BLASTN	551	3e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
8380	GM_138_B2_D11_T7	g1709885	BLASTX	183	8e-13	55	PHYTOENE SYNTHASE PRECURSOR gi 1086122 pir S54135
8381	GM_138_B2_E02_T7	g3599418	BLASTN	503	9e-16	71	phytoene synthase - Narcissus pseudonarcissus]
8382	GM_138_B2_E04_T7	g3327393	BLASTX	151	2e-13	35	phytoene synthase [Narcissus pseudonarcissus]
8383	GM_138_B2_E08_MR	g507910	BLASTN	497	7e-16	76	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
8384	GM_138_B2_E08_T7	g507910	BLASTN	599	2e-20	82	(AC004483) hypothetical protein [Arabidopsis thaliana]
8385	GM_138_B2_E10_MR	g3777527	BLASTX	424	1e-46	98	Glycine max BSR-101 satellite SB92 genomic sequence.
8386	GM_138_B2_E12_MR	g507910	BLASTN	356	2e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8387	GM_138_B2_E12_T7	g507910	BLASTN	390	5e-11	72	(AF053008) gag-pol polyprotein [Glycine max]
8388	GM_138_B2_F06_MR	g3142328	BLASTN	1334	2e-53	93	Glycine max BSR-101 satellite SB92 genomic sequence.
8389	GM_138_B2_F10_T7	g629693	BLASTX	214	2e-16	50	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8390	GM_138_B2_G04_T7	g3599418	BLASTN	829	1e-30	77	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8391	GM_138_B2_G07_MR	g3176806	BLASTN	345	2e-09	68	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
8392	GM_138_B2_G09_MR	g3777527	BLASTX	220	2e-17	53	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite. 5' sequence
8393	GM_138_B2_G10_T7	g507910	BLASTN	386	8e-11	71	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	Cloned	NCBI gi	Method	Score	P-value	%Ident	Description
8394	GM_138_B2_G12_MR	g3445210	BLASTX	197	8e-19	50	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
8395	GM_138_B2_H01_MR	g1351780	BLASTX	94	7e-11	71	HYPOTHETICAL 23.2 KD PROTEIN (ORF 203) gi 984311 (U26948) unknown [Glycine max]
8396	GM_138_B2_H03_T7	g12212	BLASTN	1049	1e-45	93	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
8397	GM_138_B2_H04_T7	g3907448	BLASTN	393	1e-10	65	Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence [Homo sapiens]
8398	GM_138_B2_H10_MR	g1184075	BLASTX	132	2e-09	50	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
8399	GM_138_B2_H10_T7	g2429543	BLASTX	221	5e-21	53	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans])
8400	GM_139_A1_A05_T7	g13767	BLASTN	362	3e-10	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
8401	GM_139_A1_B09_MR	g2443320	BLASTX	173	6e-14	52	(D85597) polyprotein [Oryza australiensis]
8402	GM_139_A1_C08_T7	g3142328	BLASTN	867	3e-32	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8403	GM_139_A1_D11_T7	g3097320	BLASTN	931	4e-35	80	Glycine max gene for Bd 30K, complete cds
8404	GM_139_A1_F04_T7	g2642431	BLASTX	166	4e-10	42	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
8405	GM_139_A1_F11_MR	g3184270	BLASTN	554	5e-18	74	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence.
8406	GM_139_A1_G08_T7	g4092470	BLASTN	600	5e-20	68	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
8407	GM_139_A1_G11_T7	g905361	BLASTX	235	5e-18	95	(U22103) gag-protease polyprotein [Glycine max]
8408	GM_139_A1_H02_T7	g1881384	BLASTX	246	3e-20	57	(AB001585) reverse transcriptase [Solanum melongena]
8409	GM_139_A1_H07_T7	g4063760	BLASTX	198	1e-13	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8410	GM_139_A2_A02_MR	g4063760	BLASTX	502	4e-46	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8411	GM_139_A2_A05_MR	g3142328	BLASTN	1033	7e-40	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
8412	GM_139_A2_A08_MR	g4063760	BLASTX	358	1e-32	70	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8413	GM_139_A2_B04_MR	g130582	BLASTX	347	2e-29	55	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
8414	GM_139_A2_C01_T7	g3645899	BLASTX	100	1e-08	42	(U68408) 5' end not determined experimentally [Zea mays]
8415	GM_139_A2_C11_MR	g3097320	BLASTN	479	1e-14	71	Glycine max gene for Bd 30K, complete cds
8416	GM_139_A2_D02_MR	g2522228	BLASTX	226	2e-22	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
8417	GM_139_A2_D03_T7	g3142328	BLASTN	398	5e-11	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8418	GM_139_A2_F05_MR	g3142379	BLASTX	268	4e-22	59	(AF053008) envelope-like [Glycine max]
8419	GM_139_A2_E10_T7	g507910	BLASTN	470	1e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
8420	GM_139_A2_F12_T7	g3097320	BLASTN	350	8e-09	72	Glycine max gene for Bd 30K, complete cds
8421	GM_139_A2_G05_T7	g507910	BLASTN	352	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8422	GM_139_A2_G08_T7	g3142379	BLASTX	256	8e-21	80	(AF053008) envelope-like [Glycine max]
8423	GM_139_A2_G11_T7	g2995405	BLASTX	329	7e-28	65	(Y12432) polyprotein [Ananas comosus]
8424	GM_139_A2_H07_MR	g3810596	BLASTX	261	1e-20	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
8425	GM_139_A2_H10_T7	g3550435	BLASTN	418	7e-12	63	Hordeum vulgare Hotr1 gene
8426	GM_139_B1_A01_T7	g456383	BLASTN	372	5e-10	74	Blastocytidia culicis ATCC 30268 kinetoplast (MURF1) and apocytochrome B (cytB) genes, partial cds, and ATPase subunit 6 (MURF4) gene, complete pre-RNA-edited DNA sequence.
8427	GM_139_B1_A09_T7	g18559	BLASTN	314	4e-11	71	G.max gene for catalase
8428	GM_139_B1_A12_MR	g733521	BLASTN	351	7e-09	67	Dictyostelium discoideum phosphatidylinositol-4,5-diphosphate 3-kinase (PIK2) mRNA, complete cds.
8429	GM_139_B1_B07_MR	g4063756	BLASTN	450	3e-13	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8430	GM_139_B1_B07_T7	g3142330	BLASTX	457	2e-42	91	(U96295) envelope-like [Glycine max]
8431	GM_139_B1_B12_T7	g2052034	BLASTN	385	2e-10	68	Human DNA sequence from PAC 450C20 on chromosome X
8432	GM_139_B1_C10_MR	g2129618	BLASTX	185	2e-12	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8433	GM_139_B1_D02_T7	g1785739	BLASTX	159	6e-11	37	(Y08502) orf240b [Arabidopsis thaliana]
8434	GM_139_B1_D06_MR	g3142328	BLASTN	961	1e-36	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8435	GM_139_B1_D08_MR	g3097320	BLASTN	634	1e-21	76	Glycine max gene for Bd 30K, complete cds
8436	GM_139_B1_D09_T7	g1435023	BLASTX	215	6e-17	70	(D26578) DNA-binding protein [Daucus carota]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8437	GM_139_B1_E04_T7	g4063760	BLASTX	192	5e-13	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8438	GM_139_B1_E06_T7	g4063760	BLASTX	243	2e-18	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8439	GM_139_B1_E08_T7	g2673917	BLASTX	205	4e-14	50	(AC005561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
8440	GM_139_B1_E09_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8441	GM_139_B1_E09_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8442	GM_139_B1_F03_T7	g4063760	BLASTX	281	2e-22	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8443	GM_139_B1_F06_MR	g4063760	BLASTX	270	2e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8444	GM_139_B1_F11_T7	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
8445	GM_139_B1_F12_T7	g3097320	BLASTN	558	3e-18	77	Glycine max gene for Bd 30K, complete cds
8446	GM_139_B1_G02_T7	g3695387	BLASTX	137	1e-13	70	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
8447	GM_139_B1_G07_T7	g507910	BLASTN	625	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
8448	GM_139_B1_G09_MR	g507910	BLASTN	532	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8449	GM_139_B1_G09_T7	g507910	BLASTN	573	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8450	GM_139_B1_G11_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8451	GM_139_B1_G11_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8452	GM_139_B1_H05_T7	g100484	BLASTX	259	2e-20	58	hypothetical protein - garden snapdragon
8453	GM_139_B1_H06_T7	g3142328	BLASTN	760	2e-27	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8454	GM_139_B1_H08_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8455	GM_139_B1_H08_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8456	GM_139_B1_H11_MR	g2443320	BLASTX	212	4e-15	42	(D85597) polypeptide [Oryza australiensis]
8457	GM_139_B1_H11_T7	g2501353	BLASTX	220	1e-23	89	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
8458	GM_139_B1_H12_MR	g3461838	BLASTX	226	8e-17	43	(AC005315) putative receptor protein kinase [Arabidopsis thaliana]
8459	GM_139_B2_A01_T71	g218269	BLASTX	180	3e-13	79	(D12839) reverse transcriptase [Glycine max]
8460	GM_139_B2_A07_MR	g4063760	BLASTX	351	6e-30	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8461	GM_139_B2_A10_T71	g2522230	BLASTX	152	3e-10	55	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8462	GM_139_B2_B10_MR	g507910	BLASTN	547	4e-18	84	Glycine max BSR-101 satellite SB92 genomic sequence.
8463	GM_139_B2_B11_T71	g2689221	BLASTX	187	4e-13	45	(Y10098) 7-ethoxycoumarin O-deethylase [Helianthus tuberosus]
	016172						

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8464	GM_139_B2_B12_T71 016172	g806299	BLASTX	95	2e-09	38	(M25427) unknown protein [Zea mays]
8465	GM_139_B2_C03_T71 016172	g1666236	BLASTX	160	2e-10	33	(U76261) unknown [Hordeum vulgare]
8466	GM_139_B2_C05_MR 016172	g3319362	BLASTX	374	1e-32	70	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
8467	GM_139_B2_C07_T71 016172	g2443320	BLASTX	213	4e-15	43	(D85597) polyprotein [Oryza australiensis]
8468	GM_139_B2_C09_T71 016172	g320565	BLASTX	257	2e-21	50	transposon TAI-1 KAS-1 - Arabidopsis thaliana (fragment)
8469	GM_139_B2_C10_MR 016172	g3142328	BLASTN	538	2e-17	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8470	GM_139_B2_D01_MR 016172	g507910	BLASTN	426	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8471	GM_139_B2_D07_MR 016172	g2264320	BLASTN	440	8e-13	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
8472	GM_139_B2_E04_T71 016172	g3142328	BLASTN	1380	1e-55	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8473	GM_139_B2_E09_MR 016172	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence
8474	GM_139_B2_E09_T71 016172	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
8475	GM_139_B2_F01_T71 016172	g3777527	BLASTX	511	7e-47	98	(AF053008) gag-pol polyprotein [Glycine max]
8476	GM_139_B2_F02_MR 016172	g2842477	BLASTX	152	3e-09	76	(AL021749) copper-binding protein-like [Arabidopsis thaliana]
8477	GM_139_B2_F03_MR 016172	g3249105	BLASTX	168	4e-11	88	(AC003114) Contains similarity to protein phosphatase 2C' (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
8478	GM_139_B2_F05_T71 016172	g1142702	BLASTN	497	6e-16	76	Glycine max satellite STR120-A.4.
8479	GM_139_B2_G01_MR 016172	g3777527	BLASTX	168	3e-10	37	(AF053008) gag-pol polyprotein [Glycine max]
8480	GM_139_B2_G04_T71 016172	g507910	BLASTN	595	3e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
8481	GM_139_B2_G05_MR 016172	g3142328	BLASTN	1400	1e-56	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8482	GM_139_B2_G06_T71 016172	g18559	BLASTN	651	2e-22	77	G-max gene for catalase
8483	GM_139_B2_G07_MR 016172	g2443320	BLASTX	275	9e-22	53	(D85597) polyprotein [Oryza australiensis]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	% Ident	Description
8484	GM_139_B2_H12_T71_016172	g436919	BLASTN	353	6e-09	62	Arabidopsis thaliana Landsburg lipoxigenase 1 gene, complete cds.
8485	GM_140_A1_A01_MR	g3080423	BLASTX	302	8e-25	51	(AL022604) putative protein [Arabidopsis thaliana]
8486	GM_140_A1_A03_MR	g2738734	BLASTN	438	5e-13	66	Cryptosporidium parvum small subunit ribosomal RNA gene, partial sequence, internal transcribed spacer 1, putative 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence, and large subunit ribosomal...
8487	GM_140_A1_A05_MR	g2995405	BLASTX	266	6e-30	56	(Y12432) polyprotein [Ananas comosus]
8488	GM_140_A1_A11_MR	g3294511	BLASTN	370	1e-09	63	Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
8489	GM_140_A1_B01_T7	g18559	BLASTN	1250	1e-49	87	G.max gene for catalase
8490	GM_140_A1_B02_T7	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8491	GM_140_A1_B03_MR	g2443320	BLASTX	258	4e-26	60	(D85597) polyprotein [Oryza australiensis]
8492	GM_140_A1_B07_T7	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8493	GM_140_A1_B10_T7	g1769898	BLASTX	125	9e-16	38	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8494	GM_140_A1_C07_T7	g1167523	BLASTX	305	5e-25	46	(D83003) ORI:(AA 1-1338) [Nicotiana tabacum]
8495	GM_140_A1_C11_T7	g857399	BLASTX	172	1e-16	69	(D50871) mitotic cyclin b1-type [Glycine max]
8496	GM_140_A1_D01_MR	g2894495	BLASTN	353	6e-09	58	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-95, complete sequence [Plasmodium falciparum]
8497	GM_140_A1_D11_T7	g18695	BLASTN	801	1e-29	91	Soybean nodulin 22 gene
8498	GM_140_A1_D12_T7	g4063760	BLASTX	533	2e-49	61	(AC005561) putative POI.3 protein [Arabidopsis thaliana]
8499	GM_140_A1_E05_T7	g3810596	BLASTX	332	4e-28	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
8500	GM_140_A1_E10_T7	g1061420	BLASTX	539	2e-54	83	(U38965) p-type H+-ATPase [Vicia faba]
8501	GM_140_A1_E12_T7	g3142328	BLASTN	480	7e-25	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8502	GM_140_A1_F01_T7	g507910	BLASTN	446	1e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8503	GM_140_A1_F02_T7	g18559	BLASTN	2487	2e-106	90	G max gene for catalase
8504	GM_140_A1_F05_MR	g3282250	BLASTX	348	3e-34	70	(AF009337) CDPK-related protein kinase [Tradescantia virginiana]
8505	GM_140_A1_F06_MR	g2522230	BLASTX	159	5e-11	32	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8506	GM_140_A1_F09_T7	g1666236	BLASTX	201	4e-15	31	(U76261) unknown [Hordeum vulgare]
8507	GM_140_A1_F12_MR	g1946355	BLASTX	137	2e-09	31	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
8508	GM_140_A1_G01_T7	g2995405	BLASTX	473	2e-43	51	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8509	GM_140_A1_G03_T7	g3273387	BLASTN	394	9e-11	60	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
8510	GM_140_A1_G04_MR	g3142328	BLASTN	675	1e-23	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8511	GM_140_A1_G05_T7	g100484	BLASTX	483	6e-45	50	hypothetical protein - garden snapdragon
8512	GM_140_A1_G07_T7	g4160362	BLASTN	339	1e-12	65	Saccharomyces cerevisiae complete mitochondrial genome
8513	GM_140_A1_G08_T7	g3097320	BLASTN	490	4e-15	69	Glycine max gene for Bd 30K, complete cds
8514	GM_140_A1_G09_T7	g101042	BLASTX	158	3e-09	31	hypothetical protein T1 - fission yeast (Schizosaccharomyces pombe) gi 173477 (M38526) T11 protein [Schizosaccharomyces pombe]
8515	GM_140_A1_H05_T7	g2880057	BLASTX	271	2e-23	52	(AC002340) putative RNA helicase A, 5' partial [Arabidopsis thaliana]
8516	GM_140_A1_H07_T7	g1666236	BLASTX	157	8e-19	36	(U76261) unknown [Hordeum vulgare]
8517	GM_140_A1_H08_MR	g3645899	BLASTX	268	5e-46	55	(U68408) 5' end not determined experimentally [Zea mays]
8518	GM_140_A1_H10_T7	g3777527	BLASTX	878	6e-91	92	(AF053008) gag-pol polypeptide [Glycine max]
8519	GM_140_A1_H11_T7	g100484	BLASTX	215	9e-16	50	hypothetical protein - garden snapdragon
8520	GM_140_A1_H12_MR	g2995405	BLASTX	208	1e-22	51	(Y12432) polypeptide [Ananas comosus]
8521	GM_140_A2_A05_T7	g629693	BLASTX	171	1e-11	43	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8522	GM_140_A2_A12_T7	g3142379	BLASTX	152	2e-09	46	(AF053008) envelope-like [Glycine max]
8523	GM_140_A2_B02_T7	g4127445	BLASTN	461	7e-14	68	Arabidopsis thaliana ucp gene, exons 1-9
8524	GM_140_A2_B03_T7	g3142379	BLASTX	433	5e-40	75	(AF053008) envelope-like [Glycine max]
8525	GM_140_A2_B07_T7	g4127445	BLASTN	427	3e-12	67	Arabidopsis thaliana ucp gene, exons 1-9
8526	GM_140_A2_D01_T7	g1142703	BLASTN	582	8e-20	82	Glycine max satellite STR120-B.1.
8527	GM_140_A2_D02_T7	g3645899	BLASTX	187	7e-14	36	(U68408) 5' end not determined experimentally [Zea mays]
8528	GM_140_A2_D11_T7	g2522228	BLASTX	405	5e-37	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
8529	GM_140_A2_E02_T7	g2522230	BLASTX	105	9e-12	52	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8530	GM_140_A2_E05_T7	g3645899	BLASTX	282	2e-25	47	(U68408) 5' end not determined experimentally [Zea mays]
8531	GM_140_A2_E06_T7	g2244761	BLASTX	419	1e-38	54	(Z97335) similar to unknown protein - Arabidopsis thaliana [Arabidopsis thaliana]
8532	GM_140_A2_F03_T7	g117822	BLASTX	248	4e-24	66	CYTOCHROME B6 gi 65635 pir CBNT6 plastoquinol-plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - common tobacco chloroplast gi 11858 (Z00044) cytochrome b6 [Nicotiana tabacum] gi 225226 prf 1211235BH cytochrome b6 [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
8533	GM_140_A2_G01_T7	g3097320	BLASTN	390	1e-10	67	Glycine max gene for Bd 30K, complete cds
8534	GM_140_A2_H02_T7	g3777527	BLASTX	435	9e-39	84	(AF053008) gag-pol polyprotein [Glycine max]
8535	GM_140_A2_H05_T7	g320569	BLASTX	165	1e-11	46	transposon TNT1 - Arabidopsis thaliana (fragment)
8536	GM_140_A2_H11_T7	g3142328	BLASTN	1065	3e-41	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8537	GM_140_B1_A04_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence
8538	GM_140_B1_A04_T7	g507910	BLASTN	387	7e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence
8539	GM_140_B1_A08_MR	g116054	BLASTX	190	2e-13	51	CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) gi 280393 pir A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean gi 169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max]
8540	GM_140_B1_A10_MR	g905361	BLASTX	487	1e-45	100	(U22103) gag-protease polyprotein [Glycine max]
8541	GM_140_B1_A11_MR	g1769898	BLASTX	325	8e-28	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8542	GM_140_B1_A11_T7	g81704	BLASTX	99	9e-12	43	S-locus-specific glycoprotein precursor - kale
8543	GM_140_B1_A12_MR	g18559	BLASTN	638	7e-22	74	G.max gene for catalase
8544	GM_140_B1_B01_T7	g2995405	BLASTX	394	7e-35	66	(Y12432) polyprotein [Ananas comosus]
8545	GM_140_B1_B03_T7	g218269	BLASTX	397	3e-36	93	(D12839) reverse transcriptase [Glycine max]
8546	GM_140_B1_B08_MR	g2995405	BLASTX	331	4e-28	60	(Y12432) polyprotein [Ananas comosus]
8547	GM_140_B1_C06_T7	g170029	BLASTN	365	2e-09	78	Glycine max cv. Dare nodulin 26 gene fragment
8548	GM_140_B1_C10_MR	g2317908	BLASTX	214	6e-16	47	(U89059) Unknown protein [Arabidopsis thaliana]
8549	GM_140_B1_C12_T7	g3810596	BLASTX	224	1e-16	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
8550	GM_140_B1_D01_T7	g3142328	BLASTN	705	6e-25	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8551	GM_140_B1_D02_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence
8552	GM_140_B1_D12_MR	g913445	BLASTX	276	2e-23	56	(S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase homolog [EC 1.1.1.1] [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 389 aa] [Lycopersicon esculentum]
8553	GM_140_B1_E06_MR	g3510347	BLASTN	476	2e-14	69	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]
8554	GM_140_B1_E06_T7	g871290	BLASTX	163	2e-23	53	(X69886) glycerol kinase [Homo sapiens]
8555	GM_140_B1_E08_T7	g2109275	BLASTX	165	5e-10	41	(U97106) downy mildew resistance protein RPP5 [Arabidopsis thaliana]
8556	GM_140_B1_E11_MR	g3047073	BLASTX	161	4e-10	42	(AF058825) contains similarity to retrotransposon-like proteins [Arabidopsis thaliana]
8557	GM_140_B1_F02_MR	g507910	BLASTN	567	5e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8558	GM_140_B1_F02_T7	g507910	BLASTN	481	4e-15	79	Glycine max BSR-101 satellite SB92 genomic sequence
8559	GM_140_B1_F05_MR	g507910	BLASTN	349	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8560	GM_140_B1_F05_T7	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8561	GM_140_B1_F07_MR	g2330651	BLASTX	153	2e-12	69	(Y14559) topoisomerase II [Pisum sativum]
8562	GM_140_B1_F08_MR	g1171642	BLASTX	159	3e-10	61	PROBABLY SERINE/THREONINE-PROTEIN KINASE NAK gi 481206 pir S38326 protein kinase - Arabidopsis thaliana gi 166809 (L07248) protein kinase [Arabidopsis thaliana]
8563	GM_140_B1_F10_MR	g1843462	BLASTX	225	1e-17	53	(L10211) isoliquiritigenin 2'-O-methyltransferase [Medicago sativa]
8564	GM_140_B1_G05_MR	g1732513	BLASTX	160	4e-11	68	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
8565	GM_140_B1_G06_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8566	GM_140_B1_G06_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8567	GM_140_B1_G07_MR	g2443320	BLASTX	227	1e-16	60	(D85597) polyprotein [Oryza australiensis]
8568	GM_140_B1_G11_T7	g2335089	BLASTN	801	4e-29	73	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]
8569	GM_140_B1_H01_T7	g4063760	BLASTX	454	5e-41	72	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8570	GM_140_B1_H10_T7	g3335376	BLASTX	212	7e-16	42	(AC003028) putative ammonium transporter [Arabidopsis thaliana]
8571	GM_140_B1_H11_T7	g4063760	BLASTX	152	3e-12	49	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8572	GM_140_B2_A03_MR	g507910	BLASTN	358	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8573	GM_140_B2_A12_T7	g4063760	BLASTX	165	4e-10	36	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8574	GM_140_B2_B05_T7	g2244965	BLASTX	161	5e-10	44	(Z97340) unnamed protein product [Arabidopsis thaliana]
8575	GM_140_B2_B06_MR	g507910	BLASTN	553	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
8576	GM_140_B2_B11_T7	g1769899	BLASTX	181	8e-18	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8577	GM_140_B2_C02_MR	g2995405	BLASTX	257	4e-20	54	(Y12432) polyprotein [Ananas comosus]
8578	GM_140_B2_C05_T7	g3645899	BLASTX	225	1e-16	48	(U68408) 5' end not determined experimentally [Zea mays]
8579	GM_140_B2_C06_T7	g100484	BLASTX	332	2e-28	58	hypothetical protein - garden snapdragon
8580	GM_140_B2_C07_MR	g3097320	BLASTN	435	1e-12	72	Glycine max gene for Bd 30K, complete cds
8581	GM_140_B2_C11_T7	g507910	BLASTN	458	4e-14	83	Glycine max BSR-101 satellite SB92 genomic sequence.
8582	GM_140_B2_D08_MR	g2829869	BLASTX	169	2e-11	96	(AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
8583	GM_140_B2_D10_T7	g507910	BLASTN	555	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
8584	GM_140_B2_E02_T7	g3142328	BLASTN	1819	1e-75	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8585	GM_140_B2_E09_T7	g507910	BLASTN	372	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8586	GM_140_B2_E12_T7	g4063760	BLASTX	126	8e-09	44	(AC005561) putative POL.3 protein [Arabidopsis thaliana]

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8587	GM_140_B2_F02_T7	g1633547	BLASTN	491	4e-15	62	Human chromosome 12p13 sequence, complete sequence [Homo sapiens]
8588	GM_140_B2_G03_MR	g3650039	BLASTX	194	1e-13	53	(AC005396) putative Em/Spm transposon protein, 5' partial [Arabidopsis thaliana]
8589	GM_140_B2_G03_T7	g3184508	BLASTN	469	4e-14	66	Homo sapiens chromosome 17, clone HRP41C23, complete sequence [Homo sapiens]
8590	GM_140_B2_G07_T7	g130582	BLASTX	168	2e-10	40	RETROVIRUS-RELATED POI POLYPROTEIN (PROTEASE; REVERSE TRANSCRIPTASE, ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
8591	GM_140_B2_H01_T7	g4063760	BLASTX	224	4e-17	50	(AC005561) putative POI.3 protein [Arabidopsis thaliana]
8592	GM_140_B2_H04_MR	g3142328	BLASTN	710	4e-25	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8593	GM_140_B2_H04_T7	g99719	BLASTX	161	9e-10	35	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 16384 (X53976) orf 2 [Arabidopsis thaliana]
8594	GM_140_B2_H09_MR	g3142328	BLASTN	1001	2e-38	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005897) putative transposon [Arabidopsis thaliana]
8595	GM_141_A1_A07_MR	g4038056	BLASTX	316	2e-26	51	(AC005499) unknown protein [Arabidopsis thaliana]
8596	GM_141_A1_A11_MR	g3786008	BLASTX	140	6e-09	50	(X97826) orf04 [Arabidopsis thaliana]
8597	GM_141_A1_B05_T7	g1495259	BLASTX	202	7e-15	38	(AC005388) Strong similarity to F22O13.22 gi 3063460 myosin homolog from A. thaliana BAC gb AC003981 [Arabidopsis thaliana]
8598	GM_141_A1_B07_MR	g3776579	BLASTX	179	2e-11	82	(AF053008) gag-pol polyprotein [Glycine max]
8599	GM_141_A1_B09_MR	g3777527	BLASTX	248	3e-25	48	Glycine max BSR-101 satellite SB92 genomic sequence.
8600	GM_141_A1_B11_MR	g507910	BLASTN	371	4e-10	73	(AC003952) putative histidine kinase [Arabidopsis thaliana]
8601	GM_141_A1_C01_T7	g2708752	BLASTX	379	2e-34	69	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]
8602	GM_141_A1_C04_MR	g2760832	BLASTX	115	4e-10	44	Glycine max BSR-101 satellite SB92 genomic sequence.
8603	GM_141_A1_C06_MR	g507910	BLASTN	562	9e-19	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF053008) gag-pol polyprotein [Glycine max]
8604	GM_141_A1_C11_MR	g3142328	BLASTN	624	3e-21	85	(U22103) gag-protease polyprotein [Glycine max]
8605	GM_141_A1_D01_T7	g3777527	BLASTX	603	1e-56	98	
8606	GM_141_A1_F04_MR	g905361	BLASTX	548	2e-58	95	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8607	GM_141_A1_F03_MR	g2522230	BLASTX	243	3e-28	39	(AB007467) retrotransposon-like gene, the first amino acid was determined to be leucine [Vicia faba]
8608	GM_141_A1_F06_MR	g905361	BLASTX	182	2e-12	37	(U22103) gag-protease polyprotein [Glycine max]
8609	GM_141_A1_F09_MR	g342964	BLASTN	373	8e-11	61	parametium species 5.311 mt dna dimer: replication init. region.
8610	GM_141_A1_F12_MR	g1277164	BLASTX	202	8e-21	93	(U51853) cysteine proteinase inhibitor [Glycine max]
8611	GM_141_A1_G01_T7	g3885341	BLASTX	162	5e-10	35	(AC005623) unknown protein [Arabidopsis thaliana]
8612	GM_141_A1_G03_MR	g3193290	BLASTX	405	2e-36	54	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido...
8613	GM_141_A1_G04_T7	g1813979	BLASTX	134	4e-12	50	(Y10860) hypothetical protein [Musa acuminata]
8614	GM_141_A1_G06_T7	g886376	BLASTN	366	2e-09	60	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds.
8615	GM_141_A1_G12_MR	g99755	BLASTX	390	3e-35	45	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
8616	GM_141_A1_G12_T7	g2995405	BLASTX	150	1e-08	36	(Y12432) polyprotein [Ananas comosus]
8617	GM_141_A1_H04_MR	g3645899	BLASTX	202	3e-21	51	(U68408) 5' end not determined experimentally [Zea mays]
8618	GM_141_A1_H05_MR	g3645899	BLASTX	293	7e-24	56	(U68408) 5' end not determined experimentally [Zea mays]
8619	GM_141_A1_H08_T7	g3540184	BLASTX	311	8e-26	61	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]
8620	GM_141_A2_C01_T7	g507910	BLASTN	425	1e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8621	GM_141_A2_C11_T7	g3650039	BLASTX	257	2e-20	44	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
8622	GM_141_A2_E01_T7	g1666236	BLASTX	175	3e-12	28	(U76261) unknown [Hordeum vulgare]
8623	GM_141_A2_E05_MR	g2085783	BLASTN	507	7e-16	64	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
8624	GM_141_A2_F06_T7	g976178	BLASTX	112	2e-09	41	(L47183) reverse transcriptase [Arabidopsis thaliana]
8625	GM_141_A2_F08_T7	g3319351	BLASTX	208	3e-20	52	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
8626	GM_141_A2_G05_T7	g3097320	BLASTN	1455	7e-59	80	Glycine max gene for Bd 30K, complete cds
8627	GM_141_A2_G11_T7	g507910	BLASTN	526	4e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8628	GM_141_A2_G12_MR	g3142328	BLASTN	412	1e-11	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF036706) similar to S. cerevisiae Lpg15p (GIB:1143281) [Caenorhabditis elegans]
8629	GM_141_A2_H03_T7	g2702365	BLASTX	319	5e-27	57	

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8630	GM_141_A2_H06_T7	g3845197	BLASTN	522	1e-16	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
8631	GM_141_A2_H11_T7	g3142328	BLASTN	783	2e-28	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8632	GM_141_B1_A06_MR	g3283026	BLASTX	182	1e-13	45	putative transposase [Arabidopsis thaliana]
8633	GM_141_B1_A06_T7	g3184291	BLASTX	196	2e-13	51	(AC004136) putative DNA polymerase III gamma subunit [Arabidopsis thaliana]
8634	GM_141_B1_B07_MR	g4063760	BLASTX	170	3e-25	60	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8635	GM_141_B1_C06_MR	g507910	BLASTN	353	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8636	GM_141_B1_C06_T7	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8637	GM_141_B1_C07_T7	g170606	BLASTN	586	8e-20	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
8638	GM_141_B1_C09_T7	g3142328	BLASTN	492	3e-15	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U68408) 5' end not determined experimentally [Zea mays]
8639	GM_141_B1_C10_T7	g3645899	BLASTX	229	5e-17	53	branching enzyme II BEII [Zea mays, cultivar B73, endosperms, Peptide, 738 aa]
8640	GM_141_B1_D10_T7	g913865	BLASTX	152	5e-09	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005957) hypothetical protein [Arabidopsis thaliana]
8641	GM_141_B1_E03_MR	g3142328	BLASTN	564	1e-18	86	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST
8642	GM_141_B1_E04_MR	g4115362	BLASTX	149	9e-09	50	PRECURSOR gi 541947 pir JQ2339 omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean gi 408792 (L22965) omega-3 fatty acid desaturase [Glycine soja]
8643	GM_141_B1_E07_T7	g1345971	BLASTX	409	2e-37	88	Glycine max BSR-101 satellite SB92 genomic sequence.
8644	GM_141_B1_F02_T7	g507910	BLASTN	407	9e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8645	GM_141_B1_F09_MR	g507910	BLASTN	472	1e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8646	GM_141_B1_F09_T7	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8647	GM_141_B1_G02_T7	g3777527	BLASTX	176	3e-11	44	(AF053008) gag-pol polyprotein [Glycine max]
8648	GM_141_B1_G04_T7	g18559	BLASTN	589	1e-19	74	G max gene for catalase
8649	GM_141_B1_G08_MR	g4063760	BLASTX	236	1e-17	44	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8650	GM_141_B1_G10_MR	g1498335	BLASTN	1369	6e-56	96	Glycine max actin (Soy120) gene, partial cds
8651	GM_141_B1_H04_MR	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8652	GM_141_B1_H06_MR	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8653	GM_141_B1_H06_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8654	GM_141_B1_H07_MR	g3096945	BLASTX	328	7e-29	78	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]
8655	GM_142_A1_A04_T7	g18559	BLASTN	544	1e-17	77	G max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8656	GM_142_A1_A05_MR	g226407	BLASTX	393	2e-34	46	retrotransposon del-46 [Lilium henryi]
8657	GM_142_A1_A05_T7	g507910	BLASTN	711	2e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
8658	GM_142_A1_A06_MR	g1769899	BLASTX	203	1e-15	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8659	GM_142_A1_A10_MR	g3250688	BLASTX	216	5e-17	35	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
8660	GM_142_A1_A11_MR	g3876092	BLASTX	165	2e-10	47	(Z69635) Similarity to Drosophila white protein (SW:WHIT_DROME); cDNA EST EMBL:M89346 comes from this gene; cDNA EST yk311f2.3 comes from this gene; cDNA EST yk311f2.5 comes from this gene [Caenorhabditis elegans] (X88864) cyclin [Medicago sativa]
8661	GM_142_A1_A11_T7	g1150932	BLASTX	154	1e-09	80	l-aminocyclopropane-1-carboxylate synthase (FC 4 4 1 14) 5 - mung bean (fragment) gi 297850 (Z12134) ACC synthase [Vigna radiata]
8662	GM_142_A1_B01_MR	g421894	BLASTX	226	1e-17	91	gi 553115 (M94863) l-aminocyclopropane-1-carboxylate synthase [Vigna radiata]
8663	GM_142_A1_B01_T7	g2244870	BLASTN	374	7e-10	66	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 3
8664	GM_142_A1_B03_MR	g629693	BLASTX	187	2e-13	34	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8665	GM_142_A1_B09_MR	g4160362	BLASTN	381	7e-15	66	Saccharomyces cerevisiae complete mitochondrial genome
8666	GM_142_A1_B10_MR	g1769898	BLASTX	172	1e-18	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8667	GM_142_A1_C06_MR	g933559	BLASTX	191	1e-12	33	ORF3 protein - rice tungro bacilliform virus gi 333967 (M65026) ORF3 [Rice tungro bacilliform virus]
8668	GM_142_A1_C11_MR	g507910	BLASTN	424	2e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8669	GM_142_A1_C11_T7	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence
8670	GM_142_A1_D02_T7	g4063760	BLASTX	218	8e-16	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8671	GM_142_A1_D05_T7	g3386534	BLASTX	174	8e-12	39	(AF078934) mariner transposase [Glycine max]
8672	GM_142_A1_D06_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8673	GM_142_A1_D09_MR	g2522230	BLASTX	216	5e-17	46	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8674	GM_142_A1_D10_T7	g1840106	BLASTN	352	2e-09	63	Human fragile site locus (FRA16B) minisatellite repeat
8675	GM_142_A1_D11_MR	g2258315	BLASTX	229	6e-17	42	(AF004878) resistance complex protein 12C-1 [Lycopersicon esculentum]
8676	GM_142_A1_D12_T7	g469153	BLASTN	372	8e-10	72	P.sativum (Birte) Lox1.Ps.2 gene.
8677	GM_142_A1_E09_MR	g905361	BLASTX	315	1e-26	75	(U22103) gag-protease polyprotein [Glycine max]
8678	GM_142_A1_E12_T7	g3953471	BLASTX	170	3e-11	54	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8679	GM_142_A1_F01_MR	g2129618	BLASTX	196	1e-13	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8680	GM_142_A1_F03_T7	g343917	BLASTN	346	2e-09	69	yeast (s.cerevisiae) mitochondrial repl region & repetitive unit.
8681	GM_142_A1_F05_T7	g2522230	BLASTX	107	2e-13	32	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8682	GM_142_A1_F06_MR	g3142328	BLASTN	1474	6e-60	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8683	GM_142_A1_F08_MR	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8684	GM_142_A1_F10_MR	g505129	BLASTN	398	5e-11	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
8685	GM_142_A1_F11_T7	g2995405	BLASTX	328	8e-28	61	(Y12432) polyprotein [Ananas comosus]
8686	GM_142_A1_G02_T7	g3810596	BLASTX	99	7e-11	29	(AC005308) reverse-transcriptase-like protein [Arabidopsis thaliana]
8687	GM_142_A1_G06_MR	g1171591	BLASTN	364	2e-09	62	P.falciparum complete gene map of plastid-like DNA (IR-B)
8688	GM_142_A1_G07_MR	g18559	BLASTN	1448	1e-58	86	Gi.max gene for catalase
8689	GM_142_A1_G12_MR	g3777527	BLASTX	279	4e-22	96	(AF053008) gag-pol polyprotein [Glycine max]
8690	GM_142_A1_H01_MR	g3695393	BLASTX	209	8e-15	33	(AF096371) contains similarity to retroviral aspartyl proteases (Pfam: rvp.hmm, score: 11.80) [Arabidopsis thaliana]
8691	GM_142_A1_H02_MR	g4063760	BLASTX	237	8e-18	56	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8692	GM_142_A1_H02_T7	g4063760	BLASTX	309	2e-25	56	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8693	GM_142_A1_H04_MR	g3171875	BLASTN	389	2e-10	61	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylamine Monooxygenase (N-Oxide 3, ECT.14.1...
8694	GM_142_A1_H06_MR	g4063760	BLASTX	190	1e-28	62	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8695	GM_142_A1_H06_T7	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8696	GM_142_A1_H07_MR	g1362108	BLASTX	199	4e-19	74	histone H3 homolog - common tobacco
8697	GM_142_A1_H08_MR	g1946355	BLASTX	196	1e-13	28	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
8698	GM_142_A2_A03_MR	g3777527	BLASTX	338	1e-35	76	(AF053008) gag-pol polyprotein [Glycine max]
8699	GM_142_A2_A03_T7	g2443320	BLASTX	165	3e-23	53	(D85597) polyprotein [Oryza australiensis]
8700	GM_142_A2_B04_T7	g3810596	BLASTX	158	1e-09	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
8701	GM_142_A2_C11_MR	g3805850	BLASTX	237	3e-19	86	(AL031986) putative protein [Arabidopsis thaliana]
8702	GM_142_A2_F03_T7	g3599418	BLASTN	777	3e-28	85	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
8703	GM_142_A2_F11_MR	g4063760	BLASTX	170	1e-10	47	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8704	GM_142_A2_F12_T7	g4063760	BLASTX	208	1e-14	55	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8705	GM_142_A2_H12_MR	g507910	BLASTN	430	8e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8706	GM_142_B1_A04_MR	g2465577	BLASTN	367	1e-09	69	Plasmodium falciparum microsatellite P4 sequence
8707	GM_142_B1_A05_T7	g4063760	BLASTX	525	1e-48	60	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8708	GM_142_B1_A11_MR	g3777527	BLASTX	423	2e-37	89	(AF053008) gag-pol polyprotein [Glycine max]
8709	GM_142_B1_B05_T7	g3777526	BLASTN	1155	3e-45	93	Glycine max env pseudogene, partial sequence, uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
8710	GM_142_B1_B06_T7	g2829924	BLASTX	112	6e-10	48	(AC002291) Unknown protein [Arabidopsis thaliana]
8711	GM_142_B1_B11_MR	g3097320	BLASTN	538	2e-17	68	Glycine max gene for Bd 30K, complete cds
8712	GM_142_B1_C03_MR	g462669	BLASTX	195	1e-15	76	MYB-RELATED PROTEIN PP2 gi 99453 pir S24244 Pp2 protein - moss (Physcomitrella patens) gi 22638 (X67050) Pp2 [Physcomitrella patens]
8713	GM_142_B1_C05_T7	g2982459	BLASTX	225	6e-18	81	(AL022223) putative protein [Arabidopsis thaliana]
8714	GM_142_B1_C09_MR	g130582	BLASTX	330	1e-27	64	RETROVIRUS-RELATED POL. POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
8715	GM_142_B1_C11_T7	g2618731	BLASTX	194	4e-14	44	(U49077) IAA21 [Arabidopsis thaliana]
8716	GM_142_B1_D01_MR	g2351176	BLASTX	253	2e-20	46	(D85222) S glycoprotein [Brassica rapa]
8717	GM_142_B1_D02_MR	g2995405	BLASTX	154	4e-09	44	(Y12432) polyprotein [Ananas comosus]
8718	GM_142_B1_D03_MR	g3142328	BLASTN	557	3e-18	94	Glycine max partial SIRF-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8719	GM_142_B1_D10_MR	g507910	BLASTN	514	1e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
8720	GM_142_B1_D10_T7	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8721	GM_142_B1_E02_MR	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8722	GM_142_B1_E03_T7	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8723	GM_142_B1_E07_T7	g2827718	BLASTX	300	1e-24	45	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]
8724	GM_142_B1_E10_T7	g2522228	BLASTX	359	7e-42	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
8725	GM_142_B1_F02_T7	g2522230	BLASTX	164	2e-11	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8726	GM_142_B1_F04_MR	g4063760	BLASTX	197	1e-13	38	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8727	GM_142_B1_F04_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8728	GM_142_B1_F09_MR	g3777527	BLASTX	473	8e-43	95	(AF053008) gag-pol polyprotein [Glycine max]
8729	GM_142_B1_F11_MR	g3367534	BLASTX	465	4e-42	89	(AC004392) Strong similarity to coatmer alpha subunit (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis thaliana]
8730	GM_142_B1_F11_T7	g2506139	BLASTX	126	7e-14	73	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) gi 1314049 gnl PID e209222 (Z67962) archain/delta-COP [Oryza sativa]
8731	GM_142_B1_G03_T7	g1666236	BLASTX	261	9e-22	36	(U76261) unknown [Hordeum vulgare]
8732	GM_142_B1_G05_MR	g3142328	BLASTN	623	4e-23	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
8733	GM_142_B1_G05_T7	g2244915	BLASTX	229	4e-17	36	
8734	GM_142_B1_G07_T7	g3142328	BLASTN	1682	2e-69	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF069299) contains similarity to Arabidopsis scarecrow (GB:U62798) [Arabidopsis thaliana]
8735	GM_142_B1_G08_MR	g3193314	BLASTX	215	5e-16	51	(AF077407) contains similarity to reverse transcriptases (PFam: rvt_hmm, score: 116.22) [Arabidopsis thaliana]
8736	GM_142_B1_G08_T7	g3319351	BLASTX	209	9e-24	47	(AF001453) Dc3 promoter-binding factor-1 [Helianthus annuus]
8737	GM_142_B1_G09_T7	g2228771	BLASTX	145	9e-09	47	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8738	GM_142_B1_G12_MR	g4063760	BLASTX	260	3e-20	56	Glycine max BSR-101 satellite SB92 genomic sequence.
8739	GM_142_B1_G12_T7	g507910	BLASTN	589	5e-20	82	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8740	GM_142_B1_H03_T7	g2522227	BLASTX	213	1e-16	53	(U22103) gag-protease polyprotein [Glycine max]
8741	GM_142_B1_H04_MR	g905361	BLASTX	460	8e-43	93	Glycine max BSR-101 satellite SB92 genomic sequence.
8742	GM_142_B1_H07_MR	g507910	BLASTN	572	3e-19	81	Soybean Tgm6 transposable element 3' end
8743	GM_142_B1_H08_T7	g18768	BLASTN	463	1e-14	69	Glycine max gene for Bd 30K, complete cds
8744	GM_142_B2_A01_T7	g3097320	BLASTN	432	2e-12	67	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL.3 protein [Arabidopsis thaliana]
8745	GM_142_B2_A02_MR	g3142328	BLASTN	665	4e-23	78	(U68408) 5' end not determined experimentally [Zea mays]
8746	GM_142_B2_A02_T7	g4063760	BLASTX	392	3e-34	65	(Y13368) reverse transcriptase [Beta vulgaris]
8747	GM_142_B2_A04_T7	g3645899	BLASTX	296	3e-24	50	Glycine max BSR-101 satellite SB92 genomic sequence.
8748	GM_142_B2_B04_T7	g2462134	BLASTX	325	9e-31	52	Glycine max BSR-101 satellite SB92 genomic sequence.
8749	GM_142_B2_B08_T7	g507910	BLASTN	420	2e-12	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8750	GM_142_B2_B09_MR	g507910	BLASTN	398	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8751	GM_142_B2_B09_T7	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8752	GM_142_B2_C06_MR	g507910	BLASTN	533	2e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
8753	GM_142_B2_C09_MR	g3777527	BLASTX	696	1e-66	97	(AF053008) gag-pol polyprotein [Glycine max]
8754	GM_142_B2_C12_MR	g905361	BLASTX	193	2e-13	38	(U22103) gag-protease polyprotein [Glycine max]
8755	GM_142_B2_D08_MR	g4038056	BLASTX	277	3e-22	47	(AC005897) putative transposon [Arabidopsis thaliana]
8756	GM_142_B2_D10_MR	g1402883	BLASTX	280	2e-23	43	(X98130) unknown [Arabidopsis thaliana] gi 1495263 gnl PID e242837 (X97487) orf09 [Arabidopsis thaliana]
8757	GM_142_B2_D12_MR	g3142328	BLASTN	671	2e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8758	GM_142_B2_D12_T7	g905361	BLASTX	98	1e-13	51	(U22103) gag-protease polyprotein [Glycine max]
8759	GM_142_B2_F08_T7	g3283026	BLASTX	185	1e-12	39	putative transposase [Arabidopsis thaliana]
8760	GM_142_B2_F03_T7	g1666236	BLASTX	183	4e-13	33	(U76261) unknown [Hordeum vulgare]
8761	GM_142_B2_F04_MR	g905361	BLASTX	432	1e-39	97	(U22103) gag-protease polyprotein [Glycine max]
8762	GM_142_B2_F05_MR	g3033400	BLASTX	318	2e-26	56	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
8763	GM_142_B2_F09_T7	g3777527	BLASTX	192	8e-14	39	(AF053008) gag-pol polyprotein [Glycine max]
8764	GM_142_B2_F11_T7	g3135969	BLASTN	358	4e-09	64	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
8765	GM_142_B2_G06_T7	g3269281	BLASTX	192	3e-13	48	(AL030978) putative protein [Arabidopsis thaliana]
8766	GM_142_B2_H03_MR	g4115942	BLASTX	170	4e-11	80	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=238.4, E= 1e-67, N=1) and EF-hand domains (Pfam: PF00036, score=109.0, F=8.9e-29, N=5) [Arabidopsis thaliana]
8767	GM_143_A2_A07_MR	g421955	BLASTX	369	9e-36	64	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
8768	GM_143_A2_A09_MR	g2827663	BLASTX	390	7e-35	67	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]
8769	GM_143_A2_A09_T7	g3738114	BLASTN	377	5e-10	64	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
8770	GM_143_A2_B08_MR	g507910	BLASTN	525	4e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
8771	GM_143_A2_B08_T7	g3777527	BLASTX	587	6e-55	95	(AF053008) gag-pol polyprotein [Glycine max]
8772	GM_143_A2_B09_MR	g13581	BLASTN	352	1e-09	62	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrial DNA segment.
8773	GM_143_A2_B09_T7	g1144554	BLASTN	357	6e-10	61	Anopheles merus 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8774	GM_143_A2_C05_MR	g18767	BLASTN	339	2e-22	75	Soybean Tgm6 transposable element 5' end
8775	GM_143_A2_C07_T7	g2995405	BLASTX	203	2e-23	56	(Y12432) polyprotein [Ananas comosus]
8776	GM_143_A2_C10_MR	g3777527	BLASTX	290	3e-23	44	(AF053008) gag-pol polyprotein [Glycine max]
8777	GM_143_A2_C10_T7	g990189	BLASTN	367	1e-09	75	dihydrofolate reductase-thymidylate synthase=bifunctional enzyme [Glycine max, seedling, mRNA, 1794 nt]
8778	GM_143_A2_D02_MR	g3426334	BLASTN	546	1e-17	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
8779	GM_143_A2_D04_MR	g218269	BLASTX	157	9e-11	53	(D12839) reverse transcriptase [Glycine max]
8780	GM_143_A2_D07_T7	g4049350	BLASTX	208	4e-16	51	(AL034567) putative protein [Arabidopsis thaliana]
8781	GM_143_A2_D08_MR	g343898	BLASTN	238	4e-10	70	Yeast (S. Cerevisiae) mitochondrial hypersuppressive (HS) rho-mutant, rep2 DNA.
8782	GM_143_A2_D11_MR	g3097320	BLASTN	521	1e-16	80	Glycine max gene for Bd 30K, complete cds
8783	GM_143_A2_F02_MR	g3599418	BLASTN	1055	7e-41	84	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
8784	GM_143_A2_F04_T7	g2316016	BLASTX	278	5e-22	56	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
8785	GM_143_A2_F07_MR	g99755	BLASTX	338	2e-29	58	RNA-directed DNA polymerase (F:C 2 7 7 49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
8786	GM_143_A2_F08_MR	g4063760	BLASTX	188	1e-12	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8787	GM_143_A2_F10_MR	g4063760	BLASTX	226	1e-16	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8788	GM_143_A2_F10_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8789	GM_143_A2_F09_T7	g1666236	BLASTX	156	4e-10	28	(U76261) unknown [Hordeum vulgare]
8790	GM_143_A2_F12_T7	g2244915	BLASTX	171	4e-12	37	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
8791	GM_143_A2_G02_MR	g3777527	BLASTX	696	1e-66	93	(AF053008) gag-pol polyprotein [Glycine max]
8792	GM_143_A2_G03_MR	g2522230	BLASTX	219	5e-27	44	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8793	GM_143_A2_G03_T7	g2129618	BLASTX	197	1e-13	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8794	GM_143_A2_G05_T7	g18559	BLASTN	772	6e-28	74	G-max gene for catalase
8795	GM_143_A2_G07_T7	g3287696	BLASTX	357	5e-31	65	(AC003979) Strong similarity to phosphoribosylanthranilate transferase glb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
8796	GM_143_A2_G10_T7	g3687234	BLASTX	154	6e-09	49	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
8797	GM_143_A2_H05_T7	g3763969	BLASTN	410	2e-11	64	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE ...
8798	GM_143_A2_H09_T7	g1142699	BLASTN	573	1e-19	82	Glycine max satellite STR120-A.1.
8799	GM_143_B1_C09_MR	g3097320	BLASTN	466	5e-14	67	Glycine max gene for Bd 30K, complete cds
8800	GM_143_B1_E04_MR	g3777527	BLASTX	436	4e-43	90	(AF053008) gag-pol polyprotein [Glycine max]
8801	GM_143_B1_E05_MR	g507910	BLASTN	490	1e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8802	GM_143_B1_E12_MR	g629693	BLASTX	159	3e-10	44	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8803	GM_143_B1_F04_MR	g3047119	BLASTX	252	4e-23	60	(AF058919) No definition line found [Arabidopsis thaliana]
8804	GM_143_B1_F05_MR	g3097320	BLASTN	393	9e-11	66	Glycine max gene for Bd 30K, complete cds
8805	GM_143_B1_H04_MR	g1813979	BLASTX	173	3e-15	53	(Y10860) hypothetical protein [Musa acuminata]
8806	GM_143_B1_H09_MR	g2108140	BLASTN	379	8e-11	63	Malurus cyaneus microsatellite McyU8
8807	GM_143_B2_A03_T7	g308769	BLASTN	262	6e-10	64	Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene.
8808	GM_143_B2_A04_T7	g3645899	BLASTX	322	6e-27	49	(U68408) 5' end not determined experimentally [Zea mays]
8809	GM_143_B2_A05_T7	g3128136	BLASTN	382	8e-15	75	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: KIF13, complete sequence [Arabidopsis thaliana]
8810	GM_143_B2_A06_MR	g3142328	BLASTN	709	4e-25	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8811	GM_143_B2_A08_T7	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8812	GM_143_B2_B01_MR	g2522228	BLASTX	440	1e-40	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
8813	GM_143_B2_B02_T7	g3098290	BLASTN	392	1e-11	60	Plasmodium falciparum sexual stage antigen (sl6) gene, promoter and partial cds
8814	GM_143_B2_B03_T7	g3928097	BLASTX	184	1e-13	39	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]
8815	GM_143_B2_B09_T7	g4115365	BLASTX	155	5e-09	31	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
8816	GM_143_B2_B11_MR	g4063760	BLASTX	154	8e-10	63	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8817	GM_143_B2_C07_T7	g18559	BLASTN	779	3e-28	73	G max gene for catalase
8818	GM_143_B2_C09_T7	g3645899	BLASTX	166	2e-20	46	(U68408) 5' end not determined experimentally [Zea mays]
8819	GM_143_B2_C11_MR	g4063760	BLASTX	202	4e-14	45	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8820	GM_143_B2_D01_MR	g1669680	BLASTN	451	2e-13	64	Human DNA sequence from PAC 293E14 contains ESTs, STS
8821	GM_143_B2_D01_T7	g2443320	BLASTX	301	2e-25	44	(D85597) polyprotein [Oryza australiensis]
8822	GM_143_B2_D02_MR	g1685091	BLASTX	185	5e-13	93	(U45243) diphenol oxidase [Nicotiana tabacum]
8823	GM_143_B2_D03_T7	g2462058	BLASTX	192	2e-14	43	(Y13389) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8824	GM_143_B2_D12_T7	g3645899	BLASTX	348	9e-30	58	(U68408) 5' end not determined experimentally [Zea mays]
8825	GM_143_B2_F01_T7	g99922	BLASTX	560	2e-53	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8826	GM_143_B2_F10_T7	g4063760	BLASTX	434	8e-39	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8827	GM_143_B2_F12_T7	g4063756	BLASTN	444	5e-13	75	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8828	GM_143_B2_F02_T7	g2959767	BLASTX	355	3e-30	43	(AJ002584) AtMRP4 [Arabidopsis thaliana]
8829	GM_143_B2_F04_T7	g3461840	BLASTX	284	1e-22	43	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
8830	GM_143_B2_F06_T7	g18559	BLASTN	956	3e-36	76	G max gene for catalase
8831	GM_143_B2_F07_T7	g2522230	BLASTX	102	3e-09	33	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8832	GM_143_B2_G08_T7	g343036	BLASTN	389	3e-11	74	Pea chloroplast gene encoding Gly-tRNA, 3' end, and Arg-tRNA.
8833	GM_143_B2_G11_MR	g18559	BLASTN	529	6e-17	74	G max gene for catalase
8834	GM_143_B2_G11_T7	g507910	BLASTN	518	8e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8835	GM_143_B2_H06_T7	g4063760	BLASTX	108	1e-09	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8836	GM_144_A1_A06_MR	g3645899	BLASTX	150	6e-13	47	(U68408) 5' end not determined experimentally [Zea mays]
8837	GM_144_A1_A09_T7	g3319362	BLASTX	184	3e-14	51	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
8838	GM_144_A1_A10_MR	g507910	BLASTN	344	6e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8839	GM_144_A1_A12_T7	g1946279	BLASTX	183	1e-13	43	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
8840	GM_144_A1_B03_MR	g2288887	BLASTX	147	5e-13	63	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] gi 3250736 gnt PID e1301175 (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]
8841	GM_144_A1_B04_MR	g2827514	BLASTX	184	2e-16	72	(AL021633) predicted protein [Arabidopsis thaliana]
8842	GM_144_A1_B08_T7	g3142328	BLASTN	505	7e-16	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
8843	GM_144_A1_B11_MR	g3097320	BLASTN	938	2e-35	74	Glycine max gene for Bd 30K, complete cds
8844	GM_144_A1_B12_MR	g283035	BLASTX	121	1e-14	81	chaperonin hsp60 - maize gi 22248 (Z12114) mitochondrial chaperonin-60 [Zea mays]
8845	GM_144_A1_C03_MR	g905361	BLASTX	428	3e-39	96	(U22103) gag-protease polyprotein [Glycine max]
8846	GM_144_A1_C06_MR	g2995405	BLASTX	251	2e-19	50	(Y12432) polyprotein [Ananas comosus]
8847	GM_144_A1_C08_MR	g2656032	BLASTN	431	2e-12	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZFI8
8848	GM_144_A1_D03_MR	g1769897	BLASTX	134	1e-09	35	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8849	GM_144_A1_D04_MR	g543632	BLASTX	141	7e-19	75	aldehyde reductase (EC 1.1.1.21), NADPH-dependent - bromegrass gi 167113 (L12042) aldose reductase-related protein [Bromus inermis]
8850	GM_144_A1_D06_MR	g2995405	BLASTX	460	5e-42	61	(Y12432) polyprotein [Ananas comosus]
8851	GM_144_A1_D08_T7	g4063760	BLASTX	195	3e-13	42	(AC005561) putative POI.3 protein [Arabidopsis thaliana]
8852	GM_144_A1_D11_MR	g2129618	BLASTX	172	5e-11	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8853	GM_144_A1_F09_MR	g3334667	BLASTX	430	1e-39	74	(Y10493) putative cytochrome P450 [Glycine max]
8854	GM_144_A1_F12_MR	g2995405	BLASTX	433	4e-39	67	(Y12432) polyprotein [Ananas comosus]
8855	GM_144_A1_F04_T7	g2879886	BLASTN	365	1e-09	60	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
8856	GM_144_A1_F06_MR	g3193221	BLASTN	375	6e-10	65	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8857	GM_144_A1_F08_MR	g2995405	BLASTX	324	2e-27	50	(Y12432) polyprotein [Ananas comosus]
8858	GM_144_A1_G02_MR	g2276310	BLASTN	403	4e-11	63	Human DNA sequence from PAC 332011 on chromosome 1q24- 1q25. Contains ESTs and STSs
8859	GM_144_A1_G09_T7	g3142328	BLASTN	1134	2e-44	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
8860	GM_144_A1_G11_MR	g3810595	BLASTX	162	1e-16	46	(AC005398) putative reverse transcriptase [Arabidopsis thaliana]
8861	GM_144_A1_G12_MR	g2191182	BLASTX	155	2e-09	50	(AF007271) similar to N. tabacum membrane-associated salt- inducible protein (PID:g473874) [Arabidopsis thaliana]
8862	GM_144_A1_H12_MR	g2827699	BLASTX	182	5e-12	72	(AI-021684) predicted protein [Arabidopsis thaliana]
8863	GM_144_A2_A10_MR	g2738248	BLASTX	268	7e-26	96	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]
8864	GM_144_A2_B08_MR	g3777527	BLASTX	684	3e-65	98	(AF053008) gag-pol polyprotein [Glycine max]
8865	GM_144_A2_C10_MR	g1813979	BLASTX	335	1e-29	55	(Y10860) hypothetical protein [Musa acuminata]
8866	GM_144_A2_C12_MR	g3142328	BLASTN	1609	6e-73	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
8867	GM_144_A2_D09_MR	g507910	BLASTN	378	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8868	GM_144_A2_E07_MR	g2443320	BLASTX	295	6e-24	45	(D85597) polyprotein [Oryza australiensis]
8869	GM_144_A2_F01_MR	g2995405	BLASTX	489	4e-45	62	(Y12432) polyprotein [Ananas comosus]
8870	GM_144_A2_F03_MR	g4063756	BLASTN	393	1e-10	72	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8871	GM_144_A2_F09_MR	g2275215	BLASTX	215	7e-17	65	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8872	GM_144_A2_F10_MR	g421954	BLASTX	329	4e-28	44	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
8873	GM_144_A2_G08_MR	g3171159	BLASTN	599	5e-20	65	Homo sapiens chromosome 21q22.3 PAC 21H.13, complete sequence [Homo sapiens]
8874	GM_144_A2_G10_MR	g3097320	BLASTN	1208	1e-47	81	Glycine max gene for Bd 30K, complete cds
8875	GM_144_A2_H03_MR	g4049345	BLASTX	248	1e-31	54	(AL034567) putative protein [Arabidopsis thaliana]
8876	GM_144_A2_H08_MR	g3777527	BLASTX	694	2e-66	98	(AF053008) gag-pol polypeptide [Glycine max]
8877	GM_144_A2_H09_MR	g2924730	BLASTN	371	1e-09	77	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MP17, complete sequence [Arabidopsis thaliana]
8878	GM_144_A2_H10_MR	g3426062	BLASTX	225	2e-17	39	(AJ007587) monooxygenase [Arabidopsis thaliana]
8879	GM_144_B1_A02_T7	g100484	BLASTX	184	2e-12	39	hypothetical protein - garden snapdragon
8880	GM_144_B1_A03_T7	g421955	BLASTX	166	1e-19	61	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
8881	GM_144_B1_A04_T7	g2792208	BLASTX	286	2e-24	39	(AF032682) NBS-LRR type resistance protein [Hordeum vulgare]
8882	GM_144_B1_A05_MR	g2244915	BLASTX	250	2e-19	49	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
8883	GM_144_B1_A09_MR	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8884	GM_144_B1_A09_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8885	GM_144_B1_B03_T7	g296873	BLASTN	358	3e-09	61	W.mrakii mitochondrial DNA
8886	GM_144_B1_B04_T7	g3426334	BLASTN	570	8e-19	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds (U68408) 5' end not determined experimentally [Zea mays]
8887	GM_144_B1_B08_T7	g3645899	BLASTX	153	6e-09	38	, complete sequence [Homo sapiens]
8888	GM_144_B1_B09_T7	g3928116	BLASTN	361	3e-09	59	G.max gene for catalase
8889	GM_144_B1_B10_MR	g18559	BLASTN	642	4e-22	68	gag protein - maize gi 507845 (U11059) gag gene product [Zea mays]
8890	GM_144_B1_B12_T7	g1363528	BLASTX	146	6e-09	27	
8891	GM_144_B1_C03_T7	g4063760	BLASTX	229	6e-17	45	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8892	GM_144_B1_C07_MR	g2462134	BLASTX	163	2e-10	49	(Y13368) reverse transcriptase [Beta vulgaris]
8893	GM_144_B1_C08_MR	g4160362	BLASTN	346	2e-09	60	Saccharomyces cerevisiae complete mitochondrial genome
8894	GM_144_B1_C08_T7	g100484	BLASTX	470	2e-43	52	hypothetical protein - garden snapdragon
8895	GM_144_B1_C12_T7	g507910	BLASTN	582	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8896	GM_144_B1_D06_T7	g2864621	BLASTX	150	2e-18	52	hypothetical protein [Arabidopsis thaliana]
8897	GM_144_B1_F02_T7	g2801681	BLASTN	1016	1e-39	83	Glycine max telomere-associated sequence STAS10
8898	GM_144_B1_F12_T7	g507910	BLASTN	522	6e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8899	GM_144_B1_F03_T7	g507910	BLASTN	520	7e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8900	GM_144_B1_F05_T7	g3810596	BLASTX	238	5e-18	31	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8901	GM_144_B1_F09_MR	g3142328	BLASTN	636	8e-22	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
8902	GM_144_B1_G02_T7	g4063760	BLASTX	202	2e-26	59	Glycine max gene for Bd 30K, complete cds
8903	GM_144_B1_G03_T7	g3097320	BLASTN	1005	2e-38	73	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
8904	GM_144_B1_G05_T7	g2583130	BLASTX	216	2e-15	36	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranyltransferase component A 1, Choroideraemia protein, T...
8905	GM_144_B1_G07_T7	g3059060	BLASTN	358	4e-09	58	(AJ004901) resistance protein [Glycine max]
8906	GM_144_B1_G10_MR	g3452140	BLASTX	124	1e-09	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8907	GM_144_B1_H03_T7	g4063760	BLASTX	238	6e-18	49	Glycine max gene for Bd 30K, complete cds
8908	GM_144_B2_A05_MR	g3097320	BLASTN	480	1e-14	68	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8909	GM_144_B2_A06_MR	g3142328	BLASTN	380	3e-10	71	putative protein [Arabidopsis thaliana]
8910	GM_144_B2_A09_MR	g3367570	BLASTX	131	3e-14	86	(AC002329) putative Mlo-like protein [Arabidopsis thaliana]
8911	GM_144_B2_A09_T7	g2262178	BLASTX	185	9e-13	56	Glycine max BSR-101 satellite SB92 genomic sequence.
8912	GM_144_B2_B04_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
8913	GM_144_B2_B04_T7	g507910	BLASTN	543	6e-18	78	(AC004473) Contains similarity to 21 KD subunit of the Arp2/3 protein complex (ARC21) gb AF006086 from Homo sapiens. EST
8914	GM_144_B2_B05_T7	g3249086	BLASTX	194	1e-14	70	gb Z37222 comes [Arabidopsis thaliana]
8915	GM_144_B2_B10_T7	g4038056	BLASTX	325	2e-27	56	(AC005897) putative transposon [Arabidopsis thaliana]
8916	GM_144_B2_C03_MR	g2129618	BLASTX	215	1e-15	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8917	GM_144_B2_C03_T7	g905361	BLASTX	654	2e-63	95	(U22103) gag-protease polyprotein [Glycine max]
8918	GM_144_B2_C06_T7	g18563	BLASTN	362	2e-09	73	G max intergenic region DNA (between Gmachs1 and Gmachs3)
8919	GM_144_B2_C10_T7	g1142699	BLASTN	287	6e-15	68	Glycine max satellite STR120-A 1
8920	GM_144_B2_C12_MR	g1142701	BLASTN	263	1e-19	76	Glycine max satellite STR120-A.3.
8921	GM_144_B2_D04_MR	g2245104	BLASTX	327	3e-27	44	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
8922	GM_144_B2_D04_T7	g130582	BLASTX	363	3e-31	47	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
							(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
8923	GM_144_B2_D05_T7	g2522228	BLASTX	285	2e-31	55	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
8924	GM_144_B2_D07_MR	g507910	BLASTN	695	8e-25	86	Glycine max BSR-101 satellite SB92 genomic sequence.
8925	GM_144_B2_F03_MR	g99922	BLASTX	182	6e-13	55	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:150225 [Glycine max]
8926	GM_144_B2_F04_T7	g3645899	BLASTX	197	1e-13	36	(U68408) 5' end not determined experimentally [Zea mays]
8927	GM_144_B2_F05_T7	g3650039	BLASTX	288	1e-23	45	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
8928	GM_144_B2_F07_MR	g2522227	BLASTX	208	3e-16	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8929	GM_144_B2_F08_T7	g2262177	BLASTX	121	8e-17	50	(AC002329) hypothetical protein similar to T18A10.3 [Arabidopsis thaliana]
8930	GM_144_B2_F10_MR	g3142328	BLASTN	1094	1e-42	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
8931	GM_144_B2_F10_T7	g905361	BLASTX	648	9e-63	92	(U22103) gag-protease polyprotein [Glycine max]
8932	GM_144_B2_F04_MR	g3142303	BLASTX	195	6e-16	45	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana]
8933	GM_144_B2_F04_T7	g20854	BLASTN	386	1e-10	67	Pea rbcS-3A gene for ribulose 1,5-bisphosphate carboxylase (RBC) small subunit
8934	GM_144_B2_F07_MR	g3461839	BLASTX	142	4e-14	52	(AC005315) putative receptor protein kinase [Arabidopsis thaliana]
8935	GM_144_B2_F08_MR	g4063760	BLASTX	585	5e-55	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8936	GM_144_B2_F08_T7	g125889	BLASTX	156	8e-10	36	PROBABLE PECTATE LYASE P59 PRECURSOR gi 280400 pir S27098 pectate lyase (EC 4.2.2.2) LAT59 - tomato gi 19271 (X15499) P59 protein [Lycopersicon esculentum]
8937	GM_144_B2_F09_T7	g178823	BLASTN	337	4e-09	62	Human apolipoprotein B gene hypervariable region, 3' flank.
8938	GM_144_B2_G03_MR	g507910	BLASTN	362	9e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8939	GM_144_B2_G03_T7	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8940	GM_144_B2_G04_T7	g3142328	BLASTN	700	1e-24	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope- like genes, partial cds, and long terminal repeat, complete sequence
8941	GM_144_B2_G06_MR	g3097320	BLASTN	444	5e-13	68	Glycine max gene for Bd 30K, complete cds
8942	GM_144_B2_G07_MR	g507910	BLASTN	666	2e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
8943	GM_144_B2_G10_T7	g1717949	BLASTX	404	7e-37	86	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1 PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1) gi 100375 pir B41607 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - common tobacco (fragment) gi 170322 (M77225) Rieske Fe-S protein [Nicotiana tabacum]
8944	GM_144_B2_H02_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8945	GM_144_B2_H05_MR	g4056496	BLASTX	181	1e-12	62	(AC005896) unknown protein [Arabidopsis thaliana]
8946	GM_144_B2_H07_MR	g2995405	BLASTX	237	5e-18	45	(Y12432) polyprotein [Ananas comosus]
8947	GM_144_B2_H08_T7	g3702323	BLASTX	358	8e-32	76	(AC005397) unknown protein [Arabidopsis thaliana]
8948	GM_144_B2_H10_MR	g18559	BLASTN	378	4e-10	65	G.max gene for catalase
8949	GM_144_B2_H12_T7	g4063760	BLASTX	250	3e-19	68	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8950	GM_145_A1_A09_MR	g3097320	BLASTN	653	1e-22	75	Glycine max gene for Bd 30K, complete cds
8951	GM_145_A1_A10_T7	g3550435	BLASTN	553	6e-18	64	Hordeum vulgare Hov1 gene
8952	GM_145_A1_A11_T7	g4063760	BLASTX	175	7e-13	63	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8953	GM_145_A1_B01_T7	g1172495	BLASTX	582	8e-55	93	PHYTOCHROME: A gi 515749 (L34842) phytochrome A [Glycine max] gi 515751 (L34844) phytochrome A [Glycine max]
8954	GM_145_A1_B02_T7	g4063760	BLASTX	437	4e-39	65	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8955	GM_145_A1_B03_MR	g3142328	BLASTN	2065	4e-87	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8956	GM_145_A1_B03_T7	g4063760	BLASTX	298	2e-24	48	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8957	GM_145_A1_B05_MR	g3097320	BLASTN	426	3e-12	73	Glycine max gene for Bd 30K, complete cds
8958	GM_145_A1_B05_T7	g3142328	BLASTN	837	6e-31	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8959	GM_145_A1_B06_MR	g3046854	BLASTN	654	2e-22	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]
8960	GM_145_A1_B06_T7	g1769897	BLASTX	224	5e-17	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8961	GM_145_A1_B09_MR	g181904	BLASTN	483	7e-16	63	Homo sapiens DZY2 satellite sequence HinfA fragment.
8962	GM_145_A1_B11_MR	g3779030	BLASTX	160	4e-11	34	(AC005171) putative gag-protease polypeptide [Arabidopsis thaliana]
8963	GM_145_A1_B12_T7	g3097320	BLASTN	972	5e-37	81	Glycine max gene for Bd 30K, complete cds
8964	GM_145_A1_C01_MR	g2522230	BLASTX	176	9e-13	35	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8965	GM_145_A1_C03_MR	g2522228	BLASTX	248	3e-28	50	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
8966	GM_145_A1_C04_MR	g114268	BLASTX	269	5e-40	65	L-ASCORBATE OXIDASE HOMOLOG PRECURSOR (ASCORBATE) gi 541907 pir S23763 gene Bp10 protein - rape gi 17789 (X64257) protein homologous to ascorbate oxidase [Brassica napus]
8967	GM_145_A1_C06_MR	g4063760	BLASTX	148	3e-13	49	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8968	GM_145_A1_C08_T7	g100484	BLASTX	302	4e-25	49	hypothetical protein - garden snapdragon
8969	GM_145_A1_C10_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8970	GM_145_A1_C10_T7	g4063760	BLASTX	484	3e-44	63	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8971	GM_145_A1_D07_T7	g3786007	BLASTX	159	6e-10	38	(AC005499) hypothetical protein [Arabidopsis thaliana]
8972	GM_145_A1_D08_T7	g3426334	BLASTN	453	2e-13	63	Pisum sativum pectin methylesterase (repmel) gene, complete cds
8973	GM_145_A1_D11_T7	g3777527	BLASTX	285	9e-23	73	(AF053008) gag-pol polyprotein [Glycine max]
8974	GM_145_A1_E02_MR	g2443320	BLASTX	296	5e-24	39	(D85597) polyprotein [Oryza australiensis]
8975	GM_145_A1_E10_MR	g4063760	BLASTX	581	1e-54	73	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
8976	GM_145_A1_E10_T7	g3930515	BLASTX	122	2e-12	38	(AF059674) putative gag protein [Nicotiana tabacum]
8977	GM_145_A1_E11_MR	g3097320	BLASTN	739	2e-26	78	Glycine max gene for Bd 30K, complete cds
8978	GM_145_A1_F01_T7	g19642	BLASTN	380	4e-10	69	Medicago sativa nodulin-25 gene
8979	GM_145_A1_F02_MR	g522302	BLASTX	206	1e-14	34	(L35053) endonuclease [Magnaporthe grisea]
8980	GM_145_A1_F05_MR	g3421413	BLASTX	195	7e-14	81	(AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] gi 3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
8981	GM_145_A1_F06_T7	g3142379	BLASTX	310	5e-27	65	(AF053008) envelope-like [Glycine max]
8982	GM_145_A1_F07_T7	g1707642	BLASTX	205	1e-14	33	(Y07748) TMK [Oryza sativa]
8983	GM_145_A1_F09_T7	g3820757	BLASTN	545	5e-18	67	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
8984	GM_145_A1_F10_MR	g421955	BLASTX	206	2e-15	42	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
8985	GM_145_A1_F11_T7	g3859610	BLASTN	414	1e-11	65	Arabidopsis thaliana BAC T9E19
8986	GM_145_A1_F12_MR	g322663	BLASTX	223	9e-18	68	S-receptor kinase-related protein - Chinese kale gi 17917 (Z18884)
8987	GM_145_A1_G01_MR	g507910	BLASTN	420	2e-12	75	S-receptor kinase related protein [Brassica oleracea]
8988	GM_145_A1_G01_T7	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8989	GM_145_A1_G02_MR	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
8990	GM_145_A1_G03_T7	g3777527	BLASTX	226	1e-20	57	(AF053008) gag-pol polyprotein [Glycine max]
8991	GM_145_A1_G08_T7	g3176711	BLASTX	256	5e-20	51	(AC002392) bZIP-like protein [Arabidopsis thaliana]
8992	GM_145_A1_G10_MR	g1663551	BLASTX	367	5e-33	66	(U55810) disease resistance protein homolog [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
8993	GM_145_A1_G10_T7	g1314277	BLASTX	154	3e-09	55	(U34919) white homolog [Homo sapiens]
8994	GM_145_A1_H01_T7	g2443320	BLASTX	433	1e-38	58	(D85597) polyprotein [Oryza australiensis]
8995	GM_145_A1_H02_MR	g1084606	BLASTX	157	5e-11	35	TyB protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty3-2
8996	GM_145_A1_H04_MR	g2244915	BLASTX	261	1e-20	41	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
8997	GM_145_A1_H05_T7	g18559	BLASTN	1307	3e-52	90	G max gene for catalase
8998	GM_145_A1_H08_MR	g4063760	BLASTX	443	8e-40	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8999	GM_145_A1_H10_MR	g507910	BLASTN	505	3e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9000	GM_145_A1_H10_T7	g507910	BLASTN	415	4e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
9001	GM_145_A2_A08_T7	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9002	GM_145_A2_A09_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9003	GM_145_A2_A10_T7	g3080448	BLASTX	217	4e-16	64	(AL022605) putative protein [Arabidopsis thaliana]
9004	GM_145_A2_B02_MR	g3116020	BLASTX	329	5e-29	80	(Y15383) FtsZ protein [Pisum sativum]
9005	GM_145_A2_B03_MR	g3097320	BLASTN	365	2e-09	73	Glycine max gene for Bd 30K, complete cds
9006	GM_145_A2_B03_T7	g3142328	BLASTN	984	1e-37	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB007466) reverse transcriptase-like protein [Vicia faba]
9007	GM_145_A2_B05_MR	g2522228	BLASTX	161	2e-10	78	G max gene for catalase
9008	GM_145_A2_B08_MR	g18559	BLASTN	874	1e-32	74	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
9009	GM_145_A2_B09_MR	g3513747	BLASTX	310	2e-25	51	Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence
9010	GM_145_A2_B12_MR	g3845264	BLASTN	366	2e-09	63	hypothetical protein [Lycopersicon esculentum]
9011	GM_145_A2_C05_T7	g2995279	BLASTX	141	3e-12	46	(U76261) unknown [Hordeum vulgare]
9012	GM_145_A2_C09_MR	g1666236	BLASTX	229	2e-18	35	(Z11985) 70-Kd heat shock protein [Solanum tuberosum]
9013	GM_145_A2_C09_T7	g21479	BLASTX	226	4e-18	81	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
9014	GM_145_A2_C11_T7	g3650039	BLASTX	248	2e-19	43	Soybean nodulin 22 gene
9015	GM_145_A2_D01_T7	g18695	BLASTN	353	5e-09	62	Glycine max gene for Bd 30K, complete cds
9016	GM_145_A2_D02_MR	g3097320	BLASTN	352	7e-09	73	(D85597) polyprotein [Oryza australiensis]
9017	GM_145_A2_D02_T7	g2443320	BLASTX	215	2e-15	35	hypothetical protein [Arabidopsis thaliana]
9018	GM_145_A2_D03_MR	g2864621	BLASTX	185	6e-13	41	Pea chloroplast photosystem II gene encoding the D2 and 44kd chlorophyll a-binding proteins, complete cds.
9019	GM_145_A2_D07_T7	g343022	BLASTN	454	1e-13	85	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9020	GM_145_A2_D09_MR	g3142328	BLASTN	1033	7e-40	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
9021	GM_145_A2_D10_MR	g4063760	BLASTX	355	2e-30	62	(AF059674) putative gag protein [Nicotiana tabacum]
9022	GM_145_A2_D10_T7	g3930515	BLASTX	122	1e-11	38	Glycine max BSR-101 satellite SB92 genomic sequence.
9023	GM_145_A2_D12_MR	g507910	BLASTN	421	2e-12	72	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
9024	GM_145_A2_F03_MR	g422418	BLASTX	207	1e-14	37	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]
9025	GM_145_A2_F05_T7	g2947063	BLASTX	165	2e-10	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9026	GM_145_A2_F09_MR	g3810596	BLASTX	192	4e-13	52	COP9 PROTEIN (FUSCA PROTEIN FUS7) gi 625971 pir A54842
9027	GM_145_A2_F12_T7	g1169013	BLASTX	148	8e-10	81	COP9 protein - Arabidopsis thaliana gi 530870 (L32874) COP9 [Arabidopsis thaliana] gi 2244767 gnt PID e326869 (Z97335) COP9 protein [Arabidopsis thaliana]
9028	GM_145_A2_F01_MR	g2764526	BLASTN	541	2e-17	66	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
9029	GM_145_A2_F02_T7	g3142328	BLASTN	1151	3e-45	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9030	GM_145_A2_F07_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9031	GM_145_A2_F07_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9032	GM_145_A2_F09_MR	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9033	GM_145_A2_F09_T7	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9034	GM_145_A2_F10_MR	g421955	BLASTX	194	4e-14	44	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
9035	GM_145_A2_F12_MR	g18559	BLASTN	1616	2e-69	90	G.max gene for catalase
9036	GM_145_A2_F12_T7	g1769897	BLASTX	343	1e-31	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9037	GM_145_A2_G05_T7	g3319682	BLASTX	156	2e-09	64	(Y17720) SPINDLY protein [Petunia x hybrida]
9038	GM_145_A2_G09_T7	g421955	BLASTX	216	9e-20	50	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
9039	GM_145_A2_G11_MR	g3777527	BLASTX	204	1e-19	39	(AF053008) gag-pol polyprotein [Glycine max]
9040	GM_145_A2_H01_MR	g4063760	BLASTX	272	1e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9041	GM_145_A2_H02_T7	g18768	BLASTN	557	8e-19	73	Soybean Tgm6 transposable element 3' end
9042	GM_145_A2_H03_T7	g3142379	BLASTX	311	4e-27	68	(AF053008) envelope-like [Glycine max]
9043	GM_145_A2_H05_T7	g3777527	BLASTX	215	2e-15	36	(AF053008) gag-pol polyprotein [Glycine max]
9044	GM_145_A2_H07_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9045	GM_145_A2_H07_T7	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
9046	GM_145_A2_H09_MR	g294042	BLASTN	416	9e-12	63	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
9047	GM_145_B1_A04_T7	g2911075	BLASTX	184	5e-14	76	(AL021960) putative protein [Arabidopsis thaliana]
9048	GM_145_B1_B03_T7	g3142328	BLASTN	1067	2e-41	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9049	GM_145_B1_D02_T7	g507910	BLASTN	456	5e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9050	GM_145_B1_D04_T7	g505129	BLASTN	323	1e-10	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9051	GM_145_B1_E02_T7	g507910	BLASTN	358	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9052	GM_145_B1_E05_T7	g3924609	BLASTX	189	1e-12	39	(AF069442) putative polypeptide of LTR transposon [Arabidopsis thaliana]
9053	GM_145_B1_F06_T7	g2970554	BLASTN	407	2e-11	69	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
9054	GM_145_B2_A03_MR	g507910	BLASTN	526	4e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9055	GM_145_B2_A03_T7	g507910	BLASTN	588	6e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9056	GM_145_B2_A04_MR	g507910	BLASTN	679	4e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
9057	GM_145_B2_A04_T7	g507910	BLASTN	558	1e-18	85	Glycine max BSR-101 satellite SB92 genomic sequence.
9058	GM_145_B2_A05_MR	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
9059	GM_145_B2_A05_T7	g4063756	BLASTN	359	3e-09	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9060	GM_145_B2_A06_MR	g4115365	BLASTX	293	1e-23	44	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
9061	GM_145_B2_A07_T7	g2522226	BLASTN	829	1e-30	68	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
9062	GM_145_B2_A08_T7	g505129	BLASTN	315	8e-10	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9063	GM_145_B2_A09_T7	g4115365	BLASTX	253	2e-19	41	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
9064	GM_145_B2_A12_T7	g2129618	BLASTX	239	3e-18	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9065	GM_145_B2_B04_T7	g1204057	BLASTN	442	6e-13	61	Caenorhabditis elegans cosmid C04B4, complete sequence [Caenorhabditis elegans]
9066	GM_145_B2_B05_MR	g559261	BLASTN	291	1e-09	66	Saccharomyces cerevisiae mitochondrion 21S R2 ribosomal RNA, 3' end.
9067	GM_145_B2_B09_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9068	GM_145_B2_B11_MR	g2522228	BLASTX	247	5e-20	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
9069	GM_145_B2_B12_MR	g3599418	BLASTN	370	1e-09	67	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9070	GM_145_B2_B12_T7	g3097320	BLASTN	786	2e-28	74	Glycine max gene for Bd 30K, complete cds
9071	GM_145_B2_C03_MR	g4038056	BLASTX	337	1e-28	54	(AC005897) putative transposon [Arabidopsis thaliana]
9072	GM_145_B2_C03_T7	g4098966	BLASTN	344	6e-09	70	Glycine max putative resistance gene analog genomic sequence
9073	GM_145_B2_C04_T7	g3600044	BLASTX	116	4e-21	48	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
9074	GM_145_B2_C06_T7	g2738248	BLASTX	420	7e-38	81	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]
9075	GM_145_B2_C07_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
9076	GM_145_B2_C09_T7	g18559	BLASTN	604	2e-20	71	G.max gene for catalase
9077	GM_145_B2_C11_T7	g505129	BLASTN	356	2e-11	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9078	GM_145_B2_D02_MR	g2494132	BLASTX	415	4e-38	64	(AC002376) Contains similarity to human dimethylalanine monoxygenase (gb M64082). [Arabidopsis thaliana]
9079	GM_145_B2_D06_T7	g18559	BLASTN	949	5e-36	77	G.max gene for catalase
9080	GM_145_B2_D08_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
9081	GM_145_B2_D09_T7	g4038056	BLASTX	367	6e-32	49	(AC005897) putative transposon [Arabidopsis thaliana]
9082	GM_145_B2_F04_MR	g2462134	BLASTX	299	2e-25	40	(Y13368) reverse transcriptase [Beta vulgaris]
9083	GM_145_B2_F04_T7	g2129618	BLASTX	182	4e-12	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9084	GM_145_B2_F05_T7	g4063760	BLASTX	207	1e-14	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9085	GM_145_B2_F09_MR	g2462134	BLASTX	192	7e-18	36	(Y13368) reverse transcriptase [Beta vulgaris]
9086	GM_145_B2_F01_MR	g3097320	BLASTN	1063	4e-41	77	Glycine max gene for Bd 30K, complete cds
9087	GM_145_B2_F03_MR	g3746069	BLASTX	182	6e-14	39	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
9088	GM_145_B2_F06_MR	g507910	BLASTN	384	9e-11	77	Glycine max BSR-101 satellite SB92 genomic sequence.
9089	GM_145_B2_F06_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence
9090	GM_145_B2_F08_T7	g3123745	BLASTX	203	4e-31	92	(AB013447) aluminum-induced [Brassica napus]
9091	GM_145_B2_F09_T7	g3097320	BLASTN	487	5e-15	73	Glycine max gene for Bd 30K, complete cds
9092	GM_145_B2_G02_T7	g18559	BLASTN	1136	2e-44	75	G.max gene for catalase
9093	GM_145_B2_G05_T7	g1840106	BLASTN	375	2e-10	61	Human fragile site locus (FRA16B) minisatellite repeat
9094	GM_145_B2_G06_MR	g99922	BLASTX	263	4e-26	53	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA): pid:e150225 [Glycine max]
9095	GM_145_B2_G08_T7	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence
9096	GM_145_B2_G11_MR	g3142328	BLASTN	1104	4e-43	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9097	GM_145_B2_H04_MR	g3894211	BLASTN	456	1e-13	62	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9098	GM_145_B2_H06_MR	g507910	BLASTN	481	4e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9099	GM_145_B2_H07_T7	g3142328	BLASTN	1008	1e-38	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (L46702) kinesin heavy chain-like protein [Solanum tuberosum] (AC005561) putative POL3 protein [Arabidopsis thaliana]
9100	GM_145_B2_H11_MR	g1369852	BLASTX	324	5e-27	81	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9101	GM_145_B2_H12_MR	g4063760	BLASTX	252	2e-19	46	(AC005561) putative reverse transcriptase [Arabidopsis thaliana]
9102	GM_146_A1_A01_MR	g2129618	BLASTX	190	6e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9103	GM_146_A1_A02_MR	g3779021	BLASTX	397	9e-35	53	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9104	GM_146_A1_A08_MR	g2129618	BLASTX	187	1e-12	36	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9105	GM_146_A1_A09_MR	g3599418	BLASTN	673	2e-23	73	Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete sequence [Homo sapiens]
9106	GM_146_A1_A09_T7	g3935200	BLASTN	386	2e-10	65	retrotransposon del1-46 [Lilium henryi]
9107	GM_146_A1_B06_MR	g226407	BLASTX	158	3e-09	42	Zerene cesonia large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
9108	GM_146_A1_B08_T7	g2895633	BLASTN	462	3e-14	63	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9109	GM_146_A1_B11_T7	g2129618	BLASTX	213	2e-15	41	G.max gene for catalase
9110	GM_146_A1_C01_T7	g18559	BLASTN	839	5e-31	78	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9111	GM_146_A1_C03_MR	g2522230	BLASTX	241	5e-22	40	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9112	GM_146_A1_C06_MR	g3599418	BLASTN	351	7e-09	65	DNA Mismatch REPAIR PROTEIN MSH2 >gi 2522362 (AF002706) MutS homolog 2 [Arabidopsis thaliana] >gi 2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana] >gi 2547236 (AF026549) DNA mismatch repair protein MSH2 [Arabidopsis thaliana]
9113	GM_146_A1_C09_MR	g3914056	BLASTX	140	2e-12	82	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit 1 (COXI) gene, complete cds
9114	GM_146_A1_C10_T7	g294042	BLASTN	372	8e-10	64	G max gene for catalase
9115	GM_146_A1_C11_MR	g18559	BLASTN	781	2e-28	78	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9116	GM_146_A1_D02_MR	g3142295	BLASTX	417	4e-37	56	(AC002411) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from <i>Pisum sativum</i> . [Arabidopsis thaliana] (AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
9117	GM_146_A1_D03_MR	g3319351	BLASTX	215	3e-25	51	(AF069298) contains similarity to a protein kinase domain (PFam: pkinase.hmm, score: 165.48), to legume lectins beta domain (PFam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (PFam: lectin_legA.hmm, score: 16.72) [Arabidopsis thaliana]
9118	GM_146_A1_D04_T7	g3193290	BLASTX	383	5e-34	56	activator-like transposable element [Pennisetum glaucum]
9119	GM_146_A1_D06_T7	g1091678	BLASTX	186	1e-12	36	Homo sapiens BAC clone GS180J15 from 7q31, complete sequence [Homo sapiens]
9120	GM_146_A1_D07_T7	g3894208	BLASTN	365	2e-09	61	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9121	GM_146_A1_D08_MR	g4063760	BLASTX	465	4e-42	61	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9122	GM_146_A1_D08_T7	g4063760	BLASTX	408	5e-36	70	(AF053008) gag-pol polyprotein [Glycine max]
9123	GM_146_A1_D11_MR	g3777527	BLASTX	673	4e-64	95	(D26578) DNA-binding protein [Daucus carota]
9124	GM_146_A1_E01_T7	g1435023	BLASTX	280	4e-28	77	(Y12432) polyprotein [Ananas comosus]
9125	GM_146_A1_E07_T7	g2995405	BLASTX	367	6e-35	64	(Y12432) polyprotein [Ananas comosus]
9126	GM_146_A1_E10_MR	g2995405	BLASTX	214	1e-39	56	(AF053008) gag-pol polyprotein [Glycine max]
9127	GM_146_A1_E11_T7	g3777527	BLASTX	207	4e-15	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9128	GM_146_A1_F01_MR	g3810596	BLASTX	282	9e-23	41	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9129	GM_146_A1_F01_T7	g4063760	BLASTX	210	6e-15	45	(AF053008) gag-pol polyprotein [Glycine max]
9130	GM_146_A1_F06_T7	g3777527	BLASTX	773	7e-75	96	Glycine max BSR-101 satellite SB92 genomic sequence.
9131	GM_146_A1_F07_MR	g507910	BLASTN	373	3e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9132	GM_146_A1_F07_T7	g507910	BLASTN	373	3e-10	70	(U22103) gag-protease polyprotein [Glycine max]
9133	GM_146_A1_F08_MR	g905361	BLASTX	226	5e-17	41	G.max gene for catalase
9134	GM_146_A1_F11_MR	g18559	BLASTN	676	1e-23	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9135	GM_146_A1_G02_T7	g507910	BLASTN	599	2e-20	82	Glycine max cdc2 protein kinase (cdc2(1)) nonprocessed pseudogene
9136	GM_146_A1_G05_MR	g1480927	BLASTN	843	2e-31	92	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9137	GM_146_A1_G05_T7	g2129618	BLASTX	206	1e-14	48	Glycine max partial SIRE-1 sequence ribonuclease II and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9138	GM_146_A1_G07_T7	g3142328	BLASTN	1117	1e-43	93	Saccharomyces cerevisiae mitochondrial Tyr-tRNA, Asn-tRNA and Met-tRNA genes
9139	GM_146_A1_G09_MR	g2924341	BLASTN	356	3e-09	64	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9140	GM_146_A1_G09_T7	g927574	BLASTN	377	3e-10	74	Glycine max williams alpha galactosidase mRNA, complete cds. >gi 2086979 gb 136466 136466 Sequence 8 from patent US 5606042
9141	GM_146_A1_G11_MR	g2264320	BLASTN	563	2e-18	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
9142	GM_146_A1_G12_MR	g3319345	BLASTX	233	1e-17	43	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
9143	GM_146_A1_G12_T7	g3142328	BLASTN	993	5e-38	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
9144	GM_146_A1_H05_MR	g4063760	BLASTX	261	2e-20	55	G.max gene for catalase
9145	GM_146_A1_H08_T7	g18559	BLASTN	997	3e-38	74	(U76261) unknown [Hordeum vulgare]
9146	GM_146_A2_A01_MR	g1666236	BLASTX	207	7e-16	31	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXF12, complete sequence [Arabidopsis thaliana]
9147	GM_146_A2_A03_T7	g3449333	BLASTN	388	2e-10	68	Glycine max BSR-101 satellite SB92 genomic sequence.
9148	GM_146_A2_A07_T7	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
9149	GM_146_A2_A08_MR	g507910	BLASTN	392	4e-11	75	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
9150	GM_146_A2_A11_MR	g170606	BLASTN	752	2e-27	67	(U76261) unknown [Hordeum vulgare]
9151	GM_146_A2_A11_T7	g1666236	BLASTX	181	7e-13	31	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
9152	GM_146_A2_B03_MR	g2708743	BLASTX	116	6e-15	41	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005169) putative copia-like transposable element [Arabidopsis thaliana]
9153	GM_146_A2_B12_MR	g3142328	BLASTN	818	4e-30	81	(U95973) BRC A1-associated RING domain protein isolog [Arabidopsis thaliana]
9154	GM_146_A2_C03_T7	g3687234	BLASTX	186	2e-14	43	Soybean nodulin-24 gene 5' end
9155	GM_146_A2_C04_MR	g1931654	BLASTX	266	1e-21	45	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
9156	GM_146_A2_C06_MR	g18702	BLASTN	347	2e-09	60	(Z35162) beta-fructofuranosidase; cell wall invertase 1; fructosidase [Vicia faba]
9157	GM_146_A2_C10_MR	g2316016	BLASTX	286	6e-23	60	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE
9158	GM_146_A2_C11_MR	g861155	BLASTX	203	1e-14	83	PRECURSOR (AIR CARBOXYLASE) (AIRC) gi 629656 pir
9159	GM_146_A2_D05_MR	g1709930	BLASTX	171	3e-11	94	S43322 phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) - moth bean gi 349159 (L22584) 5-aminoimidazole ribonucleotide carboxylase [Vigna aconitifolia]
9160	GM_146_A2_D08_MR	g4006831	BLASTX	267	6e-23	42	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9161	GM_146_A2_D09_MR	g507910	BLASTN	359	1e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
9162	GM_146_A2_E02_MR	g18695	BLASTN	487	3e-15	83	Soybean nodulin 22 gene
9163	GM_146_A2_E03_T7	g100484	BLASTX	374	6e-33	61	hypothetical protein - garden snapdragon
9164	GM_146_A2_E08_T7	g100484	BLASTX	187	6e-14	47	hypothetical protein - garden snapdragon
9165	GM_146_A2_E10_MR	g3746069	BLASTX	156	2e-22	50	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
9166	GM_146_A2_E11_T7	g509768	BLASTN	417	6e-12	67	Glycine max seed-specific low molecular weight sulfur-rich protein.
9167	GM_146_A2_E12_T7	g2497538	BLASTX	147	9e-09	55	PYRUVATE KINASE, CYTOSOLIC ISOZYME gi 466350 (L08632) pyruvate kinase [Glycine max]
9168	GM_146_A2_F04_MR	g2815075	BLASTN	390	1e-10	60	Caenorhabditis elegans cosmid Y38H8A, complete sequence [Caenorhabditis elegans]
9169	GM_146_A2_F05_T7	g4063756	BLASTN	514	4e-16	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9170	GM_146_A2_F08_MR	g3319362	BLASTX	210	7e-30	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
9171	GM_146_A2_F11_MR	g170606	BLASTN	787	4e-29	68	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
9172	GM_146_A2_F12_T7	g3810596	BLASTX	152	7e-09	62	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9173	GM_146_A2_G08_MR	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
9174	GM_146_A2_G10_MR	g4159709	BLASTN	593	9e-20	67	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence [Arabidopsis thaliana]
9175	GM_146_A2_H04_T7	g4063770	BLASTX	167	1e-10	49	(AB004906) transposase [Ipomoea purpurea]
9176	GM_146_A2_H06_T7	g3142379	BLASTX	319	6e-28	82	(AF053008) envelope-like [Glycine max]
9177	GM_146_A2_H07_T7	g2443899	BLASTN	402	4e-11	62	A. thaliana BAC T3F12 from chromosome IV, likely from the long arm, complete sequence [Arabidopsis thaliana]
9178	GM_146_A2_H08_MR	g507910	BLASTN	659	4e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
9179	GM_146_A2_H11_T7	g1174779	BLASTX	195	6e-14	84	TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR gi 166894 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
9180	GM_146_B1_A01_T7	g1769897	BLASTX	425	7e-45	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9181	GM_146_B1_A02_MR	g3645899	BLASTX	140	7e-16	35	(U68408) 5' end not determined experimentally [Zea mays]
9182	GM_146_B1_A02_T7	g4063760	BLASTX	236	1e-17	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9183	GM_146_B1_A03_MR	g4006838	BLASTN	380	4e-10	62	Homo sapiens chromosome 17, clone HRPK.855_D_21, complete sequence [Homo sapiens]
9184	GM_146_B1_A03_T7	g3402755	BLASTX	189	3e-19	38	(AL031187) putative transposable element [Arabidopsis thaliana]
9185	GM_146_B1_A04_T7	g1142702	BLASTN	354	2e-09	78	Glycine max satellite STR120-A.4.
9186	GM_146_B1_A05_T7	g3142330	BLASTX	732	1e-71	85	(U96295) envelope-like [Glycine max]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	%Ident	Description
9187	GM_146_B1_A06_T7	g2062167	BLASTX	247	8e-42	79	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]
9188	GM_146_B1_A07_T7	g294042	BLASTN	350	8e-09	61	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
9189	GM_146_B1_A08_MR	g4049647	BLASTN	349	1e-08	61	Melanoplus sanguinipes entomopoxvirus, complete genome
9190	GM_146_B1_A09_T7	g1142702	BLASTN	338	9e-09	78	Glycine max satellite STR120-A.4.
9191	GM_146_B1_B05_T7	g170080	BLASTN	441	3e-15	74	Soybean seed lectin gene transposable element tgml.
9192	GM_146_B1_B06_MR	g507910	BLASTN	405	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9193	GM_146_B1_B06_T7	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9194	GM_146_B1_B07_T7	g1666236	BLASTX	287	1e-24	36	(U76261) unknown [Hordeum vulgare]
9195	GM_146_B1_B12_MR	g13096	BLASTN	359	3e-09	59	Leishmania tarentolae maxicircle DNA fragment
9196	GM_146_B1_C04_MR	g2213599	BLASTX	251	2e-22	37	(AC000348) T7N9.19 [Arabidopsis thaliana]
9197	GM_146_B1_C05_MR	g3142328	BLASTN	2400	4e-103	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF104919) contains similarity to expansins [Arabidopsis thaliana]
9198	GM_146_B1_C08_T7	g3859592	BLASTX	338	2e-55	74	G.max gene for catalase
9199	GM_146_B1_C09_MR	g18559	BLASTN	556	3e-18	72	hypothetical protein - garden snapdragon
9200	GM_146_B1_D02_T7	g100484	BLASTX	356	4e-43	60	Glycine max BSR-101 satellite SB92 genomic sequence.
9201	GM_146_B1_D06_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9202	GM_146_B1_D08_MR	g507910	BLASTN	372	3e-10	71	(AC002333) hypothetical protein [Arabidopsis thaliana]
9203	GM_146_B1_D11_T7	g2281092	BLASTX	144	2e-09	72	(AC002333) hypothetical protein [Arabidopsis thaliana]
9204	GM_146_B1_E01_T7	g2281092	BLASTX	206	6e-16	64	(AC002333) hypothetical protein [Arabidopsis thaliana]
9205	GM_146_B1_E02_T7	g3217506	BLASTN	389	1e-10	62	Caenorhabditis elegans cosmid F55C9, complete sequence [Caenorhabditis elegans]
9206	GM_146_B1_E03_MR	g4063760	BLASTX	264	1e-20	35	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9207	GM_146_B1_E05_T7	g18559	BLASTN	631	1e-21	76	G.max gene for catalase
9208	GM_146_B1_E06_T7	g3845307	BLASTN	379	4e-10	58	Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence
9209	GM_146_B1_E08_MR	g3746069	BLASTX	163	3e-27	51	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
9210	GM_146_B1_E09_MR	g1142701	BLASTN	1083	1e-42	83	Glycine max satellite STR120-A.3.
9211	GM_146_B1_E11_MR	g1666236	BLASTX	144	9e-09	35	(U76261) unknown [Hordeum vulgare]
9212	GM_146_B1_F06_T7	g3097320	BLASTN	1114	2e-43	79	Glycine max gene for Bd 30K, complete cds
9213	GM_146_B1_G01_MR	g507910	BLASTN	407	9e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence
9214	GM_146_B1_G01_T7	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9215	GM_146_B1_G03_T7	g1871192	BLASTX	143	7e-10	37	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]
9216	GM_146_B1_G06_T7	g2245120	BLASTX	208	1e-14	39	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9217	GM_146_B1_G07_T7	g543905	BLASTX	176	1e-12	69	BRASSINOSTEROID-REGULATED PROTEIN BRU1 gi 347459 (L22162) brassinosteroid-regulated protein [Glycine max]
9218	GM_146_B1_H01_T7	g905361	BLASTX	362	7e-32	85	(U22103) gag-protease polypeptide [Glycine max]
9219	GM_146_B1_H02_MR	g4063760	BLASTX	279	3e-22	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9220	GM_146_B1_H03_T7	g3845197	BLASTN	594	8e-20	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
9221	GM_146_B1_H07_MR	g1769897	BLASTX	364	2e-32	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9222	GM_146_B1_H11_MR	g1769897	BLASTX	282	3e-23	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9223	GM_146_B1_H12_T7	g3142379	BLASTX	262	2e-21	85	(AF053008) envelope-like [Glycine max]
9224	GM_146_B2_A05_MR	g3777527	BLASTX	726	8e-70	97	(AF053008) gag-pol polypeptide [Glycine max]
9225	GM_146_B2_A11_MR	g507910	BLASTN	396	3e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
9226	GM_146_B2_B03_MR	g3142328	BLASTN	662	5e-23	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9227	GM_146_B2_C11_MR	g3142379	BLASTX	291	8e-25	68	(AF053008) envelope-like [Glycine max]
9228	GM_146_B2_C12_MR	g4063760	BLASTX	189	1e-12	31	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9229	GM_146_B2_D01_MR	g3777527	BLASTX	260	5e-21	46	(AF053008) gag-pol polypeptide [Glycine max]
9230	GM_146_B2_D04_MR	g3873182	BLASTN	385	2e-10	63	Homo sapiens chromosome 17, clone hRPK.235_1 10, complete sequence [Homo sapiens]
9231	GM_146_B2_D08_MR	g18559	BLASTN	363	2e-09	62	G max gene for catalase
9232	GM_146_B2_D11_MR	g2130096	BLASTX	353	4e-31	55	cytochrome P450tyr - sorghum gi 984543 (U32624) cytochrome P-450 [Sorghum bicolor]
9233	GM_146_B2_E01_MR	g905361	BLASTX	709	3e-69	95	(U22103) gag-protease polypeptide [Glycine max]
9234	GM_146_B2_E10_MR	g505129	BLASTN	315	3e-10	67	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9235	GM_146_B2_F11_MR	g4063760	BLASTX	401	3e-35	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9236	GM_146_B2_F05_MR	g320565	BLASTX	219	3e-17	48	transposon TAI-1 KAS-1 - Arabidopsis thaliana (fragment)
9237	GM_146_B2_G01_MR	g3097320	BLASTN	416	8e-12	73	Glycine max gene for Bd 30K, complete cds
9238	GM_146_B2_G05_MR	g1142701	BLASTN	1383	4e-56	86	Glycine max satellite STR120-A.3.
9239	GM_146_B2_G12_MR	g4063760	BLASTX	339	1e-28	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9240	GM_146_B2_H03_MR	g505129	BLASTN	356	4e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9241	GM_147_A1_A01_MR	g100728	BLASTX	156	8e-10	87	aspartate transaminase (EC 2.6.1.1) AAT3 precursor - proso millet gi 1084464 pir S53304 aspartate aminotransferase - proso millet gi 20601 (X63430) aspartate aminotransferase [Panicum miliaceum] gi 435459 gnl PID d1005534 (D25323) aspartate aminotransferase [Panicum miliaceum]
9242	GM_147_A1_A04_MR	g18559	BLASTN	906	5e-34	77	G.max gene for catalase
9243	GM_147_A1_A06_MR	g905361	BLASTX	206	6e-15	36	(U22103) gag-protease polyprotein [Glycine max]
9244	GM_147_A1_A06_T7	g100484	BLASTX	359	3e-31	61	hypothetical protein - garden snapdragon
9245	GM_147_A1_A07_MR	g507910	BLASTN	517	9e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9246	GM_147_A1_A07_T7	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence
9247	GM_147_A1_A08_MR	g1236949	BLASTX	303	4e-25	98	(U50075) lipoygenase 1-5 [Glycine max]
9248	GM_147_A1_A09_T7	g4050011	BLASTN	398	6e-11	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
9249	GM_147_A1_A12_MR	g3097320	BLASTN	1037	6e-40	81	Glycine max gene for Bd 30K, complete cds
9250	GM_147_A1_B02_T7	g2129473	BLASTX	234	6e-19	38	arabinogalactan-like protein - loblolly pine gi 607774 (U09556)
9251	GM_147_A1_B05_T7	g8540	BLASTN	383	4e-11	70	arabinogalactan-like protein [Pinus taeda]
9252	GM_147_A1_B11_T7	g4063760	BLASTX	255	9e-20	52	Drosophila satellite DNA fragment 1.672-614 >gi 158379 gb
9253	GM_147_A1_C01_T7	g4063760	BLASTX	155	6e-11	37	M29744 DROSAT02 Drosophila satellite DNA fragment 1.672-614 (AC005561) putative POL3 protein [Arabidopsis thaliana]
9254	GM_147_A1_C02_T7	g1769897	BLASTX	326	7e-30	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9255	GM_147_A1_C07_MR	g3142328	BLASTN	691	3e-24	92	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9256	GM_147_A1_C10_MR	g33599418	BLASTN	533	4e-17	69	Glycine max partial SIRI5-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9257	GM_147_A1_C11_MR	g421954	BLASTX	339	3e-29	55	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9258	GM_147_A1_D01_MR	g2764526	BLASTN	372	9e-10	60	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
9259	GM_147_A1_D03_T7	g25222228	BLASTX	210	8e-16	35	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
9260	GM_147_A1_D04_MR	g507910	BLASTN	560	1e-18	81	(AB007466) reverse transcriptase-like protein [Vicia faba]
9261	GM_147_A1_E03_T7	g507910	BLASTN	401	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence
9262	GM_147_A1_E05_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9263	GM_147_A1_E11_T7	g13596	BLASTN	398	8e-12	62	Glycine max BSR-101 satellite SB92 genomic sequence
9264	GM_147_A1_E12_MR	g507910	BLASTN	394	3e-11	75	Yeast mit DNA for promoter upstream of tRNA-Leu gene 3 *Source: Glycine max BSR-101 satellite SB92 genomic sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9265	GM_147_A1_E12_T7	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9266	GM_147_A1_F01_MR	g3777527	BLASTX	512	6e-47	97	(AF053008) gag-pol polyprotein [Glycine max]
9267	GM_147_A1_F01_T7	g1666236	BLASTX	193	3e-14	30	(U76261) unknown [Hordeum vulgare]
9268	GM_147_A1_G01_T7	g3097320	BLASTN	891	3e-33	73	Glycine max gene for Bd 30K, complete cds
9269	GM_147_A1_G02_MR	g1335862	BLASTX	204	5e-30	90	(U42608) clathrin heavy chain [Glycine max]
9270	GM_147_A1_G06_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9271	GM_147_A1_G07_MR	g2522226	BLASTN	623	3e-21	70	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
9272	GM_147_A1_G08_MR	g3599418	BLASTN	523	1e-16	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9273	GM_147_A1_G12_T7	g3097320	BLASTN	446	4e-13	70	Glycine max gene for Bd 30K, complete cds
9274	GM_147_A1_H03_MR	g2244965	BLASTX	166	1e-10	38	(Z97340) unnamed protein product [Arabidopsis thaliana]
9275	GM_147_A1_H05_T7	g99755	BLASTX	248	1e-19	59	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
9276	GM_147_A1_H08_MR	g3281868	BLASTX	319	5e-27	55	(AL031004) putative protein [Arabidopsis thaliana]
9277	GM_147_A1_H09_T7	g3599418	BLASTN	354	5e-09	86	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9278	GM_147_A2_A06_T7	g3645899	BLASTX	193	3e-13	57	(U68408) 5' end not determined experimentally [Zea mays]
9279	GM_147_A2_A07_T7	g3142328	BLASTN	603	3e-20	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9280	GM_147_A2_A08_MR	g3650039	BLASTX	159	8e-10	40	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
9281	GM_147_A2_A11_T7	g2462745	BLASTX	216	6e-16	58	(AC002292) Hypothetical protein [Arabidopsis thaliana]
9282	GM_147_A2_B07_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9283	GM_147_A2_B07_T7	g4063760	BLASTX	270	2e-21	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9284	GM_147_A2_B09_T7	g507910	BLASTN	570	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9285	GM_147_A2_B11_MR	g3645899	BLASTX	337	1e-28	51	(U68408) 5' end not determined experimentally [Zea mays]
9286	GM_147_A2_C05_MR	g4063760	BLASTX	172	5e-16	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9287	GM_147_A2_C06_MR	g4063760	BLASTX	312	8e-26	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9288	GM_147_A2_C09_MR	g2522227	BLASTX	150	1e-09	36	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9289	GM_147_A2_C09_T7	g507910	BLASTN	380	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
9290	GM_147_A2_C11_T7	g3097320	BLASTN	429	2e-12	71	Glycine max gene for Bd 30K, complete cds
9291	GM_147_A2_C12_T7	g3894385	BLASTX	187	1e-12	36	(AF053094) Hcr2-0A [Lycopersicon esculentum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9292	GM_147_A2_D01_MR	g2982444	BLASTX	158	1e-13	37	(AL022224) CLV1 receptor kinase like protein [Arabidopsis thaliana]
9293	GM_147_A2_D01_T7	g3779021	BLASTX	233	2e-17	43	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
9294	GM_147_A2_D03_T7	g18559	BLASTN	922	9e-35	77	G max gene for catalase
9295	GM_147_A2_D05_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9296	GM_147_A2_D07_MR	g507910	BLASTN	391	5e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9297	GM_147_A2_D12_T7	g3645899	BLASTX	146	7e-11	46	(U68408) 5' end not determined experimentally [Zea mays]
9298	GM_147_A2_E01_T7	g507910	BLASTN	408	8e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9299	GM_147_A2_E02_T7	g4092471	BLASTN	483	9e-15	67	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
9300	GM_147_A2_E04_MR	g507910	BLASTN	566	6e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9301	GM_147_A2_E05_MR	g130582	BLASTX	208	1e-15	44	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
9302	GM_147_A2_F06_T7	g507910	BLASTN	584	9e-20	82	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9303	GM_147_A2_F07_T7	g2996647	BLASTN	357	4e-09	62	Glycine max BSR-101 satellite SB92 genomic sequence.
9304	GM_147_A2_F08_T7	g3860272	BLASTX	100	2e-11	68	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
9305	GM_147_A2_E10_T7	g2764526	BLASTN	467	4e-14	68	(AC005824) putative suppressor protein [Arabidopsis thaliana]
9306	GM_147_A2_F05_MR	g4160362	BLASTN	401	4e-11	61	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
9307	GM_147_A2_F08_MR	g3402703	BLASTX	201	8e-15	70	Saccharomyces cerevisiae complete mitochondrial genome (AC004261) hypothetical protein [Arabidopsis thaliana]
9308	GM_147_A2_F11_T7	g3142379	BLASTX	215	3e-16	78	(AF053008) envelope-like [Glycine max]
9309	GM_147_A2_G02_T7	g4063760	BLASTX	152	3e-12	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9310	GM_147_A2_G08_T7	g99922	BLASTX	240	1e-19	78	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
9311	GM_147_A2_G10_T7	g3810595	BLASTX	367	1e-31	55	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
9312	GM_147_A2_H02_T7	g2244802	BLASTX	142	5e-10	45	(Z97336) retrovirus-related polypeptide homolog [Arabidopsis thaliana]
9313	GM_147_A2_H04_T7	g18695	BLASTN	792	3e-29	91	Soybean nodulin 22 gene
9314	GM_147_A2_H05_T7	g99755	BLASTX	302	2e-25	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9315	GM_147_A2_H11_T7	g507910	BLASTN	382	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
9316	GM_147_A2_H12_MR	g4063756	BLASTN	430	2e-12	64	Arabidopsis thaliana chromosome II BAC T9f8 genomic sequence, complete sequence [Arabidopsis thaliana]
9317	GM_147_A2_H12_T7	g3930515	BLASTX	126	2e-11	50	(AF059674) putative gag protein [Nicotiana tabacum]
9318	GM_147_B1_A02_MR	g507910	BLASTN	747	4e-27	90	Glycine max BSR-101 satellite SB92 genomic sequence
9319	GM_147_B1_A02_T7	g4063760	BLASTX	252	2e-19	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9320	GM_147_B1_A04_MR	g2996576	BLASTN	371	1e-09	60	Homo sapiens DNA sequence from PAC 29C18 on chromosome 22
9321	GM_147_B1_A05_T7	g13557	BLASTN	380	3e-10	72	Yeast mitochondrial genes for 15S rRNA and tRNA-Trp
9322	GM_147_B1_A06_T7	g99922	BLASTX	579	4e-62	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
9323	GM_147_B1_A07_T7	g4003350	BLASTN	344	9e-10	68	Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map
9324	GM_147_B1_A08_T7	g2708743	BLASTX	314	6e-26	42	10q25.1, complete sequence [Homo sapiens]
9325	GM_147_B1_B02_MR	g2914707	BLASTX	155	1e-10	34	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
9326	GM_147_B1_B05_T7	g1769897	BLASTX	213	3e-17	36	(AC003974) putative disease resistance protein (Ct-2.2) [Arabidopsis thaliana] gi 3298554 (AC004681) putative disease resistance protein [Arabidopsis thaliana]
9327	GM_147_B1_B08_MR	g507910	BLASTN	387	7e-11	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9328	GM_147_B1_B08_T7	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9329	GM_147_B1_B10_T7	g507910	BLASTN	429	9e-13	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9330	GM_147_B1_C04_MR	g3097320	BLASTN	474	2e-14	71	Glycine max gene for Bd 30K, complete cds
9331	GM_147_B1_C09_T7	g18559	BLASTN	1692	8e-70	90	G max gene for catalase
9332	GM_147_B1_C10_T7	g4092470	BLASTN	695	2e-24	67	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
9333	GM_147_B1_C11_MR	g507910	BLASTN	346	5e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence
9334	GM_147_B1_D04_MR	g3152629	BLASTN	384	3e-10	65	Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence [Homo sapiens]
9335	GM_147_B1_D05_T7	g3820757	BLASTN	374	4e-10	62	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
9336	GM_147_B1_D06_MR	g4063760	BLASTX	277	5e-22	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9337	GM_147_B1_E03_T7	g3319362	BLASTX	183	3e-12	31	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt hrm, score 19.29) [Arabidopsis thaliana]
9338	GM_147_B1_E04_MR	g18559	BLASTN	1043	3e-40	75	G max gene for catalase

Seq No.	ClonID	NCBI gi	Method	Score	P-value	% Ident	Description
9339	GM_147_B1_F05_MR	g422418	BLASTX	139	2e-09	41	pol protein - fruit fly (<i>Drosophila ananassae</i>) transposon Tom (fragment) gi 394705 (Z24451) pol protein [<i>Drosophila ananassae</i>]
9340	GM_147_B1_F07_T7	g3036785	BLASTN	465	6e-14	60	Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A1, H2B.1A, H4, H2A.1b, H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island
9341	GM_147_B1_F01_T7	g4115365	BLASTX	367	1e-31	47	(AC005957) reverse transcriptase-like protein [<i>Arabidopsis thaliana</i>]
9342	GM_147_B1_F04_MR	g3097320	BLASTN	476	2e-14	72	Glycine max gene for Bd 30K, complete cds
9343	GM_147_B1_F04_T7	g3097320	BLASTN	693	2e-24	76	Glycine max gene for Bd 30K, complete cds
9344	GM_147_B1_F05_MR	g3319362	BLASTX	430	1e-38	61	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [<i>Arabidopsis thaliana</i>]
9345	GM_147_B1_F08_MR	g1658457	BLASTX	137	1e-12	61	(U75248) reverse transcriptase [<i>Gossypium barbadense</i>]
9346	GM_147_B1_F09_T7	g2522227	BLASTX	218	3e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [<i>Vicia faba</i>]
9347	GM_147_B1_F10_MR	g421954	BLASTX	163	1e-14	37	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [<i>Solanum tuberosum</i>]
9348	GM_147_B1_G02_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
9349	GM_147_B1_G02_T7	g507910	BLASTN	414	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9350	GM_147_B1_G03_T7	g1171591	BLASTN	371	1e-09	62	<i>P. falciparum</i> complete gene map of plastid-like DNA (IR-B)
9351	GM_147_B1_G05_T7	g469153	BLASTN	402	4e-11	65	<i>P. sativum</i> (Birte) Lox1:Ps2 gene.
9352	GM_147_B1_G06_MR	g507910	BLASTN	535	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
9353	GM_147_B1_G06_T7	g4063760	BLASTX	290	2e-23	52	(AC005561) putative POL3 protein [<i>Arabidopsis thaliana</i>]
9354	GM_147_B1_G07_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9355	GM_147_B1_G07_T7	g507910	BLASTN	597	2e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9356	GM_147_B1_G08_T7	g4038056	BLASTX	256	5e-20	52	(AC005897) putative transposon [<i>Arabidopsis thaliana</i>]
9357	GM_147_B1_H05_MR	g4063756	BLASTN	421	6e-12	69	<i>Arabidopsis thaliana</i> chromosome II BAC T9F8 genomic sequence, complete sequence [<i>Arabidopsis thaliana</i>]
9358	GM_147_B1_H07_MR	g505129	BLASTN	441	5e-13	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9359	GM_147_B1_H08_MR	g3645899	BLASTX	342	4e-29	47	(U68408) 5' end not determined experimentally [<i>Zea mays</i>]
9360	GM_147_B1_H09_MR	g4063760	BLASTX	650	5e-62	70	(AC005561) putative POL3 protein [<i>Arabidopsis thaliana</i>]
9361	GM_147_B1_H10_T7	g100484	BLASTX	320	4e-27	58	hypothetical protein - garden snapdragon
9362	GM_147_B1_H12_T7	g3142328	BLASTN	433	1e-12	69	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9363	GM_147_B2_A04_MR	g4063760	BLASTX	559	3e-52	71	(AC005561) putative POL3 protein [<i>Arabidopsis thaliana</i>]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9364	GM_147_B2_A08_T7	g3097320	BLASTN	403	3e-11	70	Glycine max gene for Bd 30K, complete cds
9365	GM_147_B2_A09_T7	g1431738	BLASTN	630	1e-21	74	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
9366	GM_147_B2_B01_MR	g2995405	BLASTX	291	7e-46	64	(Y12432) polyprotein [Ananas comosus]
9367	GM_147_B2_B04_MR	g1769897	BLASTX	209	2e-15	35	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9368	GM_147_B2_B12_MR	g2894575	BLASTX	157	1e-10	67	(AL021890) putative protein [Arabidopsis thaliana]
9369	GM_147_B2_C04_T7	g4038056	BLASTX	296	3e-24	48	(AC005897) putative transposon [Arabidopsis thaliana]
9370	GM_147_B2_C06_T7	g1142702	BLASTN	605	8e-21	79	Glycine max satellite STR120-A.4.
9371	GM_147_B2_C11_T7	g2995405	BLASTX	260	2e-20	46	(Y12432) polyprotein [Ananas comosus]
9372	GM_147_B2_D02_MR	g507910	BLASTN	559	1e-18	86	Glycine max BSR-101 satellite SB92 genomic sequence
9373	GM_147_B2_D02_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9374	GM_147_B2_D03_MR	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9375	GM_147_B2_D04_MR	g2997694	BLASTX	232	1e-18	42	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
9376	GM_147_B2_D11_MR	g3746062	BLASTX	140	7e-14	60	(AC005311) hypothetical protein [Arabidopsis thaliana]
9377	GM_147_B2_E06_MR	g3924609	BLASTX	260	7e-24	50	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
9378	GM_147_B2_E09_MR	g905361	BLASTX	141	4e-20	69	(U22103) gag-protease polyprotein [Glycine max]
9379	GM_147_B2_E11_T7	g2522227	BLASTX	170	3e-14	57	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9380	GM_147_B2_F02_MR	g3097320	BLASTN	474	2e-14	69	Glycine max gene for Bd 30K, complete cds
9381	GM_147_B2_F05_MR	g2894575	BLASTX	172	2e-12	71	(AL021890) putative protein [Arabidopsis thaliana]
9382	GM_147_B2_F07_MR	g505129	BLASTN	347	1e-08	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9383	GM_147_B2_F08_MR	g1666236	BLASTX	155	6e-10	29	(U76261) unknown [Hordeum vulgare]
9384	GM_147_B2_G10_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9385	GM_147_B2_G11_MR	g4063760	BLASTX	216	1e-15	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9386	GM_147_B2_G12_T7	g3097320	BLASTN	682	8e-24	75	Glycine max gene for Bd 30K, complete cds
9387	GM_147_B2_H05_MR	g4038056	BLASTX	394	8e-35	55	(AC005897) putative transposon [Arabidopsis thaliana]
9388	GM_147_B2_H06_MR	g3777527	BLASTX	241	4e-18	38	(AF053008) gag-pol polyprotein [Glycine max]
9389	GM_147_B2_H07_MR	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9390	GM_147_B2_H07_T7	g507910	BLASTN	476	7e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
9391	GM_148_A1_A02_MR	g2459422	BLASTX	115	2e-09	42	(AC002332) unknown protein [Arabidopsis thaliana]
9392	GM_148_A1_A05_MR	g1488266	BLASTN	370	5e-10	60	Arabidopsis thaliana low affinity calcium antiporter CAX2 mRNA, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9393	GM_148_A1_A08_T7	g3668091	BLASTX	181	3e-12	29	(AC004667) hypothetical protein [Arabidopsis thaliana]
9394	GM_148_A1_A11_MR	g3142328	BLASTN	974	4e-37	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF053008) gag-pol polyprotein [Glycine max]
9395	GM_148_A1_B09_MR	g3777527	BLASTX	310	2e-25	52	(AF004879) resistance complex protein 12C-2 [Lycopersicon esculentum]
9396	GM_148_A1_B11_T7	g2258317	BLASTX	114	2e-12	33	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
9397	GM_148_A1_C03_MR	g3695387	BLASTX	259	3e-20	68	(AB004906) transposase [Ipomoea purpurea]
9398	GM_148_A1_C06_MR	g4063770	BLASTX	186	1e-12	39	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
9399	GM_148_A1_D10_MR	g3695395	BLASTX	217	4e-16	37	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U76261) unknown [Hordeum vulgare]
9400	GM_148_A1_E02_MR	g3142328	BLASTN	1045	2e-40	95	(AC000103) F2119.2 [Arabidopsis thaliana]
9401	GM_148_A1_E02_T7	g1666236	BLASTX	157	3e-10	30	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence Pisum sativum pectin methyltransferase (rcpme1) gene, complete cds
9402	GM_148_A1_F03_MR	g2213608	BLASTX	177	1e-12	38	Torulopsis glabrata mitochondrial DNA for tRNA-Thr, -His and -Glu upstream of cytochrome b gene >gi 343951 gb M11856
9403	GM_148_A1_F04_MR	g3142328	BLASTN	847	5e-61	89	YSLMTIG01 Yeast (T.glabrata) mitochondrial DNA between L. rRNA and cytochrome b genes.
9404	GM_148_A1_F07_T7	g3426334	BLASTN	354	5e-09	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9405	GM_148_A1_F12_MR	g13768	BLASTN	276	1e-09	69	(U22103) gag-protease polyprotein [Glycine max]
9406	GM_148_A1_G04_T7	g4063760	BLASTX	270	2e-21	54	Drosophila satellite DNA fragment 1.672-573
9407	GM_148_A1_G05_T7	g905361	BLASTX	587	3e-56	94	G max gene for catalase
9408	GM_148_A1_G08_MR	g8543	BLASTN	372	1e-10	67	(AB004906) transposase [Ipomoea purpurea]
9409	GM_148_A1_H07_MR	g18559	BLASTN	992	6e-38	73	(U76261) unknown [Hordeum vulgare]
9410	GM_148_A1_H07_T7	g4063770	BLASTX	186	3e-16	53	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]
9411	GM_148_A1_H11_T7	g1666236	BLASTX	139	9e-13	44	Glycine max BSR-101 satellite SB92 genomic sequence.
9412	GM_148_A1_H12_T7	g3004564	BLASTX	134	5e-17	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9413	GM_148_A2_A02_MR	g507910	BLASTN	531	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9414	GM_148_A2_A02_T7	g507910	BLASTN	599	2e-20	82	Hansenula wingei mitochondrial DNA, complete sequence
9415	GM_148_A2_A03_T7	g1000971	BLASTN	382	3e-10	62	Glycine max BSR-101 satellite SB92 genomic sequence.
9416	GM_148_A2_A05_MR	g507910	BLASTN	508	2e-20	83	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9417	GM_148_A2_A05_T7	g3777527	BLASTX	728	5e-70	97	(AF053008) gag-pol polyprotein [Glycine max]
9418	GM_148_A2_A08_MR	g905361	BLASTX	181	3e-12	29	(U22103) gag-protease polyprotein [Glycine max]
9419	GM_148_A2_B07_T7	g2347190	BLASTX	274	5e-22	38	(AC002338) Na/H antiporter isolog [Arabidopsis thaliana] gi 3150398 (AC004165) putative Na/H antiporter [Arabidopsis thaliana]
9420	GM_148_A2_B09_MR	g3510337	BLASTN	359	3e-09	69	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]
9421	GM_148_A2_B11_T7	g4063760	BLASTX	557	5e-52	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9422	GM_148_A2_B12_MR	g3777527	BLASTX	191	9e-13	34	(AF053008) gag-pol polyprotein [Glycine max]
9423	GM_148_A2_C05_T7	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9424	GM_148_A2_C06_MR	g505129	BLASTN	371	5e-12	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9425	GM_148_A2_C06_T7	g507910	BLASTN	607	8e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
9426	GM_148_A2_C07_T7	g1666236	BLASTX	136	4e-15	34	(U76261) unknown [Hordeum vulgare]
9427	GM_148_A2_C10_MR	g100484	BLASTX	363	9e-32	60	hypothetical protein - garden snapdragon
9428	GM_148_A2_D04_T7	g3650039	BLASTX	272	6e-22	43	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
9429	GM_148_A2_D09_MR	g3426334	BLASTN	503	9e-16	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
9430	GM_148_A2_D10_MR	g3873182	BLASTN	427	3e-12	62	Homo sapiens chromosome 17, clone hRPK.235_1_10, complete sequence [Homo sapiens]
9431	GM_148_A2_D10_T7	g18768	BLASTN	507	1e-16	67	Soybean Tgm6 transposable element 3' end
9432	GM_148_A2_E06_T7	g2522228	BLASTX	281	1e-36	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
9433	GM_148_A2_E08_T7	g3273120	BLASTN	352	7e-09	63	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-57, complete sequence [Plasmodium falciparum] (U68408) 5' end not determined experimentally [Zea mays]
9434	GM_148_A2_E10_MR	g3645899	BLASTX	263	1e-20	45	Glycine max gene for Bd 30K, complete cds
9435	GM_148_A2_E12_T7	g3097320	BLASTN	416	8e-12	73	hypothetical protein - garden snapdragon
9436	GM_148_A2_F01_T7	g100484	BLASTX	284	4e-23	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9437	GM_148_A2_F04_MR	g4063760	BLASTX	539	5e-50	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
9438	GM_148_A2_F04_T7	g2264312	BLASTN	420	6e-12	70	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]
9439	GM_148_A2_F10_T7	g3096945	BLASTX	244	6e-20	67	Glycine max gene for Bd 30K, complete cds
9440	GM_148_A2_G01_MR	g3097320	BLASTN	463	6e-14	72	(AJ003387) protease [Drosophila melanogaster]
9441	GM_148_A2_G04_T7	g2791289	BLASTX	193	4e-13	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9442	GM_148_A2_G05_T7	g4063760	BLASTX	252	2e-19	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9443	GM_148_A2_G08_MR	g4063760	BLASTX	212	4e-15	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9444	GM_148_A2_H03_MR	g507910	BLASTN	576	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9445	GM_148_A2_H03_T7	g507910	BLASTN	492	1e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence
9446	GM_148_A2_H04_MR	g4063760	BLASTX	473	5e-43	61	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9447	GM_148_A2_H04_T7	g3645899	BLASTX	188	3e-17	46	(U68408) 5' end not determined experimentally [Zea mays]
9448	GM_148_A2_H06_MR	g507910	BLASTN	371	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9449	GM_148_A2_H06_T7	g507910	BLASTN	422	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence
9450	GM_148_A2_H10_MR	g18559	BLASTN	544	1e-17	81	Gi max gene for catalase
9451	GM_148_A2_H10_T7	g3777527	BLASTX	726	8e-70	97	(AF053008) gag-pol polyprotein [Glycine max]
9452	GM_148_A2_H11_MR	g4150933	BLASTN	390	1e-10	63	Homo sapiens BAC clone NH0520M18 from 7q31.1-q31.2, complete sequence [Homo sapiens]
9453	GM_148_A2_H12_MR	g2443320	BLASTX	235	1e-17	37	(D85597) polyprotein [Oryza australiensis]
9454	GM_148_B1_A02_MR	g3777527	BLASTX	628	2e-59	93	(AF053008) gag-pol polyprotein [Glycine max]
9455	GM_148_B1_A05_MR	g4092470	BLASTN	632	2e-21	66	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
9456	GM_148_B1_A05_T7	g2443320	BLASTX	246	1e-18	39	(D85597) polyprotein [Oryza australiensis]
9457	GM_148_B1_A06_MR	g840618	BLASTN	375	4e-10	60	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
9458	GM_148_B1_A07_MR	g4063760	BLASTX	574	8e-54	62	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9459	GM_148_B1_A07_T7	g3645899	BLASTX	188	1e-19	46	(U68408) 5' end not determined experimentally [Zea mays]
9460	GM_148_B1_A08_T7	g4063760	BLASTX	213	3e-15	66	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9461	GM_148_B1_A10_MR	g3142328	BLASTN	597	2e-27	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9462	GM_148_B1_B05_MR	g18559	BLASTN	907	4e-34	79	Gi max gene for catalase
9463	GM_148_B1_B08_T7	g166421	BLASTN	375	2e-10	66	Medicago sativa ubiquitin carrier protein mRNA, complete cds.
9464	GM_148_B1_B10_T7	g18559	BLASTN	584	5e-31	78	Gi max gene for catalase
9465	GM_148_B1_B12_T7	g1769897	BLASTX	308	3e-26	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9466	GM_148_B1_C01_MR	g1899158	BLASTN	555	2e-18	64	Saccharomyces cerevisiae synthetic green fluorescent protein (cox3::GFPm) gene, mitochondrial gene construct, complete cds
9467	GM_148_B1_C04_MR	g2443320	BLASTX	238	4e-30	46	(D85597) polyprotein [Oryza australiensis]
9468	GM_148_B1_C07_T7	g4138265	BLASTX	197	2e-14	91	(AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]
9469	GM_148_B1_C08_MR	g2583130	BLASTX	178	1e-12	37	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
9470	GM_148_B1_C08_T7	g4038056	BLASTX	275	5e-25	52	(AC005897) putative transposon [Arabidopsis thaliana]
9471	GM_148_B1_C12_MR	g3036806	BLASTX	108	3e-09	30	(AL022373) glycine-rich protein [Arabidopsis thaliana]
9472	GM_148_B1_C12_T7	g3096945	BLASTX	219	2e-17	59	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]
9473	GM_148_B1_D03_MR	g3777527	BLASTX	335	4e-28	45	(AF053008) gag-pol polyprotein [Glycine max]
9474	GM_148_B1_D04_MR	g3645899	BLASTX	234	1e-17	45	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9475	GM_148_B1_D10_MR	g3097320	BLASTN	1016	6e-39	80	Glycine max gene for Bd 30K, complete cds
9476	GM_148_B1_D10_T7	g4050011	BLASTN	499	1e-15	67	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
9477	GM_148_B1_D12_MR	g1769897	BLASTX	127	1e-17	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9478	GM_148_B1_E01_MR	g2828293	BLASTX	201	4e-14	49	(A1021687) putative protein [Arabidopsis thaliana]
9479	GM_148_B1_E03_T7	g3777527	BLASTX	702	3e-67	97	(AF053008) gag-pol polypeptide [Glycine max]
9480	GM_148_B1_E04_T7	g100484	BLASTX	321	3e-27	50	hypothetical protein - garden snapdragon
9481	GM_148_B1_E06_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9482	GM_148_B1_F06_T7	g507910	BLASTN	407	9e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9483	GM_148_B1_F07_MR	g130582	BLASTX	468	2e-42	57	RETROVIRUS-RELATED POL POLYPYRROLINE (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
							(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9484	GM_148_B1_E12_T7	g2522230	BLASTX	189	1e-17	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9485	GM_148_B1_F03_T7	g1769898	BLASTX	146	3e-17	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9486	GM_148_B1_F06_MR	g342964	BLASTN	383	3e-11	61	parametrium species 5.311 mt dna dimer: replication init. region.
9487	GM_148_B1_F06_T7	g1144553	BLASTN	365	2e-10	65	Anopheles melas 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
9488	GM_148_B1_F07_MR	g4160362	BLASTN	349	1e-08	61	Saccharomyces cerevisiae complete mitochondrial genome
9489	GM_148_B1_F07_T7	g3097320	BLASTN	1168	7e-46	80	Glycine max gene for Bd 30K, complete cds
9490	GM_148_B1_F08_T7	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
9491	GM_148_B1_F09_MR	g4063756	BLASTN	438	9e-13	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9492	GM_148_B1_F09_T7	g507910	BLASTN	719	7e-26	88	Glycine max BSR-101 satellite SB92 genomic sequence.
9493	GM_148_B1_F10_MR	g1142702	BLASTN	362	7e-10	74	Glycine max satellite STR120-A.4.
9494	GM_148_B1_F12_T7	g2995405	BLASTX	312	5e-26	61	(Y12432) polypeptide [Ananas comosus]
9495	GM_148_B1_G02_T7	g2522227	BLASTX	237	1e-21	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9496	GM_148_B1_G03_T7	g3763998	BLASTN	449	3e-13	60	Plasmodium falciparum MAL3P4, complete sequence [Plasmodium falciparum]
9497	GM_148_B1_G04_MR	g99922	BLASTX	315	2e-27	57	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9498	GM_148_B1_G05_T7	g2656029	BLASTN	429	2e-12	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2
9499	GM_148_B1_G07_MR	g18559	BLASTN	1143	8e-45	74	G.max gene for catalase
9500	GM_148_B1_G07_T7	g4063770	BLASTX	159	2e-23	48	(AB004906) transposase [Ipomoea purpurea]
9501	GM_148_B1_G09_MR	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9502	GM_148_B1_G12_MR	g4063756	BLASTN	474	2e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9503	GM_148_B1_G12_T7	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9504	GM_148_B1_H01_MR	g3777527	BLASTX	569	5e-53	87	(AF053008) gag-pol polyprotein [Glycine max]
9505	GM_148_B1_H03_T7	g1173624	BLASTX	477	1e-44	75	(U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid SM9108']
9506	GM_148_B1_H06_T7	g100484	BLASTX	401	7e-36	56	hypothetical protein - garden snapdragon
9507	GM_148_B1_H11_MR	g905361	BLASTX	200	3e-14	32	(U22103) gag-protease polyprotein [Glycine max]
9508	GM_148_B2_A02_MR	g130582	BLASTX	394	2e-34	60	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
9509	GM_148_B2_A05_MR	g3777527	BLASTX	687	1e-65	95	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9510	GM_148_B2_A07_MR	g1167523	BLASTX	195	3e-13	47	(AF053008) gag-pol polyprotein [Glycine max]
9511	GM_148_B2_A08_MR	g507910	BLASTN	434	5e-13	75	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
9512	GM_148_B2_B06_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9513	GM_148_B2_B11_MR	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence
9514	GM_148_B2_C03_MR	g3142328	BLASTN	460	8e-14	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9515	GM_148_B2_C11_MR	g3097320	BLASTN	846	3e-31	80	Glycine max gene for Bd 30K, complete cds
9516	GM_148_B2_D06_MR	g100484	BLASTX	220	1e-18	51	hypothetical protein - garden snapdragon
9517	GM_148_B2_E03_MR	g3777527	BLASTX	683	3e-65	94	(AF053008) gag-pol polyprotein [Glycine max]
9518	GM_148_B2_E06_MR	g4063756	BLASTN	495	2e-15	69	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9519	GM_148_B2_E10_MR	g100484	BLASTX	261	1e-20	46	hypothetical protein - garden snapdragon
9520	GM_148_B2_F02_MR	g2443320	BLASTX	228	9e-17	46	(D85597) polyprotein [Oryza australiensis]
9521	GM_148_B2_F10_MR	g3776013	BLASTX	298	1e-25	70	(AJ010470) RNA helicase [Arabidopsis thaliana]
9522	GM_148_B2_G03_MR	g2828293	BLASTX	172	6e-11	66	(AL021687) putative protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9523	GM_148_B2_G04_MR	g2769655	BLASTN	476	2e-14	65	Human DNA sequence from PAC 1271.4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Contain...
9524	GM_149_A1_A01_MR	g3645899	BLASTX	142	6e-22	57	(U68408) 5' end not determined experimentally [Zea mays]
9525	GM_149_A1_A05_T7	g130582	BLASTX	393	2e-34	68	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9526	GM_149_A1_A09_T7	g3869075	BLASTN	406	3e-11	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
9527	GM_149_A1_B03_T7	g3021268	BLASTX	134	4e-15	50	(AL022347) putative protein [Arabidopsis thaliana]
9528	GM_149_A1_B04_MR	g4063760	BLASTX	191	7e-13	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9529	GM_149_A1_B06_T7	g3142379	BLASTX	262	2e-21	80	(AF053008) envelope-like [Glycine max]
9530	GM_149_A1_B11_MR	g3599418	BLASTN	441	6e-13	78	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9531	GM_149_A1_B11_T7	g2522227	BLASTX	157	2e-10	39	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9532	GM_149_A1_C03_MR	g100484	BLASTX	352	1e-30	52	hypothetical protein - garden snapdragon
9533	GM_149_A1_C05_MR	g18559	BLASTN	757	2e-44	75	Gmax gene for catalase
9534	GM_149_A1_C09_MR	g2880051	BLASTX	161	3e-22	78	(AC002340) putative protein kinase [Arabidopsis thaliana]
9535	GM_149_A1_C09_T7	g2462058	BLASTX	298	1e-25	56	(Y13389) reverse transcriptase [Antirrhinum majus]
9536	GM_149_A1_D02_MR	g3695395	BLASTX	151	5e-12	42	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
9537	GM_149_A1_D04_MR	g3930515	BLASTX	115	7e-12	46	(AF059674) putative gag protein [Nicotiana tabacum]
9538	GM_149_A1_D12_MR	g3142328	BLASTN	836	7e-31	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9539	GM_149_A1_E12_MR	g3810596	BLASTX	142	2e-11	52	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9540	GM_149_A1_F02_T7	g507910	BLASTN	541	8e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
9541	GM_149_A1_F07_MR	g3695395	BLASTX	200	3e-14	38	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
9542	GM_149_A1_F09_T7	g896244	BLASTX	206	6e-16	39	(S75260) pol [Drosophila buzzatii, BU-24, Peptide Transposon, 263 aa] [Drosophila buzzatii]
9543	GM_149_A1_G01_T7	g3785980	BLASTX	151	5e-09	35	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9544	GM_149_A1_G03_MR	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
9545	GM_149_A1_G03_T7	g3142328	BLASTN	764	1e-27	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9546	GM_149_A1_G09_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9547	GM_149_A1_G10_T7	g639722	BLASTX	292	9e-25	81	(L27484) calcium-dependent protein kinase [Zea mays]
9548	GM_149_A1_G12_T7	g2244915	BLASTX	169	1e-10	37	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
9549	GM_149_A1_H02_MR	g3377856	BLASTX	164	4e-15	43	(AF076274) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zfcch.hmm, score: 12.35) [Arabidopsis thaliana]
9550	GM_149_A1_H03_MR	g2522230	BLASTX	226	5e-18	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9551	GM_149_A2_A01_MR	g3426334	BLASTN	355	5e-09	61	Pisum sativum pectin methylesterase (repm1) gene, complete cds
9552	GM_149_A2_A02_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9553	GM_149_A2_A03_MR	g3377834	BLASTX	219	3e-16	35	(AF075598) No definition line found [Arabidopsis thaliana]
9554	GM_149_A2_A03_T7	g3004564	BLASTX	198	1e-14	87	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]
9555	GM_149_A2_A04_T7	g550118	BLASTN	335	5e-09	63	L.tarentolae mRNA encoding putative NADH subunit (G rich region 4)
9556	GM_149_A2_A11_T7	g2262177	BLASTX	102	2e-11	51	(AC002329) hypothetical protein similar to T18A10.3 [Arabidopsis thaliana]
9557	GM_149_A2_B03_MR	g1167523	BLASTX	475	4e-43	68	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
9558	GM_149_A2_B05_MR	g3820757	BLASTN	380	2e-10	61	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
9559	GM_149_A2_B06_MR	g3834322	BLASTX	146	5e-09	46	(AC005679) EST gb R30300 comes from this gene. [Arabidopsis thaliana]
9560	GM_149_A2_B08_MR	g3786414	BLASTN	473	2e-14	64	Caenorhabditis elegans cosmid H28G03
9561	GM_149_A2_B11_MR	g3142379	BLASTX	282	9e-24	84	(AF053008) envelope-like [Glycine max]
9562	GM_149_A2_C01_MR	g505129	BLASTN	353	2e-11	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9563	GM_149_A2_C02_MR	g4038056	BLASTX	237	5e-18	50	(AC005897) putative transposon [Arabidopsis thaliana]
9564	GM_149_A2_C02_T7	g2104945	BLASTN	626	2e-21	66	Glycine max copia-like retrotransposon Tgm, complete sequence
9565	GM_149_A2_C04_MR	g185559	BLASTN	351	7e-09	71	G.max gene for catalase
9566	GM_149_A2_C07_T7	g3142328	BLASTN	810	1e-29	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9567	GM_149_A2_C08_MR	g2244859	BLASTX	137	2e-17	41	(Z97337) hypothetical protein [Arabidopsis thaliana]
9568	GM_149_A2_C08_T7	g3785980	BLASTX	149	5e-14	44	(AC005560) hypothetical protein [Arabidopsis thaliana]
9569	GM_149_A2_C09_MR	g3845310	BLASTN	353	6e-09	61	Plasmodium falciparum chromosome 2, section 62 of 73 of the complete sequence
9570	GM_149_A2_D03_MR	g414665	BLASTN	391	1e-10	66	G.max gene for coproporphyrinogen oxidase
9571	GM_149_A2_D04_MR	g12212	BLASTN	998	2e-43	91	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
9572	GM_149_A2_D07_MR	g3645899	BLASTX	291	1e-24	51	(U68408) 5' end not determined experimentally [Zea mays]
9573	GM_149_A2_D08_T7	g4063756	BLASTN	383	3e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9574	GM_149_A2_D10_MR	g2462134	BLASTX	252	4e-20	33	(Y13368) reverse transcriptase [Beta vulgaris]
9575	GM_149_A2_D11_T7	g3097320	BLASTN	741	2e-26	77	Glycine max gene for Bd 30K, complete cds
9576	GM_149_A2_F01_T7	g3097320	BLASTN	777	4e-28	77	Glycine max gene for Bd 30K, complete cds
9577	GM_149_A2_F02_T7	g2522230	BLASTX	241	1e-19	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9578	GM_149_A2_F03_MR	g100484	BLASTX	321	3e-27	49	hypothetical protein - garden snapdragon
9579	GM_149_A2_F04_MR	g4063760	BLASTX	268	4e-21	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9580	GM_149_A2_F06_MR	g3777526	BLASTN	502	1e-15	73	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
9581	GM_149_A2_F07_MR	g2522227	BLASTX	200	3e-15	52	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9582	GM_149_A2_F11_MR	g2335061	BLASTN	503	1e-15	65	Homo sapiens chromosome 16 BAC clone CTT987SK-334D11 complete sequence [Homo sapiens]
9583	GM_149_A2_F11_T7	g2121303	BLASTN	356	5e-09	66	Homo sapiens cosmid Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
9584	GM_149_A2_F02_MR	g2326363	BLASTX	171	2e-23	82	(AJ001037) DNA-directed RNA polymerase [Arabidopsis thaliana]
9585	GM_149_A2_F03_T7	g3080423	BLASTX	312	6e-26	51	(AL022604) putative protein [Arabidopsis thaliana]
9586	GM_149_A2_F06_T7	g3142379	BLASTX	298	1e-25	67	(AF053008) envelope-like [Glycine max]
9587	GM_149_A2_F12_MR	g2443320	BLASTX	463	7e-42	59	(D85597) polyprotein [Oryza australiensis]
9588	GM_149_A2_G01_MR	g396249	BLASTN	399	3e-11	63	S. douglasii mitochondrial ATP subunit 9 gene, complete CDS

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9589	GM_149_A2_G01_T7	g130582	BLASTX	326	3e-27	49	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9590	GM_149_A2_G02_MR	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
9591	GM_149_A2_G05_MR	g18559	BLASTN	948	6e-36	75	G.max gene for catalase
9592	GM_149_A2_G05_T7	g905361	BLASTX	636	2e-61	98	(U22103) gag-protease polyprotein [Glycine max]
9593	GM_149_A2_G06_T7	g3645899	BLASTX	312	6e-26	51	(U68408) 5' end not determined experimentally [Zea mays]
9594	GM_149_A2_G07_MR	g2444271	BLASTX	206	4e-15	66	(AF019637) putative amino acid or GABA permease [Arabidopsis thaliana]
9595	GM_149_A2_G08_MR	g3242708	BLASTX	235	6e-18	52	(AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]
9596	GM_149_A2_G09_T7	g18559	BLASTN	699	1e-24	72	G.max gene for catalase
9597	GM_149_A2_G11_MR	g3810596	BLASTX	285	4e-23	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9598	GM_149_A2_G12_T7	g3702964	BLASTX	117	9e-10	95	(AF079485) rac GTP binding protein Atac10 [Arabidopsis thaliana]
9599	GM_149_A2_H05_T7	g3097320	BLASTN	597	5e-20	85	Glycine max gene for Bd 30K, complete cds
9600	GM_149_A2_H09_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
9601	GM_149_A2_H10_T7	g3135263	BLASTX	152	1e-09	80	(AC003058) hypothetical protein [Arabidopsis thaliana]
9602	GM_149_A2_H11_T7	g3097320	BLASTN	896	2e-33	77	Glycine max gene for Bd 30K, complete cds
9603	GM_149_B1_A02_MR	g1335695	BLASTX	257	2e-21	45	(X02600) unidentified open reading frame II (146 aa) [Drosophila melanogaster]
9604	GM_149_B1_A04_MR	g3171159	BLASTN	615	1e-20	66	Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence [Homo sapiens]
9605	GM_149_B1_A08_MR	g2801682	BLASTN	676	5e-24	81	Glycine max telomere-associated sequence STAS11
9606	GM_149_B1_A09_MR	g3600062	BLASTN	398	6e-11	68	Arabidopsis thaliana BAC T25C13
9607	GM_149_B1_B02_MR	g3645899	BLASTX	455	3e-41	61	(U68408) 5' end not determined experimentally [Zea mays]
9608	GM_149_B1_B08_MR	g1666236	BLASTX	149	2e-11	31	(U76261) unknown [Hordeum vulgare]
9609	GM_149_B1_C06_MR	g1944188	BLASTN	388	9e-11	72	Soybean DNA for nodulin 35, partial cds
9610	GM_149_B1_C11_MR	g2160165	BLASTX	246	6e-19	45	(AC000132) F21M12.11 gene product [Arabidopsis thaliana]
9611	GM_149_B1_E06_MR	g3695401	BLASTX	170	1e-11	43	(AF096373) No definition line found [Arabidopsis thaliana]
9612	GM_149_B1_E09_MR	g18559	BLASTN	968	7e-37	73	G.max gene for catalase
9613	GM_149_B1_E10_MR	g3142303	BLASTX	498	1e-45	68	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb I.49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9614	GIM_149_B1_E11_MR	g1769898	BLASTX	388	9e-35	71	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9615	GIM_149_B1_E12_MR	g1769898	BLASTX	425	5e-39	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9616	GIM_149_B1_F02_MR	g507910	BLASTN	553	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9617	GIM_149_B1_F03_MR	g1769898	BLASTX	408	5e-37	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9618	GIM_149_B1_F12_MR	g3845197	BLASTN	445	4e-13	64	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
9619	GIM_149_B1_G02_MR	g18559	BLASTN	406	2e-11	72	G. max gene for catalase
9620	GIM_149_B1_G03_MR	g2129618	BLASTX	254	8e-20	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9621	GIM_149_B1_G05_MR	g3777527	BLASTX	156	1e-14	44	(AF053008) gag-pol polyprotein [Glycine max]
9622	GIM_149_B1_H02_MR	g280492	BLASTX	199	7e-14	44	pol polyprotein homolog - fungus (Cladosporium fulvum) transposon CFT-1 (fragment) gi 2564 (Z11866) Reverse Transcriptase [Cladosporium fulvum]
9623	GIM_149_B1_H03_MR	g2055374	BLASTX	136	1e-19	60	(U29095) serine-threonine protein kinase [Triticum aestivum]
9624	GIM_149_B1_H09_MR	g3687234	BLASTX	172	6e-11	47	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
9625	GIM_153_A2_A05_MR	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
9626	GIM_153_A2_A05_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9627	GIM_153_A2_A06_T7	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9628	GIM_153_A2_A08_T7	g1769898	BLASTX	313	2e-26	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9629	GIM_153_A2_A11_MR	g4140712	BLASTX	148	8e-10	52	(AF110183) putative integrase [Oryza sativa]
9630	GIM_153_A2_A12_MR	g2921625	BLASTN	498	2e-15	75	Lupinus luteus leghemoglobin (Lb1) gene, complete cds
9631	GIM_153_A2_B01_MR	g3645899	BLASTX	253	3e-24	63	(U68408) 5' end not determined experimentally [Zea mays]
9632	GIM_153_A2_B03_T7	g3645899	BLASTX	174	1e-15	37	(U68408) 5' end not determined experimentally [Zea mays]
9633	GIM_153_A2_B04_MR	g3142328	BLASTN	1791	2e-74	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9634	GIM_153_A2_B04_T7	g3097320	BLASTN	437	9e-13	67	Glycine max gene for Bd 30K, complete cds
9635	GIM_153_A2_B06_T7	g2982550	BLASTN	370	1e-09	63	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-65, complete sequence [Plasmodium falciparum]
9636	GIM_153_A2_B10_T7	g3097320	BLASTN	1170	6e-46	81	Glycine max gene for Bd 30K, complete cds
9637	GIM_153_A2_C01_MR	g3142328	BLASTN	1847	5e-77	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9638	GIM_153_A2_C04_MR	g18737	BLASTN	411	1e-11	73	Glycine max RPRP3 gene for repetitive proline-rich protein 3
9639	GIM_153_A2_D02_MR	g3142328	BLASTN	1029	1e-39	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9640	GM_153_A2_D03_MR	g2656024	BLASTN	360	3e-09	63	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6
9641	GM_153_A2_D03_T7	g3777527	BLASTX	152	3e-18	57	(AF053008) gag-pol polyprotein [Glycine max]
9642	GM_153_A2_D05_MR	g4063760	BLASTX	208	1e-14	48	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9643	GM_153_A2_E02_MR	g2492782	BLASTX	102	2e-09	78	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) gi 504489 (L27992) alpha-galactosidase [Coffea arabica]
9644	GM_153_A2_E03_MR	g2654095	BLASTX	106	5e-09	80	(AF034210) aspartate aminotransferase cytosolic isozyme AAT2 [Glycine max]
9645	GM_153_A2_E05_T7	g1480927	BLASTN	721	7e-26	82	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
9646	GM_153_A2_E07_T7	g3645899	BLASTX	292	9e-24	53	(U68408) 5' end not determined experimentally [Zea mays]
9647	GM_153_A2_E10_MR	g3097320	BLASTN	560	3e-18	70	Glycine max gene for Bd 30K, complete cds
9648	GM_153_A2_F01_T7	g2522226	BLASTN	507	5e-16	64	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
9649	GM_153_A2_F04_T7	g166884	BLASTN	466	8e-15	77	A.thaliana telomeric DNA. >gi 589934 gb I07744 Sequence 1 from Patent EP 0338266
9650	GM_153_A2_F05_MR	g1769898	BLASTX	331	2e-28	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9651	GM_153_A2_F05_T7	g1167523	BLASTX	308	3e-25	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
9652	GM_153_A2_F06_T7	g2245104	BLASTX	311	1e-25	47	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
9653	GM_153_A2_F07_T7	g2129618	BLASTX	180	7e-12	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9654	GM_153_A2_F12_T7	g507910	BLASTN	385	9e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9655	GM_153_A2_G05_MR	g2522228	BLASTX	362	8e-42	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
9656	GM_153_A2_G08_T7	g3645899	BLASTX	170	9e-11	42	(U68408) 5' end not determined experimentally [Zea mays]
9657	GM_153_A2_G12_T7	g1040717	BLASTN	498	2e-16	65	D.polychroa microsatellite sequence (clone Dp ch1 F3)
9658	GM_153_B1_A06_T7	g2129618	BLASTX	180	7e-12	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9659	GM_153_B1_A08_MR	g3097320	BLASTN	416	8e-12	72	Glycine max gene for Bd 30K, complete cds
9660	GM_153_B1_A08_T7	g3894099	BLASTX	187	7e-24	90	(AJ012750) MCM3 protein [Pisum sativum]
9661	GM_153_B1_B02_MR	g3777527	BLASTX	571	3e-53	94	(AF053008) gag-pol polyprotein [Glycine max]
9662	GM_153_B1_B02_T7	g507910	BLASTN	386	8e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9663	GM_153_B1_B04_MR	g4038056	BLASTX	378	4e-33	50	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9664	G1M_153_B1_B05_MR	g3193290	BLASTX	208	2e-16	55	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabidopsis]
9665	G1M_153_B1_C01_T7	g3097320	BLASTN	393	9e-11	68	Glycine max gene for Bd 30K, complete cds
9666	G1M_153_B1_C04_MR	g3645899	BLASTX	251	2e-22	52	(U68408) 5' end not determined experimentally [Zea mays]
9667	G1M_153_B1_C06_MR	g1550814	BLASTX	163	7e-13	96	(Y07959) 60S acidic ribosomal protein P0 [Zea mays]
9668	G1M_153_B1_C09_MR	g4063760	BLASTX	184	3e-13	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9669	G1M_153_B1_D01_T7	g2129618	BLASTX	257	4e-20	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9670	G1M_153_B1_D04_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence
9671	G1M_153_B1_D04_T7	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence
9672	G1M_153_B1_D09_T7	g1707938	BLASTX	202	4e-30	95	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) gi 312721 (X73365) glucose-1-phosphate adenylyltransferase [Arabidopsis thaliana]
9673	G1M_153_B1_D11_T7	g18559	BLASTN	618	6e-21	75	G.max gene for catalase
9674	G1M_153_B1_E04_MR	g99730	BLASTX	148	7e-09	44	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Tal-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
9675	G1M_153_B1_E06_T7	g2980795	BLASTX	94	5e-10	78	(AF022197) putative protein [Arabidopsis thaliana]
9676	G1M_153_B1_E07_T7	g3097320	BLASTN	471	3e-14	76	Glycine max gene for Bd 30K, complete cds
9677	G1M_153_B1_E09_MR	g18559	BLASTN	795	5e-29	72	G.max gene for catalase
9678	G1M_153_B1_E11_MR	g541825	BLASTX	136	4e-18	86	protein kinase - spinach gi 457711 (Z30332) protein kinase [Spinacia oleracea]
9679	G1M_153_B1_F01_T7	g507910	BLASTN	444	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence
9680	G1M_153_B1_F10_MR	g100484	BLASTX	336	8e-29	58	hypothetical protein - garden snapdragon
9681	G1M_153_B1_G06_T7	g2522230	BLASTX	263	6e-22	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9682	G1M_153_B1_G12_T7	g2443320	BLASTX	342	6e-29	57	(D85597) polyprotein [Oryza australiensis]
9683	G1M_153_B1_H02_T7	g2443320	BLASTX	301	1e-24	50	(D85597) polyprotein [Oryza australiensis]
9684	G1M_153_B1_H03_T7	g507910	BLASTN	593	3e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence
9685	G1M_153_B1_H09_MR	g2982540	BLASTN	375	7e-10	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-30, complete sequence [Plasmodium falciparum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9686	GM_153_B1_H11_T7	g1370140	BLASTX	215	6e-17	67	(X98308) myb-related transcription factor [<i>Lycopersicon esculentum</i>]
9687	GM_153_B1_H12_T7	g100484	BLASTX	341	2e-29	56	hypothetical protein - garden snapdragon
9688	GM_153_B2_A01_T7	g3738114	BLASTN	377	5e-10	60	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
9689	GM_153_B2_A02_T7	g3386534	BLASTX	498	6e-62	59	(AF078934) mariner transposase [Glycine max]
9690	GM_153_B2_A03_MR	g1769897	BLASTX	373	1e-33	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9691	GM_153_B2_A03_T7	g2522227	BLASTX	205	7e-16	47	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9692	GM_153_B2_A04_MR	g4063756	BLASTN	630	2e-21	67	Arabidopsis thaliana chromosome II BAC T918 genomic sequence, complete sequence [Arabidopsis thaliana]
9693	GM_153_B2_A05_T7	g3367515	BLASTX	299	8e-26	78	(AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
9694	GM_153_B2_A06_T7	g2443320	BLASTX	317	1e-37	48	(D85597) polyprotein [Oryza australiensis]
9695	GM_153_B2_A07_MR	g2522227	BLASTX	192	2e-14	42	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9696	GM_153_B2_A08_MR	g18559	BLASTN	394	8e-11	71	Gi max gene for catalase
9697	GM_153_B2_A09_T7	g3142379	BLASTX	268	4e-22	48	(AF053008) envelope-like [Glycine max]
9698	GM_153_B2_B01_MR	g2316016	BLASTX	550	5e-51	60	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
9699	GM_153_B2_B03_MR	g3845197	BLASTN	544	2e-17	63	Plasmodium falci-parum chromosome 2, section 35 of 73 of the complete sequence
9700	GM_153_B2_B11_T7	g3097320	BLASTN	376	5e-10	74	Glycine max gene for Bd 30K, complete cds
9701	GM_153_B2_C01_T7	g3599418	BLASTN	533	4e-17	67	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9702	GM_153_B2_C04_MR	g1769899	BLASTX	248	2e-20	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9703	GM_153_B2_C06_MR	g3281870	BLASTX	297	3e-25	59	(AL031004) putative protein [Arabidopsis thaliana]
9704	GM_153_B2_C08_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
9705	GM_153_B2_C08_T7	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9706	GM_153_B2_C09_MR	g1769899	BLASTX	333	2e-29	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9707	GM_153_B2_C09_T7	g4063760	BLASTX	186	4e-19	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9708	GM_153_B2_C10_T7	g3273127	BLASTN	385	2e-10	62	Plasmodium falci-parum DNA *** SEQUENCING IN PROGRESS *** from contig 4-54, complete sequence [Plasmodium falci-parum]
9709	GM_153_B2_C12_MR	g3097320	BLASTN	645	4e-22	81	Glycine max gene for Bd 30K, complete cds
9710	GM_153_B2_D01_T7	g99922	BLASTX	876	6e-87	87	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
9711	GM_153_B2_D03_MR	g4063760	BLASTX	158	2e-09	31	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9712	GM_153_B2_D03_T7	g2791289	BLASTX	254	1e-19	35	(AJ000387) protease [Drosophila melanogaster]
9713	GM_153_B2_D04_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9714	GM_153_B2_D05_MR	g3283026	BLASTX	260	1e-20	38	putative transposase [Arabidopsis thaliana]
9715	GM_153_B2_D07_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9716	GM_153_B2_E02_T7	g3201682	BLASTX	451	2e-44	64	(AF060942) extra-large G-protein [Arabidopsis thaliana]
9717	GM_153_B2_E05_MR	g1666236	BLASTX	209	4e-16	32	(U76261) unknown [Hordeum vulgare]
9718	GM_153_B2_E05_T7	g3142328	BLASTN	2544	1e-109	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AB007466) reverse transcriptase-like protein [Vicia faba]
9719	GM_153_B2_E11_MR	g2522228	BLASTX	655	2e-63	72	(AC002330) putative zinc finger protein [Arabidopsis thaliana]
9720	GM_153_B2_E12_MR	g3892045	BLASTX	123	2e-09	80	(AB007466) reverse transcriptase-like protein [Vicia faba]
9721	GM_153_B2_F01_MR	g2522228	BLASTX	224	2e-17	64	Glycine max BSR-101 satellite SB92 genomic sequence.
9722	GM_153_B2_F02_T7	g507910	BLASTN	570	4e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9723	GM_153_B2_F06_T7	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
9724	GM_153_B2_F07_MR	g99721	BLASTX	153	1e-21	45	retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Tal-3 gi 16534 (X13291) polyprotein [Arabidopsis thaliana]
9725	GM_153_B2_F08_MR	g2072628	BLASTX	126	1e-14	65	(Y12641) superoxide dismutase [Arabidopsis thaliana]
9726	GM_153_B2_F09_T7	g1480927	BLASTN	352	5e-09	85	Glycine max cdc2 protein kinase (cdc2(1)) nonprocessed pseudogene
9727	GM_153_B2_F11_MR	g3152600	BLASTX	320	5e-28	59	(AC002986) Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb Z75105. ESTs gb H37409, gb AA395290, and gb T43907 come from this gene. [Arabidopsis thaliana]
9728	GM_153_B2_F11_T7	g4038056	BLASTX	208	9e-27	47	(AC005897) putative transposon [Arabidopsis thaliana]
9729	GM_153_B2_F12_T7	g100484	BLASTX	377	3e-33	62	hypothetical protein - garden snapdragon
9730	GM_153_B2_G02_MR	g3142328	BLASTN	1516	7e-62	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9731	GM_153_B2_G03_MR	g3810596	BLASTX	299	1e-24	43	Glycine max gene for Bd 30K, complete cds
9732	GM_153_B2_G03_T7	g3097320	BLASTN	437	9e-13	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9733	GM_153_B2_G05_MR	g505129	BLASTN	378	4e-10	60	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9734	GM_153_B2_G07_MR	g3142328	BLASTN	2124	8e-90	96	Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence [Homo sapiens]
9735	GM_153_B2_G09_T7	g3135962	BLASTN	353	7e-09	59	(AC005897) hypothetical protein [Arabidopsis thaliana]
9736	GM_153_B2_G10_T7	g4038057	BLASTX	174	2e-11	36	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9737	GM_153_B2_G11_MR	g3142328	BLASTN	608	1e-20	68	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9738	GM_153_B2_G12_MR	g13774	BLASTN	302	3e-10	61	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1
9739	GM_153_B2_G12_T7	g3283026	BLASTX	207	6e-15	41	putative transposase [Arabidopsis thaliana]
9740	GM_153_B2_H02_T7	g3097320	BLASTN	1010	1e-38	81	Glycine max gene for Bd 30K, complete cds
9741	GM_153_B2_H06_T7	g3097320	BLASTN	490	4e-15	71	Glycine max gene for Bd 30K, complete cds
9742	GM_153_B2_H11_T7	g3777527	BLASTX	842	3e-82	94	(AF053008) gag-pol polyprotein [Glycine max]
9743	GM_153_B2_H12_MR	g4038056	BLASTX	303	4e-27	46	(AC005897) putative transposon [Arabidopsis thaliana]
9744	GM_154_A1_A02_MR	g3914006	BLASTX	146	3e-15	70	MITOCHONDRIAL LON PROTEASE HOMOLOG 2
9745	GM_154_A1_A02_T7	g4049647	BLASTN	386	2e-10	62	PRECURSOR >gi 1816588 (U85495) LON2 [Zea mays]
9746	GM_154_A1_A05_T7	g507910	BLASTN	563	8e-19	80	Melanoplus sanguinipes entomopoxvirus, complete genome
9747	GM_154_A1_A09_T7	g13619	BLASTN	339	6e-09	63	Glycine max BSR-101 satellite SB92 genomic sequence.
9748	GM_154_A1_A12_T7	g3319372	BLASTX	189	1e-12	37	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL) (AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
9749	GM_154_A1_B03_MR	g507910	BLASTN	621	2e-21	86	Glycine max BSR-101 satellite SB92 genomic sequence.
9750	GM_154_A1_B03_T7	g507910	BLASTN	559	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9751	GM_154_A1_B04_T7	g100484	BLASTX	359	3e-31	61	hypothetical protein - garden snapdragon
9752	GM_154_A1_B10_T7	g3097320	BLASTN	480	1e-14	71	Glycine max gene for Bd 30K, complete cds
9753	GM_154_A1_B12_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9754	GM_154_A1_C01_MR	g3777527	BLASTX	576	2e-54	96	(AF053008) gag-pol polyprotein [Glycine max]
9755	GM_154_A1_C01_T7	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
9756	GM_154_A1_C03_T7	g507910	BLASTN	520	7e-17	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9757	GM_154_A1_C05_MR	g18559	BLASTN	1055	8e-41	77	G.max gene for catalase
9758	GM_154_A1_C08_MR	g905361	BLASTX	428	3e-39	95	(U22103) gag-protease polyprotein [Glycine max]
9759	GM_154_A1_C10_T7	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9760	GM_154_A1_C11_MR	g100484	BLASTX	196	2e-18	57	hypothetical protein - garden snapdragon
9761	GM_154_A1_D06_T7	g2522228	BLASTX	274	1e-28	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
9762	GM_154_A1_D09_MR	g3426334	BLASTN	398	5e-11	61	Pisum sativum pectin methylesterase (repmel) gene, complete cds
9763	GM_154_A1_D11_T7	g3660471	BLASTX	213	1e-15	88	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq No.	ClonID	NCBI gi	Method	Score	P-value	% Ident	Description
9764	GM_154_A1_F07_T7	g505129	BLASTN	364	2e-09	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9765	GM_154_A1_F09_T7	g1778843	BLASTN	424	3e-12	66	Dictyostelium discoideum LimA (limA) mRNA, partial cds
9766	GM_154_A1_F11_MR	g18559	BLASTN	767	9e-28	78	G.max gene for catalase
9767	GM_154_A1_F11_T7	g2497540	BLASTX	194	1e-19	57	PYRUVATE KINASE, CHLOROPLAST ISOZYME G
9768	GM_154_A1_F02_T7	g3097320	BLASTN	514	3e-16	79	Glycine max gene for Bd 30K, complete cds
9769	GM_154_A1_F05_T7	g2244960	BLASTX	337	8e-30	44	(Z97340) similarity to copia-like retrotransposon [Arabidopsis thaliana]
9770	GM_154_A1_F07_T7	g3097320	BLASTN	614	9e-21	80	Glycine max gene for Bd 30K, complete cds
9771	GM_154_A1_F09_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9772	GM_154_A1_F09_T7	g507910	BLASTN	388	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9773	GM_154_A1_F12_T7	g170080	BLASTN	655	1e-22	90	Soybean seed lectin gene transposable element tgm1.
9774	GM_154_A1_G01_MR	g2414681	BLASTX	156	9e-10	90	(Z99174) cysteine proteinase precursor [Vicia narbonensis]
9775	GM_154_A1_G02_T7	g3777527	BLASTX	630	1e-61	96	(AF053008) gag-pol polyprotein [Glycine max]
9776	GM_154_A1_G04_MR	g2129618	BLASTX	153	5e-09	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9777	GM_154_A1_G06_MR	g3694834	BLASTN	448	3e-13	69	Glycine max alcohol dehydrogenase Adh-1 gene, partial cds
9778	GM_154_A1_G07_T7	g1488267	BLASTX	151	2e-21	66	(U57412) low affinity calcium antiporter CAX2 [Arabidopsis thaliana]
9779	GM_154_A1_G09_MR	g2688828	BLASTX	151	1e-09	72	(U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]
9780	GM_154_A1_G12_MR	g507910	BLASTN	509	2e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9781	GM_154_A1_G12_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9782	GM_154_A1_H02_T7	g3461846	BLASTX	381	4e-33	55	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
9783	GM_154_A1_H04_T7	g507910	BLASTN	594	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9784	GM_154_A1_H05_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9785	GM_154_A1_H08_MR	g3142328	BLASTN	1120	8e-44	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans])
9786	GM_154_A1_H09_MR	g2429543	BLASTX	200	7e-14	42	(D85597) polyprotein [Oryza australiensis]
9787	GM_154_A1_H10_T7	g2443320	BLASTX	156	4e-09	35	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
9788	GM_154_A1_H12_T7	g1272349	BLASTX	188	3e-13	53	(AF053008) envelope-like [Glycine max]
9789	GM_154_B2_A02_MR	g3142379	BLASTX	258	5e-21	61	(AC005561) putative POI.3 protein [Arabidopsis thaliana]
9790	GM_154_B2_A04_MR	g4063760	BLASTX	358	2e-33	77	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9791	G1M_154_B2_A06_MR	g25222228	BLASTX	151	2e-09	30	(AB007466) reverse transcriptase-like protein [Vicia faba]
9792	G1M_154_B2_A09_MR	g1749831	BLASTX	153	4e-09	60	(Z56279) beta-xylo-glucosidase [Thermoanaerobacter brockii]
9793	G1M_154_B2_A09_T7	g2656031	BLASTN	345	8e-10	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone; MXC20
9794	G1M_154_B2_B03_T7	g629693	BLASTX	155	8e-10	43	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
9795	G1M_154_B2_B04_T7	g4160362	BLASTN	275	9e-16	68	Saccharomyces cerevisiae complete mitochondrial genome
9796	G1M_154_B2_B06_MR	g3777527	BLASTX	562	3e-52	88	(AF053008) gag-pol polypeptide [Glycine max]
9797	G1M_154_B2_B12_MR	g25222228	BLASTX	329	6e-29	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
9798	G1M_154_B2_C04_MR	g3650039	BLASTX	200	3e-14	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
9799	G1M_154_B2_C04_T7	g33874213	BLASTX	154	8e-11	37	(Z83217) Similarity to Drosophila White protein (SW:WHIT_DROME); cDNA EST EMBL: T01609 comes from this gene; cDNA EST EMBL: D67987 comes from this gene; cDNA EST EMBL: D34570 comes from this gene; cDNA EST EMBL: D32839 comes from...
9800	G1M_154_B2_C06_T7	g2995405	BLASTX	367	6e-32	56	(Y12432) polyprotein [Ananas comosus]
9801	G1M_154_B2_D02_MR	g507910	BLASTN	584	9e-20	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9802	G1M_154_B2_D04_T7	g3097320	BLASTN	437	9e-13	78	Glycine max gene for Bd 30K, complete cds
9803	G1M_154_B2_D06_MR	g2995405	BLASTX	362	2e-31	48	(Y12432) polyprotein [Ananas comosus]
9804	G1M_154_B2_D12_T7	g18559	BLASTN	719	1e-25	74	G max gene for catalase
9805	G1M_154_B2_F01_MR	g3097320	BLASTN	376	5e-10	74	Glycine max gene for Bd 30K, complete cds
9806	G1M_154_B2_F02_T7	g3097320	BLASTN	416	8e-12	77	Glycine max gene for Bd 30K, complete cds
9807	G1M_154_B2_F03_T7	g4063770	BLASTX	226	7e-17	39	(AB004906) transposase [Ipomoea purpurea]
9808	G1M_154_B2_F04_MR	g4063760	BLASTX	253	2e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9809	G1M_154_B2_F07_MR	g18559	BLASTN	358	3e-09	63	G max gene for catalase
9810	G1M_154_B2_F01_MR	g1666236	BLASTX	186	2e-13	31	(U76261) unknown [Hordeum vulgare]
9811	G1M_154_B2_F04_T7	g3645899	BLASTX	310	1e-25	51	(U68408) 5' end not determined experimentally [Zea mays]
9812	G1M_154_B2_F10_MR	g18559	BLASTN	355	5e-09	65	G max gene for catalase
9813	G1M_154_B2_F12_MR	g4063760	BLASTX	211	4e-15	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9814	G1M_154_B2_G01_T7	g1142701	BLASTN	433	1e-30	75	Glycine max satellite STR120-A.3.
9815	G1M_154_B2_G07_T7	g3426334	BLASTN	541	2e-17	60	Pisum sativum pectin methylesterase (repm1) gene, complete cds
9816	G1M_154_B2_G11_T7	g3142328	BLASTN	610	1e-20	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9817	GIM_154_B2_H04_T7	g505129	BLASTN	381	3e-10	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9818	GIM_154_B2_H05_T7	g18559	BLASTN	612	1e-20	69	G.max gene for catalase
9819	GIM_154_B2_H06_T7	g3645899	BLASTX	418	3e-37	55	(U68408) 5' end not determined experimentally [Zea mays]
9820	GIM_154_B2_H07_MR	g507910	BLASTN	344	6e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
9821	GIM_154_B2_H09_T7	g1785744	BLASTX	143	9e-16	44	(Y08502) orf158 [Arabidopsis thaliana]
9822	GIM_154_B2_H10_MR	g4063760	BLASTX	298	3e-24	47	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9823	GIM_154_B2_H10_T7	g3319345	BLASTX	189	6e-15	36	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
9824	GIM_154_B2_H11_T7	g3777526	BLASTN	414	1e-11	83	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
9825	GIM_155_A1_A03_T7	g2129618	BLASTX	200	5e-14	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9826	GIM_155_A1_A05_MR	g3650035	BLASTX	221	4e-16	40	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
9827	GIM_155_A1_A05_T7	g2443320	BLASTX	248	6e-19	40	(D85597) polyprotein [Oryza australiensis]
9828	GIM_155_A1_A07_MR	g507910	BLASTN	590	5e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9829	GIM_155_A1_A07_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9830	GIM_155_A1_A08_T7	g3033389	BLASTX	157	2e-09	30	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
9831	GIM_155_A1_A11_MR	g4006838	BLASTN	409	2e-11	65	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens]
9832	GIM_155_A1_B03_T7	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9833	GIM_155_A1_B09_MR	g1769898	BLASTX	152	2e-20	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9834	GIM_155_A1_B11_MR	g1666236	BLASTX	182	6e-13	30	(U76261) unknown [Hordeum vulgare]
9835	GIM_155_A1_B12_MR	g3777527	BLASTX	249	6e-19	47	(AF053008) gag-pol polyprotein [Glycine max]
9836	GIM_155_A1_C01_T7	g3142328	BLASTN	1258	4e-50	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (U22103) gag-protease polyprotein [Glycine max]
9837	GIM_155_A1_C03_T7	g905361	BLASTX	203	1e-14	35	Glycine max BSR-101 satellite SB92 genomic sequence.
9838	GIM_155_A1_C06_MR	g507910	BLASTN	410	6e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9839	GIM_155_A1_C06_T7	g507910	BLASTN	380	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9840	GIM_155_A1_D01_T7	g439231	BLASTN	357	7e-10	60	Human DNA-unwinding elements sequence
9841	GIM_155_A1_D08_MR	g2961349	BLASTX	162	1e-18	39	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
9842	GIM_155_A1_D08_T7	g4115365	BLASTX	227	1e-16	47	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
9843	GIM_155_A1_D10_T7	g12226168	BLASTX	108	1e-10	32	(M32662) ORF B (bases 1850-5560) first start codon at 2306 [Autographa californica nucleopolyhedrovirus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9844	GM_155_A1_E01_MR	g3097320	BLASTN	476	2e-14	75	Glycine max gene for Bd 30K, complete cds
9845	GM_155_A1_E09_T7	g4063760	BLASTX	303	7e-25	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9846	GM_155_A1_F01_MR	g3746069	BLASTX	178	1e-16	29	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
9847	GM_155_A1_F03_MR	g18559	BLASTN	406	2e-11	69	G-max gene for catalase
9848	GM_155_A1_F04_MR	g1769898	BLASTX	400	4e-36	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9849	GM_155_A1_F07_MR	g3097320	BLASTN	464	6e-14	73	Glycine max gene for Bd 30K, complete cds
9850	GM_155_A1_F12_MR	g2262135	BLASTN	432	6e-13	74	Arabidopsis thaliana BAC T10P1, complete sequence [Arabidopsis thaliana]
9851	GM_155_A1_G04_T7	g1055224	BLASTX	152	3e-10	42	(U20977) cellular nucleic acid binding protein [Xenopus laevis]
9852	GM_155_A1_G05_T7	g3142328	BLASTN	842	4e-31	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9853	GM_155_A1_G07_MR	g18683	BLASTN	486	4e-15	86	G-max N-20t gene
9854	GM_155_A1_G09_MR	g22564044	BLASTN	355	5e-09	75	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]
9855	GM_155_A1_G09_T7	g1431738	BLASTN	637	5e-22	93	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
9856	GM_155_A1_G12_MR	g3142328	BLASTN	1612	3e-66	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC004705) hypothetical protein [Arabidopsis thaliana]
9857	GM_155_A1_H02_MR	g3252807	BLASTX	485	2e-45	67	Glycine max BSR-101 satellite SB92 genomic sequence.
9858	GM_155_A1_H03_MR	g507910	BLASTN	340	9e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
9859	GM_155_A1_H03_T7	g507910	BLASTN	416	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9860	GM_155_A1_H04_MR	g4038056	BLASTX	272	9e-22	43	(AC005897) putative transposon [Arabidopsis thaliana]
9861	GM_155_A1_H04_T7	g1935006	BLASTX	152	5e-15	46	(Y12320) starch branching enzyme 1 [Triticum aestivum]
9862	GM_155_A1_H05_MR	g130582	BLASTX	98	1e-09	37	RE:TRIVIRUS-RELATED POL POLYPYRROLINE (PROTEASE); REVERSE TRANSCRIPTASE; ENDONUCLEASE
9863	GM_155_A1_H06_MR	g3695387	BLASTX	138	4e-09	42	(TRANSPONSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9864	GM_155_A1_H09_MR	g3645899	BLASTX	271	1e-21	60	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
9865	GM_155_A2_A03_MR	g507910	BLASTN	423	2e-12	73	(U68408) 5' end not determined experimentally [Zea mays]
9866	GM_155_A2_A03_T7	g507910	BLASTN	564	7e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9867	GM_155_A2_A04_T7	g3549639	BLASTX	127	2e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence. (AJ005194) receiver-like protein 3 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9868	GIM_155_A2_A12_T7	g3142328	BLASTN	409	2e-11	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9869	GIM_155_A2_B01_T7	g497835	BLASTN	375	3e-13	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9870	GIM_155_A2_B02_T7	g4063760	BLASTX	460	1e-41	67	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9871	GIM_155_A2_B06_MR	g4092470	BLASTN	719	2e-25	67	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
9872	GIM_155_A2_B07_T7	g1167523	BLASTX	351	6e-30	58	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
9873	GIM_155_A2_B09_T7	g3947433	BLASTN	352	7e-09	65	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
9874	GIM_155_A2_B10_MR	g2335097	BLASTX	281	1e-22	47	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]
9875	GIM_155_A2_B11_T7	g2244802	BLASTX	223	7e-18	47	(Z97336) retrovirus-related polypeptide homolog [Arabidopsis thaliana]
9876	GIM_155_A2_C01_MR	g1142702	BLASTN	256	1e-12	72	Glycine max satellite STR120-A.4.
9877	GIM_155_A2_C01_T7	g4063770	BLASTX	219	4e-16	40	(AB004906) transposase [Ipomoea purpurea]
9878	GIM_155_A2_C06_MR	g507910	BLASTN	422	2e-12	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9879	GIM_155_A2_C06_T7	g4063760	BLASTX	236	1e-17	51	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9880	GIM_155_A2_D01_MR	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
9881	GIM_155_A2_D01_T7	g4063760	BLASTX	422	1e-37	63	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9882	GIM_155_A2_D04_MR	g3097320	BLASTN	368	1e-09	74	Glycine max gene for Bd 30K, complete cds
9883	GIM_155_A2_D07_MR	g3097320	BLASTN	613	1e-20	78	Glycine max gene for Bd 30K, complete cds
9884	GIM_155_A2_D09_MR	g99922	BLASTX	364	1e-32	69	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
9885	GIM_155_A2_D10_MR	g1865677	BLASTX	255	7e-20	77	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
9886	GIM_155_A2_D11_T7	g2808683	BLASTX	249	2e-19	46	(AJ002235) Cf-4 [Lycopersicon hirsutum]
9887	GIM_155_A2_D12_MR	g3599418	BLASTN	706	5e-25	83	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9888	GIM_155_A2_E06_MR	g905361	BLASTX	675	1e-65	93	(U22103) gag-protease polypeptide [Glycine max]
9889	GIM_155_A2_E07_T7	g4050011	BLASTN	411	1e-11	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
9890	GIM_155_A2_E09_MR	g905361	BLASTX	235	5e-18	42	(U22103) gag-protease polypeptide [Glycine max]
9891	GIM_155_A2_E10_T7	g3702732	BLASTN	687	5e-24	68	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]
9892	GIM_155_A2_E11_MR	g1769899	BLASTX	190	3e-14	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9893	GM_155_A2_F03_MR	g3063708	BLASTX	254	2e-19	48	(AL022537) putative protein [Arabidopsis thaliana]
9894	GM_155_A2_F05_MR	g3777527	BLASTX	634	5e-60	90	(AF053008) gag-pol polyprotein [Glycine max]
9895	GM_155_A2_F07_MR	g3695395	BLASTX	256	2e-20	45	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
9896	GM_155_A2_F08_MR	g2995405	BLASTX	406	4e-36	57	(Y12432) polyprotein [Ananas comosus]
9897	GM_155_A2_F11_MR	g4100321	BLASTX	207	4e-16	41	(U96642) A sunflower resistance gene homolog, partial cds [Helianthus annuus]
9898	GM_155_A2_F12_MR	g507910	BLASTN	495	9e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9899	GM_155_A2_F12_T7	g507910	BLASTN	417	3e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
9900	GM_155_A2_G06_MR	g421954	BLASTX	225	6e-17	44	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
9901	GM_155_A2_G07_MR	g3377855	BLASTX	248	2e-20	81	(AF076274) contains similarity to reverse transcriptase (Pfam: rvt hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC hmm, score: 14.43) [Arabidopsis thaliana]
9902	GM_155_A2_G08_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9903	GM_155_A2_G08_T7	g507910	BLASTN	394	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9904	GM_155_A2_G11_T7	g3142330	BLASTX	491	4e-46	93	(U96295) envelope-like [Glycine max]
9905	GM_155_A2_H02_MR	g2522227	BLASTX	211	2e-16	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9906	GM_155_A2_H03_T7	g3395443	BLASTX	207	2e-15	41	(AC004683) putative ammonium transporter, 3' partial [Arabidopsis thaliana]
9907	GM_155_A2_H05_T7	g4115357	BLASTX	293	9e-25	45	(AC005957) hypothetical protein [Arabidopsis thaliana]
9908	GM_155_A2_H06_T7	g4063760	BLASTX	305	4e-25	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9909	GM_155_A2_H07_MR	g282881	BLASTX	412	7e-37	67	receptor-like protein kinase precursor - Arabidopsis thaliana gi 166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
9910	GM_155_A2_H08_MR	g507910	BLASTN	405	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9911	GM_155_A2_H09_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9912	GM_155_B1_A02_T7	g18559	BLASTN	403	3e-11	70	G max gene for catalase
9913	GM_155_B1_A04_T7	g1666236	BLASTX	171	9e-12	30	(U76261) unknown [Hordeum vulgare]
9914	GM_155_B1_A06_MR	g1769898	BLASTX	395	2e-35	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9915	GM_155_B1_A08_T7	g4140712	BLASTX	188	2e-22	42	(AF110183) putative integrase [Oryza sativa]
9916	GM_155_B1_A12_MR	g1769898	BLASTX	358	2e-31	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9917	GM_155_B1_B01_T7	g3869063	BLASTN	393	1e-10	64	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17022, complete sequence [Arabidopsis thaliana]
9918	GM_155_B1_B03_MR	g4063760	BLASTX	349	9e-30	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9919	GM_155_B1_B04_T7	g1666236	BLASTX	169	1e-11	28	(U76261) unknown [Hordeum vulgare]
9920	GM_155_B1_B05_MR	g3142328	BLASTN	1124	5e-44	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza] (AC005561) putative POL3 protein [Arabidopsis thaliana] (AF053008) gag-pol polyprotein [Glycine max] (AB007466) reverse transcriptase-like protein [Vicia faba] (U22103) gag-protease polyprotein [Glycine max] (U76261) unknown [Hordeum vulgare]
9921	GM_155_B1_B09_T7	g1514643	BLASTX	167	3e-10	62	Glycine max gene for Bd 30K, complete cds
9922	GM_155_B1_C04_MR	g4063760	BLASTX	188	1e-12	39	Glycine max satellite STR120-A.3.
9923	GM_155_B1_C04_T7	g3777527	BLASTX	579	4e-54	95	Swietenia humilis DNA for simple tandem repeat (341bp)
9924	GM_155_B1_C05_MR	g2522228	BLASTX	409	2e-37	76	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
9925	GM_155_B1_C07_MR	g905361	BLASTX	250	1e-19	41	(AC003952) putative Tat-1-like reverse transcriptase [Arabidopsis thaliana]
9926	GM_155_B1_C11_MR	g1666236	BLASTX	168	2e-11	28	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9927	GM_155_B1_C12_T7	g3097320	BLASTN	462	7e-14	74	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9928	GM_155_B1_D02_MR	g1142701	BLASTN	245	5e-19	75	hypothetical protein - garden snapdragon
9929	GM_155_B1_D03_MR	g2275090	BLASTN	548	2e-18	77	(U68408) 5' end not determined experimentally [Zea mays]
9930	GM_155_B1_D04_MR	g629693	BLASTX	199	1e-14	34	hypothetical protein - garden snapdragon
9931	GM_155_B1_D07_MR	g2708743	BLASTX	255	1e-19	36	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
9932	GM_155_B1_D08_T7	g3142328	BLASTN	869	2e-32	92	Glycine max BSR-101 satellite SB92 genomic sequence.
9933	GM_155_B1_E01_T7	g4063756	BLASTN	562	2e-18	62	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
9934	GM_155_B1_E02_MR	g100484	BLASTX	268	2e-21	39	(U75225) reverse transcriptase [Gossypium barbadense]
9935	GM_155_B1_E02_T7	g3645899	BLASTX	192	7e-29	54	(AC002560) F21B7.20 [Arabidopsis thaliana]
9936	GM_155_B1_E05_MR	g100484	BLASTX	333	2e-28	53	Glycine max cv. Dare nodulin 26 gene fragment.
9937	GM_155_B1_E06_MR	g629693	BLASTX	160	2e-10	44	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence (AC005561) putative POL3 protein [Arabidopsis thaliana]
9938	GM_155_B1_E07_T7	g507910	BLASTN	738	1e-26	89	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
9939	GM_155_B1_E10_T7	g170605	BLASTN	485	3e-15	64	
9940	GM_155_B1_F02_MR	g1658435	BLASTX	143	3e-09	78	
9941	GM_155_B1_F04_MR	g2809251	BLASTX	129	1e-16	53	
9942	GM_155_B1_F06_MR	g170029	BLASTN	389	1e-10	80	
9943	GM_155_B1_F06_T7	g3142328	BLASTN	1923	2e-80	95	
9944	GM_155_B1_F07_T7	g4063760	BLASTX	414	1e-36	60	
9945	GM_155_B1_F09_T7	g421955	BLASTX	270	9e-23	48	

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
9946	GM_155_B1_F11_T7	g905361	BLASTX	185	1e-12	30	(U22103) gag-protease polypeptide [Glycine max]
9947	GM_155_B1_G01_T7	g3914056	BLASTX	111	6e-10	71	DNA MISMATCH REPAIR PROTEIN MSH2 >gi 2522362 (AF002706) MutS homolog 2 [Arabidopsis thaliana] >gi 2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana] >gi 2547236 (AF026549) DNA mismatch repair protein MSH2 [Arabidopsis thaliana]
9948	GM_155_B1_G06_MR	g507910	BLASTN	494	1e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9949	GM_155_B1_G06_T7	g507910	BLASTN	569	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9950	GM_155_B1_G12_MR	g342959	BLASTN	452	2e-14	62	parametrium species 4.51er mt dna dimer: replication init. region. clone 3.
9951	GM_155_B1_H02_T7	g905361	BLASTX	202	2e-14	33	(U22103) gag-protease polypeptide [Glycine max]
9952	GM_155_B1_H07_MR	g3549672	BLASTX	155	9e-10	88	(AL031394) putative protein [Arabidopsis thaliana]
9953	GM_155_B2_A04_MR	g3097320	BLASTN	1159	2e-45	75	Glycine max gene for Bd 30K, complete cds
9954	GM_155_B2_A06_MR	g3510347	BLASTN	460	1e-13	67	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSH1, complete sequence [Arabidopsis thaliana]
9955	GM_155_B2_A08_MR	g4063760	BLASTX	551	2e-51	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9956	GM_155_B2_A11_MR	g3645899	BLASTX	301	5e-30	49	(U68408) 5' end not determined experimentally [Zea mays]
9957	GM_155_B2_A11_T7	g1165321	BLASTN	452	2e-13	68	Glycine max extensin (SbHRGP3) gene, complete cds
9958	GM_155_B2_B02_T7	g3269288	BLASTX	419	2e-38	59	(AL030978) putative protein [Arabidopsis thaliana]
9959	GM_155_B2_B03_MR	g507910	BLASTN	539	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
9960	GM_155_B2_B05_T7	g4063756	BLASTN	589	1e-19	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9961	GM_155_B2_B07_MR	g1666236	BLASTX	179	1e-12	27	(U76261) unknown [Hordeum vulgare]
9962	GM_155_B2_B08_T7	g1370140	BLASTX	215	6e-17	66	(X98308) myb-related transcription factor [Lycopersicon esculentum]
9963	GM_155_B2_B09_MR	g4063760	BLASTX	242	1e-21	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9964	GM_155_B2_B11_T7	g3777527	BLASTX	614	8e-58	95	(AF053008) gag-pol polypeptide [Glycine max]
9965	GM_155_B2_C02_MR	g507910	BLASTN	603	1e-20	85	Glycine max BSR-101 satellite SB92 genomic sequence.
9966	GM_155_B2_C02_T7	g4063756	BLASTN	437	1e-12	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9967	GM_155_B2_C03_MR	g3097320	BLASTN	1217	4e-48	76	Glycine max gene for Bd 30K, complete cds
9968	GM_155_B2_C05_MR	g3097320	BLASTN	625	3e-21	72	Glycine max gene for Bd 30K, complete cds
9969	GM_155_B2_C07_T7	g2522228	BLASTX	244	1e-19	46	(AB007466) reverse transcriptase-like protein [Vicia faba]
9970	GM_155_B2_C09_MR	g4063760	BLASTX	280	2e-22	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9971	GM_155_B2_C10_MR	g3142328	BLASTN	783	7e-57	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9972	GM_155_B2_C11_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9973	GM_155_B2_C11_T7	g4063760	BLASTX	321	9e-27	63	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9974	GM_155_B2_D01_MR	g2522230	BLASTX	335	1e-29	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9975	GM_155_B2_D01_T7	g2522228	BLASTX	371	2e-33	57	(AB007466) reverse transcriptase-like protein [Vicia faba]
9976	GM_155_B2_D02_T7	g3777527	BLASTX	394	2e-34	93	(AF053008) gag-pol polyprotein [Glycine max]
9977	GM_155_B2_D04_MR	g3777527	BLASTX	307	4e-25	93	(AF053008) gag-pol polyprotein [Glycine max]
9978	GM_155_B2_D04_T7	g2194136	BLASTX	321	1e-26	61	(AC002062) Strong similarity to Zea mays retrotransposon
9979	GM_155_B2_D06_T7	g3850630	BLASTX	235	4e-21	73	Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
9980	GM_155_B2_E01_MR	g507910	BLASTN	347	4e-09	68	(AJ012581) cytochrome P450 [Cicer arietinum]
9981	GM_155_B2_E01_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9982	GM_155_B2_E06_MR	g2114242	BLASTN	358	4e-09	61	Glycine max BSR-101 satellite SB92 genomic sequence.
9983	GM_155_B2_E07_MR	g4063760	BLASTX	171	8e-11	40	Human (lambda) DNA for immunoglobulin light chain
9984	GM_155_B2_E09_T7	g2191197	BLASTX	232	2e-18	67	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9985	GM_155_B2_E12_T7	g905361	BLASTX	534	1e-50	98	(AF007271) contains similarity to Synechococcus PCC7942 chromosomal region used as basis of neutral siteII recombinational cloning vector (PID:g1174192) [Arabidopsis thaliana]
9986	GM_155_B2_F01_MR	g905361	BLASTX	216	6e-16	32	(U22103) gag-protease polyprotein [Glycine max]
9987	GM_155_B2_F02_T7	g1326016	BLASTX	344	3e-29	50	(U22103) gag-protease polyprotein [Glycine max]
9988	GM_155_B2_F03_T7	g507910	BLASTN	626	1e-21	85	TY3-2 orfB
9989	GM_155_B2_F04_MR	g3142328	BLASTN	821	3e-30	89	Glycine max BSR-101 satellite SB92 genomic sequence.
9990	GM_155_B2_F05_T7	g1514643	BLASTX	167	3e-10	62	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9991	GM_155_B2_F08_T7	g4063760	BLASTX	274	8e-22	57	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
9992	GM_155_B2_F09_MR	g3142328	BLASTN	723	9e-26	78	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
9993	GM_155_B2_F09_T7	g3645899	BLASTX	231	3e-17	51	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9994	GM_155_B2_G03_MR	g1769897	BLASTX	166	9e-22	64	(U68408) 5' end not determined experimentally [Zea mays]
9995	GM_155_B2_G08_MR	g3386606	BLASTX	198	5e-14	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9996	GM_155_B2_G09_T7	g507910	BLASTN	566	6e-19	83	(AC004665) putative beta-amylase [Arabidopsis thaliana]
9997	GM_155_B2_G11_MR	g3979928	BLASTN	485	7e-15	65	Glycine max BSR-101 satellite SB92 genomic sequence.
9998	GM_155_B2_G11_T7	g3777527	BLASTX	207	2e-14	48	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
9999	GM_155_B2_H06_T7	g2522228	BLASTX	440	2e-47	63	(AF053008) gag-pol polyprotein [Glycine max]
			BLASTX				(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10000	GM_155_B2_H07_MR	g629693	BLASTX	260	1e-21	59	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10001	GM_155_B2_H07_T7	g99755	BLASTX	311	2e-26	50	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
10002	GM_155_B2_H10_MR	g3097320	BLASTN	940	2e-35	76	Glycine max gene for Bd 30K, complete cds
10003	GM_156_B1_A05_T7	g2522228	BLASTX	415	4e-38	77	(AB007466) reverse transcriptase-like protein [Vicia faba]
10004	GM_156_B1_A08_T7	g4063760	BLASTX	172	7e-11	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10005	GM_156_B1_B02_T7	g505129	BLASTN	363	2e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10006	GM_156_B1_B04_T7	g3440796	BLASTN	388	2e-11	62	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
10007	GM_156_B1_B08_T7	g170080	BLASTN	454	1e-13	69	Soybean seed lectin gene transposable element tgm1.
10008	GM_156_B1_B11_MR	g4038056	BLASTX	168	2e-13	45	(AC005897) putative transposon [Arabidopsis thaliana]
10009	GM_156_B1_B12_MR	g2853076	BLASTX	159	1e-09	62	(AL021768) putative protein [Arabidopsis thaliana]
10010	GM_156_B1_B12_T7	g3283026	BLASTX	153	7e-11	35	putative transposase [Arabidopsis thaliana]
10011	GM_156_B1_C05_T7	g2244915	BLASTX	147	6e-17	35	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
10012	GM_156_B1_C06_T7	g1666236	BLASTX	205	1e-15	33	(U76261) unknown [Hordeum vulgare]
10013	GM_156_B1_C10_MR	g507910	BLASTN	343	7e-09	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10014	GM_156_B1_C12_MR	g3334667	BLASTX	267	9e-22	45	(Y10493) putative cytochrome P450 [Glycine max]
10015	GM_156_B1_C12_T7	g3334667	BLASTX	453	4e-42	65	(Y10493) putative cytochrome P450 [Glycine max]
10016	GM_156_B1_D03_MR	g2827516	BLASTX	226	1e-16	73	(AL021633) DNA topoisomerase like- protein [Arabidopsis thaliana]
10017	GM_156_B1_D04_T7	g840618	BLASTN	357	3e-09	62	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
10018	GM_156_B1_D06_MR	g3377848	BLASTX	240	3e-19	51	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
10019	GM_156_B1_D06_T7	g2316016	BLASTX	122	3e-09	45	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
10020	GM_156_B1_D07_MR	g2244915	BLASTX	168	1e-10	34	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
10021	GM_156_B1_E02_T7	g3142328	BLASTN	908	4e-34	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10022	GM_156_B1_E03_T7	g3142328	BLASTN	1040	4e-40	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10023	GM_156_B1_E04_MR	g3135252	BLASTX	152	2e-09	28	(AC003058) hypothetical protein [Arabidopsis thaliana] gi 3176720 (AC002392) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10024	G1M_156_B1_E05_MR	g3513745	BLASTX	235	2e-17	40	(AF080118) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
10025	G1M_156_B1_E08_T7	g1707657	BLASTX	375	7e-34	52	(Z71640) DnaI homologue [Pisum sativum]
10026	G1M_156_B1_E12_MR	g3695395	BLASTX	268	1e-21	37	(AF096372) contains similarity to reverse transcriptase (Pfam: Pf00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
10027	G1M_156_B1_F04_MR	g3810596	BLASTX	158	2e-09	30	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
10028	G1M_156_B1_F04_T7	g1769898	BLASTX	359	1e-31	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10029	G1M_156_B1_F06_T7	g421955	BLASTX	425	4e-39	61	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
10030	G1M_156_B1_F07_T7	g507910	BLASTN	570	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10031	G1M_156_B1_F08_MR	g3810596	BLASTX	169	1e-10	32	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
10032	G1M_156_B1_G02_T7	g3142328	BLASTN	1206	1e-47	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10033	G1M_156_B1_G03_MR	g1363492	BLASTX	178	2e-24	87	outer envelope membrane protein OEP75 precursor - garden pea gi 576507 (L36858) outer membrane protein [Pisum sativum] gi 633607 (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]
10034	G1M_156_B1_G09_MR	g3482913	BLASTX	122	8e-16	48	(AC003970) Similar to MtN21, gi 2598575, Megicigo truncatula nodulation induced gene [Arabidopsis thaliana]
10035	G1M_156_B1_G11_T7	g2522228	BLASTX	157	8e-21	87	(AB007466) reverse transcriptase-like protein [Vicia faba]
10036	G1M_156_B1_H01_MR	g3142328	BLASTN	938	2e-35	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10037	G1M_156_B1_H03_T7	g2129618	BLASTX	215	1e-15	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 8065335 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10038	G1M_156_B2_A03_MR	g1666236	BLASTX	294	3e-25	34	(U76261) unknown [Hordeum vulgare]
10039	G1M_156_B2_A08_MR	g3097320	BLASTN	1809	6e-75	82	Glycine max gene for Bd 30K, complete cds
10040	G1M_156_B2_A10_MR	g629693	BLASTX	322	2e-40	51	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10041	G1M_156_B2_C03_MR	g507910	BLASTN	465	2e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10042	G1M_156_B2_C07_MR	g2244807	BLASTX	260	7e-23	56	(Z97336) hypothetical protein [Arabidopsis thaliana]
10043	G1M_156_B2_C09_MR	g2462936	BLASTX	325	1e-31	48	(Y12321) open reading frame 2 [Brassica oleracea]
10044	G1M_156_B2_C10_MR	g2576326	BLASTN	393	9e-11	65	Phaseolus vulgaris tRNA-Pro (AGG), tRNA-Pro (UGG) genes
10045	G1M_156_B2_D11_MR	g1769897	BLASTX	189	3e-13	32	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10046	G1M_156_B2_D12_MR	g2315153	BLASTX	244	6e-28	75	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
10047	GM_156_B2_E05_MR	g881595	BLASTN	372	8e-10	64	Pisum sativum cytosolic glutamine synthetase (GS3B) gene, complete cds.
10048	GM_156_B2_E07_MR	g3097320	BLASTN	417	8e-12	72	Glycine max gene for Bd 30K, complete cds
10049	GM_156_B2_E08_MR	g4063760	BLASTX	265	4e-22	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10050	GM_156_B2_E10_MR	g2739003	BLASTN	681	3e-24	86	Glycine max cytochrome P450 monooxygenase CYP82C1p (CYP82C1) mRNA, complete cds
10051	GM_156_B2_E11_MR	g3097320	BLASTN	402	4e-11	64	Glycine max gene for Bd 30K, complete cds
10052	GM_156_B2_F01_MR	g4038056	BLASTX	262	3e-36	45	(AC005897) putative transposon [Arabidopsis thaliana]
10053	GM_156_B2_F09_MR	g629693	BLASTX	225	1e-17	52	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10054	GM_156_B2_G01_MR	g3599418	BLASTN	523	6e-31	79	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
10055	GM_156_B2_G06_MR	g905361	BLASTX	219	3e-16	29	(U22103) gag-protease polypeptide [Glycine max]
10056	GM_156_B2_G08_MR	g507910	BLASTN	444	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
10057	GM_156_B2_G09_MR	g3777527	BLASTX	231	2e-19	34	(AF053008) gag-pol polypeptide [Glycine max]
10058	GM_156_B2_H01_MR	g505129	BLASTN	425	3e-12	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10059	GM_156_B2_H06_MR	g505129	BLASTN	384	1e-15	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10060	GM_156_B2_H07_MR	g1142699	BLASTN	1339	3e-54	87	Glycine max satellite STR120-A.1.
10061	GM_157_A1_A02_MR	g3810595	BLASTX	292	1e-23	57	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
10062	GM_157_A1_A04_MR	g461987	BLASTX	583	6e-56	92	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) gi 82042 pir JS0719 translation elongation factor eEF-1 alpha chain - carrot gi 217913 gnl PID d1002697 (D12709) elongation factor 1-alpha [Daucus carota]
10063	GM_157_A1_A06_T7	g3452273	BLASTX	230	2e-26	83	(AF043110) phosphatidylinositol 4-kinase alpha [Daucus carota]
10064	GM_157_A1_A08_MR	g3097320	BLASTN	1007	1e-38	84	Glycine max gene for Bd 30K, complete cds
10065	GM_157_A1_A08_T7	g3319345	BLASTX	204	2e-14	39	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
10066	GM_157_A1_A09_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10067	GM_157_A1_A09_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10068	GM_157_A1_B04_MR	g3738114	BLASTN	441	7e-13	66	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
10069	GM_157_A1_B04_T7	g18559	BLASTN	890	3e-33	75	G max gene for catalase
10070	GM_157_A1_B10_MR	g2995405	BLASTX	313	4e-26	55	(Y12432) polypeptide [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
10071	GM_157_A1_B10_T7	g507910	BLASTN	684	3e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
10072	GM_157_A1_B11_T7	g4050011	BLASTN	361	3e-09	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
10073	GM_157_A1_C07_MR	g4063760	BLASTX	267	5e-21	54	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
10074	GM_157_A1_D01_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10075	GM_157_A1_D02_MR	g342964	BLASTN	346	2e-09	66	paramesium species 5.311 mt dna dimer: replication init. region.
10076	GM_157_A1_D02_T7	g2209031	BLASTX	128	1e-11	53	(AB001569) ORF of 1.56 kb [Daucus carota]
10077	GM_157_A1_D03_T7	g505129	BLASTN	424	3e-12	65	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
10078	GM_157_A1_D04_MR	g3097320	BLASTN	473	2e-14	70	Glycine max gene for Bd 30K, complete cds
10079	GM_157_A1_D06_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10080	GM_157_A1_D06_T7	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10081	GM_157_A1_D08_MR	g4063760	BLASTX	145	9e-18	52	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
10082	GM_157_A1_D09_T7	g3941729	BLASTN	365	2e-09	68	Homo sapiens chromosome 7 BAC clone F5, complete sequence [Homo sapiens]
10083	GM_157_A1_E03_MR	g507910	BLASTN	653	7e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
10084	GM_157_A1_E03_T7	g507910	BLASTN	616	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10085	GM_157_A1_E04_T7	g905361	BLASTX	230	2e-17	39	(U22103) gag-protease polypeptide [Glycine max]
10086	GM_157_A1_E05_MR	g2443320	BLASTX	256	9e-20	50	(D85597) polypeptide [Oryza australiensis]
10087	GM_157_A1_E07_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence
10088	GM_157_A1_E10_T7	g1769899	BLASTX	299	8e-26	77	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10089	GM_157_A1_E12_T7	g1785744	BLASTX	218	1e-20	62	(Y08502) orf158 [Arabidopsis thaliana]
10090	GM_157_A1_F03_MR	g4063760	BLASTX	436	5e-39	59	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
10091	GM_157_A1_F03_T7	g3097320	BLASTN	554	5e-18	73	Glycine max gene for Bd 30K, complete cds
10092	GM_157_A1_F04_MR	g507910	BLASTN	368	5e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10093	GM_157_A1_F04_T7	g507910	BLASTN	388	6e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
10094	GM_157_A1_F05_T7	g2443320	BLASTX	329	2e-27	46	(D85597) polypeptide [Oryza australiensis]
10095	GM_157_A1_F06_MR	g2443320	BLASTX	249	5e-19	39	(D85597) polypeptide [Oryza australiensis]
10096	GM_157_A1_G05_MR	g507910	BLASTN	501	5e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10097	GM_157_A1_G05_T7	g507910	BLASTN	520	7e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10098	GM_157_A1_G07_MR	g3097320	BLASTN	650	2e-22	77	Glycine max gene for Bd 30K, complete cds
10099	GM_157_A1_H01_T7	g3142379	BLASTX	259	4e-21	56	(AF053008) envelope-like [Glycine max]
10100	GM_157_A1_H03_MR	g1431738	BLASTN	590	7e-20	94	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10101	G1M_157_A1_H10_T7	g4222418	BLASTX	116	3e-14	36	pol protein - fruit fly (<i>Drosophila ananassae</i>) transposon Tom (fragment) gi 394705 (Z24451) pol protein [<i>Drosophila ananassae</i>]
10102	G1M_157_A2_A03_MR	g21430	BLASTN	370	1e-09	63	Potato DNA for copia-like transposable element
10103	G1M_157_A2_A05_T7	g507910	BLASTN	727	3e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
10104	G1M_157_A2_A08_T7	g2827550	BLASTX	222	6e-23	60	(AL021635) leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana]
10105	G1M_157_A2_A12_T7	g4038056	BLASTX	225	4e-25	50	(AC005897) putative transposon [Arabidopsis thaliana]
10106	G1M_157_A2_B07_MR	g4063756	BLASTN	595	8e-20	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
10107	G1M_157_A2_B08_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence
10108	G1M_157_A2_B08_T7	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
10109	G1M_157_A2_B11_T7	g3142328	BLASTN	1465	2e-59	94	Glycine max partial SIRF-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10110	G1M_157_A2_C03_T7	g18559	BLASTN	595	2e-30	73	G max gene for catalase
10111	G1M_157_A2_C07_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10112	G1M_157_A2_C08_MR	g623589	BLASTN	352	5e-09	69	Nicotiana tabacum SR1 Nr-rab7b mRNA, complete cds.
10113	G1M_157_A2_C12_MR	g2586087	BLASTX	249	2e-19	38	(U72724) receptor kinase-like protein [Oryza sativa]
10114	G1M_157_A2_C12_T7	g3288442	BLASTN	351	8e-09	62	Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC- γ 1a...
10115	G1M_157_A2_D01_MR	g4038056	BLASTX	287	2e-23	39	(AC005897) putative transposon [Arabidopsis thaliana]
10116	G1M_157_A2_D04_MR	g507910	BLASTN	509	2e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
10117	G1M_157_A2_D06_MR	g3097320	BLASTN	918	1e-34	72	Glycine max gene for Bd 30K, complete cds
10118	G1M_157_A2_D09_T7	g3097320	BLASTN	455	1e-13	73	Glycine max gene for Bd 30K, complete cds
10119	G1M_157_A2_E02_T7	g507910	BLASTN	704	3e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
10120	G1M_157_A2_E08_MR	g13096	BLASTN	390	1e-10	61	Leishmania tarentolae maxicircle DNA fragment
10121	G1M_157_A2_F04_MR	g4038056	BLASTX	266	4e-21	37	(AC005897) putative transposon [Arabidopsis thaliana]
10122	G1M_157_A2_F08_MR	g2961349	BLASTX	286	4e-23	45	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
10123	G1M_157_A2_F10_T7	g1419127	BLASTX	133	8e-11	59	(Z75516) reverse transcriptase [Oryza sativa]
10124	G1M_157_A2_G01_T7	g170029	BLASTN	440	7e-13	68	Glycine max cv. Dare nodulin 26 gene fragment.
10125	G1M_157_A2_G05_T7	g4140712	BLASTX	361	2e-32	57	(AF110183) putative integrase [Oryza sativa]
10126	G1M_157_A2_G08_T7	g507910	BLASTN	628	9e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10127	G1M_157_A2_H02_T7	g2995405	BLASTX	213	2e-15	64	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
10128	GM_157_A2_H05_MR	g629693	BLASTX	185	4e-13	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10129	GM_157_A2_H07_MR	g4063760	BLASTX	211	4e-15	35	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
10130	GM_157_A2_H09_MR	g18766	BLASTN	367	6e-10	78	Soybean Tgm5 transposable element
10131	GM_157_B1_A02_MR	g3337392	BLASTN	357	4e-09	66	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence [Homo sapiens]
10132	GM_157_B1_A03_MR	g4063760	BLASTX	498	1e-45	67	(AC005561) putative POL.3 protein [Arabidopsis thaliana]
10133	GM_157_B1_A03_T7	g507910	BLASTN	389	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10134	GM_157_B1_A06_MR	g120539	BLASTX	182	2e-13	91	NADH-P1-ASTOQUINONE OXIDOREDUCTASE SUBUNIT 1 (FRXB PROTEIN) gi 65733 pir FENTB ferredoxin 2[4Fe-4S] frxB - common tobacco chloroplast gi 100289 pir S11956 iron-sulfur protein frxB - tobacco chloroplast gi 1223671 (Z00044) NADH dehydrogenase 18kD subunit [Nicotiana tabacum] gi 225259 prf 1211235CU ORF 167 [Nicotiana tabacum]
10135	GM_157_B1_A07_T7	g507910	BLASTN	527	3e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10136	GM_157_B1_A12_T7	g2583106	BLASTN	401	4e-11	64	Arabidopsis thaliana chromosome II BAC F4I.2.3 genomic sequence, complete sequence [Arabidopsis thaliana]
10137	GM_157_B1_B02_T7	g2522230	BLASTX	143	4e-09	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
10138	GM_157_B1_B03_MR	g1142703	BLASTN	286	2e-15	76	Glycine max satellite STR120-B.1.
10139	GM_157_B1_B07_MR	g2979597	BLASTN	446	4e-13	64	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
10140	GM_157_B1_B09_MR	g3097320	BLASTN	905	6e-34	77	Glycine max gene for Bd 30K, complete cds
10141	GM_157_B1_B09_T7	g1666236	BLASTX	215	9e-17	31	(U76261) unknown [Hordeum vulgare]
10142	GM_157_B1_B12_T7	g3645899	BLASTX	152	8e-09	38	(U68408) 5' end not determined experimentally [Zea mays]
10143	GM_157_B1_C08_MR	g18559	BLASTN	704	7e-25	72	G-max gene for catalase
10144	GM_157_B1_C09_MR	g421954	BLASTX	150	7e-12	39	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
10145	GM_157_B1_C10_MR	g2828780	BLASTN	349	1e-08	64	Homo sapiens chromosome 17, clone 289A8, complete sequence [Homo sapiens]
10146	GM_157_B1_D03_MR	g3687221	BLASTN	378	5e-10	61	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]
10147	GM_157_B1_D06_T7	g537319	BLASTX	176	2e-12	84	(L36158) peroxidase [Medicago sativa]
10148	GM_157_B1_D07_T7	g3645899	BLASTX	235	2e-18	47	(U68408) 5' end not determined experimentally [Zea mays]